
BigML Documentation

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The BigML Team

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BigML makes machine learning easy by taking care of the details required to add data-driven decisions and predictive power to your company. Unlike other machine learning services, BigML creates [beautiful predictive models](#) that can be easily understood and interacted with.

These BigML Python bindings allow you to interact with BigML.io, the API for BigML. You can use it to easily create, retrieve, list, update, and delete BigML resources (i.e., sources, datasets, models and, predictions).

This module is licensed under the [Apache License, Version 2.0](#).

CHAPTER 1

Support

Please report problems and bugs to our [BigML.io issue tracker](#).

Discussions about the different bindings take place in the general [BigML mailing list](#). Or join us in our [Campfire chatroom](#).

CHAPTER 2

Requirements

Python 2.7 and Python 3 are currently supported by these bindings.

The only mandatory third-party dependencies are the `requests`, `poster`, and `unidecode` libraries. These libraries are automatically installed during the setup. Support for Google App Engine has been added as of version 3.0.0, using the `urlfetch` package instead of `requests`.

The bindings will also use `simplejson` if you happen to have it installed, but that is optional: we fall back to Python's built-in JSON libraries if `simplejson` is not found.

Additional `numpy` and `scipy` libraries are needed in case you want to use local predictions for regression models (including the error information) using proportional missing strategy. As these are quite heavy libraries and they are so seldom used, they are not included in the automatic installation dependencies. The test suite includes some tests that will need these libraries to be installed.

CHAPTER 3

Installation

To install the latest stable release with `pip`

```
$ pip install bigml
```

You can also install the development version of the bindings directly from the Git repository

```
$ pip install -e git://github.com/bigmlcom/python.git#egg=bigml_python
```

Importing the module

To import the module:

```
import bigml.api
```

Alternatively you can just import the BigML class:

```
from bigml.api import BigML
```


CHAPTER 5

Authentication

All the requests to BigML.io must be authenticated using your username and [API key](#) and are always transmitted over HTTPS.

This module will look for your username and API key in the environment variables `BIGML_USERNAME` and `BIGML_API_KEY` respectively. You can add the following lines to your `.bashrc` or `.bash_profile` to set those variables automatically when you log in:

```
export BIGML_USERNAME=myusername
export BIGML_API_KEY=ae579e7e53fb9abd646a6ff8aa99d4afe83ac291
```

With that environment set up, connecting to BigML is a breeze:

```
from bigml.api import BigML
api = BigML()
```

Otherwise, you can initialize directly when instantiating the `BigML` class as follows:

```
api = BigML('myusername', 'ae579e7e53fb9abd646a6ff8aa99d4afe83ac291')
```

Also, you can initialize the library to work in the Sandbox environment by passing the parameter `dev_mode`:

```
api = BigML(dev_mode=True)
```

The main domain for the API service is `bigml.io`, but there are some alternative domains, either for Virtual Private Cloud setups or the Australian subdomain (`au.bigml.io`). You can change the remote server domain to the VPC particular one by either setting the `BIGML_DOMAIN` environment variable to your VPC subdomain:

```
export BIGML_DOMAIN=my_VPC.bigml.io
```

or setting it when instantiating your connection:

```
api = BigML(domain="my_VPC.bigml.io")
```

The corresponding SSL REST calls will be directed to your private domain henceforth.

You can also set up your connection to use a particular PredictServer only for predictions. In order to do so, you'll need to specify a `Domain` object, where you can set up the general domain name as well as the particular prediction domain name.

```
from bigml.domain import Domain
from bigml.api import BigML

domain_info = Domain(prediction_domain="my_prediction_server.bigml.com",
                    prediction_protocol="http")

api = BigML(domain=domain_info)
```

Finally, you can combine all the options and change both the general domain server, and the prediction domain server.

```
from bigml.domain import Domain
from bigml.api import BigML

domain_info = Domain(domain="my_VPC.bigml.io",
                    prediction_domain="my_prediction_server.bigml.com",
                    prediction_protocol="https")

api = BigML(domain=domain_info)
```

Some arguments for the `Domain` constructor are more unusual, but they can also be used to set your special service endpoints:

- `protocol` (string) Protocol for the service (when different from HTTPS)
- `verify` (boolean) Sets on/off the SSL verification
- `prediction_verify` (boolean) Sets on/off the SSL verification for the prediction server (when different from the general SSL verification)

Quick Start

Imagine that you want to use [this csv file](#) containing the [Iris flower dataset](#) to predict the species of a flower whose sepal length is 5 and whose sepal width is 2.5. A preview of the dataset is shown below. It has 4 numeric fields: sepal length, sepal width, petal length, petal width and a categorical field: species. By default, BigML considers the last field in the dataset as the objective field (i.e., the field that you want to generate predictions for).

```
sepal length,sepal width,petal length,petal width,species
5.1,3.5,1.4,0.2,Iris-setosa
4.9,3.0,1.4,0.2,Iris-setosa
4.7,3.2,1.3,0.2,Iris-setosa
...
5.8,2.7,3.9,1.2,Iris-versicolor
6.0,2.7,5.1,1.6,Iris-versicolor
5.4,3.0,4.5,1.5,Iris-versicolor
...
6.8,3.0,5.5,2.1,Iris-virginica
5.7,2.5,5.0,2.0,Iris-virginica
5.8,2.8,5.1,2.4,Iris-virginica
```

You can easily generate a prediction following these steps:

```
from bigml.api import BigML

api = BigML()

source = api.create_source('./data/iris.csv')
dataset = api.create_dataset(source)
model = api.create_model(dataset)
prediction = api.create_prediction(model, \
    {'sepal length': 5, 'sepal width': 2.5})
```

You can then print the prediction using the `pprint` method:

```
>>> api.pprint(prediction)
species for {"sepal width": 2.5, "sepal length": 5} is Iris-virginica
```

The `iris` dataset has a small number of instances, and usually will be instantly created, so the `api.create_` calls will probably return the finished resources outright. As BigML's API is asynchronous, in general you will need to ensure that objects are finished before using them by using `api.ok`.

```
from bigml.api import BigML

api = BigML()

source = api.create_source('./data/iris.csv')
api.ok(source)
dataset = api.create_dataset(source)
api.ok(dataset)
model = api.create_model(dataset)
api.ok(model)
prediction = api.create_prediction(model, \
    {'sepal length': 5, 'sepal width': 2.5})
```

This method retrieves the remote object in its latest state and updates the variable used as argument with this information. Note that the prediction call is not followed by the `api.ok` method. Predictions are so quick to be generated that, unlike the rest of resources, will be generated synchronously as a finished object.

You can also generate an evaluation for the model by using:

```
test_source = api.create_source('./data/test_iris.csv')
api.ok(test_source)
test_dataset = api.create_dataset(test_source)
api.ok(test_dataset)
evaluation = api.create_evaluation(model, test_dataset)
api.ok(evaluation)
```

If you set the `storage` argument in the `api` instantiation:

```
api = BigML(storage='./storage')
```

all the generated, updated or retrieved resources will be automatically saved to the chosen directory.

For an overview of the steps that you will usually need to follow to model your data and obtain predictions, please see the basic Workflow sketch document.

Fields Structure

BigML automatically generates identifiers for each field. To see the fields and the ids and types that have been assigned to a source you can use `get_fields`:

```
>>> source = api.get_source(source)
>>> api.pprint(api.get_fields(source))
{ u'000000': { u'column_number': 0,
              u'name': u'sepal length',
              u'optype': u'numeric'},
  u'000001': { u'column_number': 1,
              u'name': u'sepal width',
              u'optype': u'numeric'},
  u'000002': { u'column_number': 2,
              u'name': u'petal length',
              u'optype': u'numeric'},
  u'000003': { u'column_number': 3,
              u'name': u'petal width',
              u'optype': u'numeric'},
  u'000004': { u'column_number': 4,
              u'name': u'species',
              u'optype': u'categorical'}}
```

When the number of fields becomes very large, it can be useful to exclude or filter them. This can be done using a query string expression, for instance:

```
>>> source = api.get_source(source, "limit=10&order_by=name")
```

would include in the retrieved dictionary the first 10 fields sorted by name.

To handle the field structure you can use the `Fields` class. See the *Fields* section.

If you want to get some basic statistics for each field you can retrieve the `fields` from the dataset as follows to get a dictionary keyed by field id:

```
>>> dataset = api.get_dataset(dataset)
>>> api.pprint(api.get_fields(dataset))
{  u'000000': {  u'column_number': 0,
                u'datatype': u'double',
                u'name': u'sepal length',
                u'optype': u'numeric',
                u'summary': {  u'maximum': 7.9,
                              u'median': 5.77889,
                              u'minimum': 4.3,
                              u'missing_count': 0,
                              u'population': 150,
                              u'splits': [ 4.51526,
                                           4.67252,
                                           4.81113,

                                           [... snip ... ]

                u'000004': {  u'column_number': 4,
                              u'datatype': u'string',
                              u'name': u'species',
                              u'optype': u'categorical',
                              u'summary': {  u'categories': [ [ u'Iris-versicolor',
                                                                50],
                                                                [u'Iris-setosa', 50],
                                                                [ u'Iris-virginica',
                                                                50]],
                              u'missing_count': 0}}}
```

The field filtering options are also available using a query string expression, for instance:

```
>>> dataset = api.get_dataset(dataset, "limit=20")
```

limits the number of fields that will be included in `dataset` to 20.

One of the greatest things about BigML is that the models that it generates for you are fully white-boxed. To get the explicit tree-like predictive model for the example above:

```
>>> model = api.get_model(model)
>>> api.pprint(model['object']['model']['root'])
{u'children': [
  {u'children': [
    {u'children': [{u'count': 38,
                  u'distribution': [[u'Iris-virginica', 38]],
                  u'output': u'Iris-virginica',
                  u'predicate': {u'field': u'000002',
                                u'operator': u'>',
                                u'value': 5.05}},
                  u'children': [
                    [ ... ]
                  ]
                },
    {u'count': 50,
      u'distribution': [[u'Iris-setosa', 50]],
      u'output': u'Iris-setosa',
      u'predicate': {u'field': u'000002',
                    u'operator': u'<=',
                    u'value': 2.45}}}],
    {u'count': 150,
      u'distribution': [[u'Iris-virginica', 50],
                      [u'Iris-versicolor', 50],
                      [u'Iris-setosa', 50]],
      u'output': u'Iris-virginica',
      u'predicate': True}}]}
```

(Note that we have abbreviated the output in the snippet above for readability: the full predictive model you'll get is going to contain much more details).

Again, filtering options are also available using a query string expression, for instance:

```
>>> model = api.get_model(model, "limit=5")
```

limits the number of fields that will be included in `model` to 5.

The predictive performance of a model can be measured using many different measures. In BigML these measures can be obtained by creating evaluations. To create an evaluation you need the id of the model you are evaluating and the id of the dataset that contains the data to be tested with. The result is shown as:

```
>>> evaluation = api.get_evaluation(evaluation)
>>> api.pprint(evaluation['object']['result'])
{  'class_names': ['0', '1'],
   'mode': {  'accuracy': 0.9802,
              'average_f_measure': 0.495,
              'average_phi': 0,
              'average_precision': 0.5,
              'average_recall': 0.4901,
              'confusion_matrix': [[99, 0], [2, 0]],
              'per_class_statistics': [  {  'accuracy': 0.9801980198019802,
                                          'class_name': '0',
                                          'f_measure': 0.99,
                                          'phi_coefficient': 0,
                                          'precision': 1.0,
                                          'present_in_test_data': True,
                                          'recall': 0.9801980198019802},
                                         {  'accuracy': 0.9801980198019802,
                                          'class_name': '1',
                                          'f_measure': 0,
                                          'phi_coefficient': 0,
                                          'precision': 0.0,
                                          'present_in_test_data': True,
                                          'recall': 0}}],

   'model': {  'accuracy': 0.9901,
              'average_f_measure': 0.89746,
              'average_phi': 0.81236,
              'average_precision': 0.99495,
              'average_recall': 0.83333,
              'confusion_matrix': [[98, 1], [0, 2]],
              'per_class_statistics': [  {  'accuracy': 0.9900990099009901,
                                          'class_name': '0',
```

```

'f_measure': 0.9949238578680203,
'phi_coefficient': 0.
↪8123623944599232,
'precision': 0.98989898989899,
'present_in_test_data': True,
'recall': 1.0},
{
'accuracy': 0.9900990099009901,
'class_name': '1',
'f_measure': 0.8,
'phi_coefficient': 0.
↪8123623944599232,
'precision': 1.0,
'present_in_test_data': True,
'recall': 0.6666666666666666}}}],
'random': {
'accuracy': 0.50495,
'average_f_measure': 0.36812,
'average_phi': 0.13797,
'average_precision': 0.74747,
'average_recall': 0.51923,
'confusion_matrix': [[49, 50], [0, 2]],
'per_class_statistics': [
{
'accuracy': 0.504950495049505,
'class_name': '0',
'f_measure': 0.6621621621621622,
'phi_coefficient': 0.
↪1379728923974526,
'precision': 0.494949494949495,
'present_in_test_data': True,
'recall': 1.0},
{
'accuracy': 0.504950495049505,
'class_name': '1',
'f_measure': 0.07407407407407407,
'phi_coefficient': 0.
↪1379728923974526,
'precision': 1.0,
'present_in_test_data': True,
'recall': 0.038461538461538464}}}]

```

where two levels of detail are easily identified. For classifications, the first level shows these keys:

- **class_names:** A list with the names of all the categories for the objective field (i.e., all the classes)
- **mode:** A detailed result object. Measures of the performance of the classifier that predicts the mode class for all the instances in the dataset
- **model:** A detailed result object.
- **random:** A detailed result object. Measures the performance of the classifier that predicts a random class for all the instances in the dataset.

and the detailed result objects include accuracy, average_f_measure, average_phi, average_precision, average_recall, confusion_matrix and per_class_statistics.

For regressions first level will contain these keys:

- **mean:** A detailed result object. Measures the performance of the model that predicts the mean for all the instances in the dataset.
- **model:** A detailed result object.
- **random:** A detailed result object. Measures the performance of the model that predicts a random class for all the instances in the dataset.

where the detailed result objects include `mean_absolute_error`, `mean_squared_error` and `r_squared` (refer to [developers documentation](#) for more info on the meaning of these measures).

For unsupervised learning problems, the cluster is used to classify in a limited number of groups your training data. The cluster structure is defined by the centers of each group of data, named centroids, and the data enclosed in the group. As for in the model's case, the cluster is a white-box resource and can be retrieved as a JSON:

```
>>> cluster = api.get_cluster(cluster)
>>> api.pprint(cluster['object'])
{  'balance_fields': True,
   'category': 0,
   'cluster_datasets': {  '000000': '', '000001': '', '000002': ''},
   'cluster_datasets_ids': {  '000000': '53739b9ae4b0dad82b0a65e6',
                              '000001': '53739b9ae4b0dad82b0a65e7',
                              '000002': '53739b9ae4b0dad82b0a65e8'},
   'cluster_seed': '2c249dda00fbf54ab4cdd850532a584f286af5b6',
   'clusters': {  'clusters': [  {  'center': {  '000000': 58.5,
                                                '000001': 26.8314,
                                                '000002': 44.27907,
                                                '000003': 14.37209},
                                  'count': 56,
                                  'distance': {  'bins': [  [  0.69602,
                                                            2],
                                                            [ ... ]
                                                            [  3.77052,
                                                            1]],
                                                'maximum': 3.77052,
                                                'mean': 1.61711,
                                                'median': 1.52146,
                                                'minimum': 0.69237,
                                                'population': 56,
                                                'standard_deviation': 0.6161,
                                                'sum': 90.55805,
                                                'sum_squares': 167.31926,
                                                'variance': 0.37958},
                                  'id': '000000',
                                  'name': 'Cluster 0'},
                                {  'center': {  '000000': 50.06,
```

```

        '000001': 34.28,
        '000002': 14.62,
        '000003': 2.46},
    'count': 50,
    'distance': {
        'bins': [
            [ 0.16917,
              1],
            [ ... ]
            [ 4.94699,
              1]],
        'maximum': 4.94699,
        'mean': 1.50725,
        'median': 1.3393,
        'minimum': 0.16917,
        'population': 50,
        'standard_deviation': 1.00994,
        'sum': 75.36252,
        'sum_squares': 163.56918,
        'variance': 1.01998},
    'id': '000001',
    'name': 'Cluster 1'},
  {
    'center': {
        '000000': 68.15625,
        '000001': 31.25781,
        '000002': 55.48438,
        '000003': 19.96875},
    'count': 44,
    'distance': {
        'bins': [
            [ 0.36825,
              1],
            [ ... ]
            [ 3.87216,
              1]],
        'maximum': 3.87216,
        'mean': 1.67264,
        'median': 1.63705,
        'minimum': 0.36825,
        'population': 44,
        'standard_deviation': 0.78905,
        'sum': 73.59627,
        'sum_squares': 149.87194,
        'variance': 0.6226},
    'id': '000002',
    'name': 'Cluster 2'}],
  'fields': {
    '000000': {
        'column_number': 0,
        'datatype': 'int8',
        'name': 'sepal length',
        'optype': 'numeric',
        'order': 0,
        'preferred': True,
        'summary': {
            'bins': [
                [ 43.75,
                  4],
                [ ... ]
                [ 79,
                  1]],
            'maximum': 79,
            'mean': 58.43333,
            'median': 57.7889,
            'minimum': 43,
            'missing_count': 0,
            'population': 150,

```



```

        'splits': [ 45.15258,
                   46.72525,
                   72.04226,
                   76.
↪47461],
        'standard_deviation': 8.28066,
        'sum': 8765,
        'sum_squares': 522385,
        'variance': 68.56935}},
        [ ... ]
        [ 25,
          3]],
        'maximum': 25,
        'mean': 11.99333,
        'median': 13.28483,
        'minimum': 1,
        'missing_count': 0,
        'population': 150,
        'standard_deviation': 7.62238,
        'sum': 1799,
        'sum_squares': 30233,
        'variance': 58.10063}}}
↪},
  'code': 202,
  'columns': 4,
  'created': '2014-05-14T16:36:40.993000',
  'credits': 0.017578125,
  'credits_per_prediction': 0.0,
  'dataset': 'dataset/53739b88c8db63122b000411',
  'dataset_field_types': { 'categorical': 1,
                           'datetime': 0,
                           'numeric': 4,
                           'preferred': 5,
                           'text': 0,
                           'total': 5},
  'dataset_status': True,
  'dataset_type': 0,
  'description': '',
  'excluded_fields': ['000004'],
  'field_scales': None,
  'fields_meta': { 'count': 4,
                   'limit': 1000,
                   'offset': 0,
                   'query_total': 4,
                   'total': 4},
  'input_fields': ['000000', '000001', '000002', '000003'],
  'k': 3,
  'locale': 'es-ES',
  'max_columns': 5,
  'max_rows': 150,
  'name': 'my iris',
  'number_of_batchcentroids': 0,
  'number_of_centroids': 0,
  'number_of_public_centroids': 0,
  'out_of_bag': False,
  'price': 0.0,

```

```
'private': True,
'range': [1, 150],
'replacement': False,
'resource': 'cluster/53739b98d994972da7001de9',
'rows': 150,
'sample_rate': 1.0,
'scales': {  '000000': 0.22445382597655375,
             '000001': 0.4264213814821549,
             '000002': 0.10528680248949522,
             '000003': 0.2438379900517961},
'shared': False,
'size': 4608,
'source': 'source/53739b24d994972da7001ddd',
'source_status': True,
'status': {  'code': 5,
             'elapsed': 1009,
             'message': 'The cluster has been created',
             'progress': 1.0},
'subscription': True,
'tags': [],
'updated': '2014-05-14T16:40:26.234728',
'white_box': False}
```

(Note that we have abbreviated the output in the snippet above for readability: the full predictive cluster you'll get is going to contain much more details).

Anomaly detector

For anomaly detection problems, BigML anomaly detector uses iforest as an unsupervised kind of model that detects anomalous data in a dataset. The information it returns encloses a *top_anomalies* block that contains a list of the most anomalous points. For each, we capture a *score* from 0 to 1. The closer to 1, the more anomalous. We also capture the *row* which gives values for each field in the order defined by *input_fields*. Similarly we give a list of *importances* which match the *row* values. These importances tell us which values contributed most to the anomaly score. Thus, the structure of an anomaly detector is similar to:

```
{  'category': 0,
  'code': 200,
  'columns': 14,
  'constraints': False,
  'created': '2014-09-08T18:51:11.893000',
  'credits': 0.11653518676757812,
  'credits_per_prediction': 0.0,
  'dataset': 'dataset/540dfa9d9841fa5c88000765',
  'dataset_field_types': {  'categorical': 21,
                           'datetime': 0,
                           'numeric': 21,
                           'preferred': 14,
                           'text': 0,
                           'total': 42},
  'dataset_status': True,
  'dataset_type': 0,
  'description': '',
  'excluded_fields': [],
  'fields_meta': {  'count': 14,
                   'limit': 1000,
                   'offset': 0,
                   'query_total': 14,
                   'total': 14},
  'forest_size': 128,
  'input_fields': [  '000004',
                    '000005',
                    '000009',
```

```

        '000016',
        '000017',
        '000018',
        '000019',
        '00001e',
        '00001f',
        '000020',
        '000023',
        '000024',
        '000025',
        '000026'],
    'locale': 'en_US',
    'max_columns': 42,
    'max_rows': 200,
    'model': {
      'fields': {
        '000004': {
          'column_number': 4,
          'datatype': 'int16',
          'name': 'src_bytes',
          'optype': 'numeric',
          'order': 0,
          'preferred': True,
          'summary': {
            'bins': [
              [ 143,
                2],
              ...
              [ 370,
                2]],
            'maximum': 370,
            'mean': 248.235,
            'median': 234.57157,
            'minimum': 141,
            'missing_count': 0,
            'population': 200,
            'splits': [
              159.92462,
              173.73312,
              188,
              ...
              339.55228],
            'standard_deviation': 49.
          },
          'sum': 49647,
          'sum_squares': 12809729,
          'variance': 2440.23093}},
        '000005': {
          'column_number': 5,
          'datatype': 'int32',
          'name': 'dst_bytes',
          'optype': 'numeric',
          'order': 1,
          'preferred': True,
          ...
          'sum': 1030851,
          'sum_squares': 22764504759,
          'variance': 87694652.
        },
        '000009': {
          'column_number': 9,
          'datatype': 'string',
          'name': 'hot',
          'optype': 'categorical',
          'order': 2,
          'sum': 45224}},
      }
    }
  }
}

```

```

        'preferred': True,
        'summary': { 'categories': [ [ '0',
                                     ↪199],
                                     [ '1',
                                     1]],
                    'missing_count': 0},
        'term_analysis': { 'enabled': True}},
    '000016': { 'column_number': 22,
               'datatype': 'int8',
               'name': 'count',
               'optype': 'numeric',
               'order': 3,
               'preferred': True,
               ...
               'population': 200,
               'standard_deviation': 5.
               ↪42421,
               'sum': 1351,
               'sum_squares': 14981,
               'variance': 29.42209}},
    '000017': { ... }},
    'kind': 'iforest',
    'mean_depth': 12.314174107142858,
    'top_anomalies': [ { 'importance': [ 0.06768,
                                        0.01667,
                                        0.00081,
                                        0.02437,
                                        0.04773,
                                        0.22197,
                                        0.18208,
                                        0.01868,
                                        0.11855,
                                        0.01983,
                                        0.01898,
                                        0.05306,
                                        0.20398,
                                        0.00562],
                       'row': [ 183.0,
                                8654.0,
                                '0',
                                4.0,
                                4.0,
                                0.25,
                                0.25,
                                0.0,
                                123.0,
                                255.0,
                                0.01,
                                0.04,
                                0.01,
                                0.0],
                       'score': 0.68782},
                      { 'importance': [ 0.05645,
                                        0.02285,
                                        0.0015,
                                        0.05196,
                                        0.04435,

```



```

↪         'value': 65.14308},
↪     { 'field': '000019',
↪       'op': '=',
↪       'value': 0}}}],
↪     'population': 105,
↪     'predicates': [ {
↪ 'field': '000017',
↪ 'op': '<=',
↪ 'value': 13.21754},
↪ 'field': '000009',
↪ 'op': 'in',
↪ 'value': [ '0']}]},
↪     'population': 126,
↪     'predicates': [ True,
↪       { 'field': '000018',
↪         'op': '=',
↪         'value': 0}}],
↪     'training_mean_depth': 11.071428571428571}}],
'name': "tiny_kdd's dataset anomaly detector",
'number_of_batchscores': 0,
'number_of_public_predictions': 0,
'number_of_scores': 0,
'out_of_bag': False,
'price': 0.0,
'private': True,
'project': None,
'range': [1, 200],
'replacement': False,
'resource': 'anomaly/540dfa9f9841fa5c8800076a',
'rows': 200,
'sample_rate': 1.0,
'sample_size': 126,
'seed': 'BigML',
'shared': False,
'size': 30549,
'source': 'source/540dfa979841fa5c7f000363',
'source_status': True,
'status': { 'code': 5,
            'elapsed': 32397,
            'message': 'The anomaly detector has been created',
            'progress': 1.0},
'subscription': False,
'tags': [],
'updated': '2014-09-08T23:54:28.647000',
'white_box': False}

```

Note that we have abbreviated the output in the snippet above for readability: the full anomaly detector you'll get is going to contain much more details).

The *trees* list contains the actual isolation forest, and it can be quite large usually. That's why, this part of the resource should only be included in downloads when needed. If you are only interested in other properties, such as *top_anomalies*, you'll improve performance by excluding it, using the *excluded=trees* query string in the API call:

```
anomaly = api.get_anomaly('anomaly/540dfa9f9841fa5c8800076a', \
                          query_string='excluded=trees')
```

Each node in an isolation tree can have multiple predicates. For the node to be a valid branch when evaluated with a data point, all of its predicates must be true.

Samples

To provide quick access to your row data you can create a `sample`. Samples are in-memory objects that can be queried for subsets of data by limiting their size, the fields or the rows returned. The structure of a sample would be:

Samples are not permanent objects. Once they are created, they will be available as long as GETs are requested within periods smaller than a pre-established TTL (Time to Live). The expiration timer of a sample is reset every time a new GET is received.

If requested, a sample can also perform linear regression and compute Pearson's and Spearman's correlations for either one numeric field against all other numeric fields or between two specific numeric fields.

Correlations

A `correlation` resource contains a series of computations that reflect the degree of dependence between the field set as objective for your predictions and the rest of fields in your dataset. The dependence degree is obtained by comparing the distributions in every objective and non-objective field pair, as independent fields should have probabilistic independent distributions. Depending on the types of the fields to compare, the metrics used to compute the correlation degree will be:

- for numeric to numeric pairs: [Pearson's](#) and [Spearman's correlation coefficients](#).
- for numeric to categorical pairs: [One-way Analysis of Variance](#), with the categorical field as the predictor variable.
- for categorical to categorical pairs: [contingency table \(or two-way table\)](#), [Chi-square test of independence](#), and [Cramer's V](#) and [Tschuprow's T coefficients](#).

An example of the correlation resource JSON structure is:

```
>>> from bigml.api import BigML
>>> api = BigML()
>>> correlation = api.create_correlation('dataset/55b7a6749841fa2500000d41')
>>> api.ok(correlation)
>>> api.pprint(correlation['object'])
{  u'category': 0,
   u'clones': 0,
   u'code': 200,
   u'columns': 5,
   u'correlations': {  u'correlations': [  {  u'name': u'one_way_anova',
                                             u'result': {  u'000000': {  u'eta_
↪square': 0.61871,
                                             u'f_
↪ratio': 119.2645,
                                             u'p_
↪value': 0,
                                             u
↪'significant': [  True,
                                             ↪
↪                True,
```

```

↪         True]],
↪         u'000001': { u'eta_
↪square': 0.40078,           u'f_
↪ratio': 49.16004,         u'p_
↪value': 0,                u
↪'significant': [ True,
↪         True,
↪         True]],
↪         u'000002': { u'eta_
↪square': 0.94137,           u'f_
↪ratio': 1180.16118,       u'p_
↪value': 0,                u
↪'significant': [ True,
↪         True,
↪         True]],
↪         u'000003': { u'eta_
↪square': 0.92888,           u'f_
↪ratio': 960.00715,       u'p_
↪value': 0,                u
↪'significant': [ True,
↪         True,
↪         True]]}],
↪         u'fields': { u'000000': { u'column_number': 0,
↪         u'datatype': u'double',
↪         u'idx': 0,
↪         u'name': u'sepal length',
↪         u'optype': u'numeric',
↪         u'order': 0,
↪         u'preferred': True,
↪         u'summary': { u'bins': [ [
↪ 4.3,
↪ 1],
↪ 4.425,
↪ 4],
↪ ...
↪ 7.9,
↪ 1]],

```

```

↪0.57357,
↪9,
↪84333,
↪3,
↪': 0,
↪150,
↪31175,
↪4.51526,
↪4.67252,
↪4.81113,
↪4.89582,
↪4.96139,
↪5.01131,
...
↪6.92597,
↪7.20423,
↪7.64746],
↪deviation': 0.82807,
↪': 5223.85,
↪68569}},
    u'000001': { u'column_number': 1,
                 u'datatype': u'double',
                 u'idx': 1,
                 u'name': u'sepal width',
                 u'optype': u'numeric',
                 u'order': 1,
                 u'preferred': True,
                 u'summary': { u'counts': [
↪[ 2,
↪ 1],
↪[ 2.2,
...
    u'000004': { u'column_number': 4,
                 u'datatype': u'string',
                 u'idx': 4,
u'kurtosis': -
u'maximum': 7.
u'mean': 5.
u'median': 5.8,
u'minimum': 4.
u'missing_count
u'population':
u'skewness': 0.
u'splits': [
u'standard_
u'sum': 876.5,
u'sum_squares
u'variance': 0.
u'counts': [

```

```

        u'name': u'species',
        u'optype': u'categorical',
        u'order': 4,
        u'preferred': True,
        u'summary': { u'categories': u
↪[ [ u'Iris-setosa',
↪    50],
↪ [ u'Iris-versicolor',
↪    50],
↪ [ u'Iris-virginica',
↪    50]],
        u'missing_count
↪': 0},
        u'term_analysis': { u'enabled
↪': True}}},
        u'significance_levels': [0.01, 0.05, 0.1]},
    u'created': u'2015-07-28T18:07:37.010000',
    u'credits': 0.017581939697265625,
    u'dataset': u'dataset/55b7a6749841fa2500000d41',
    u'dataset_status': True,
    u'dataset_type': 0,
    u'description': u'',
    u'excluded_fields': [],
    u'fields_meta': { u'count': 5,
        u'limit': 1000,
        u'offset': 0,
        u'query_total': 5,
        u'total': 5},
    u'input_fields': [u'000000', u'000001', u'000002', u'000003'],
    u'locale': u'en_US',
    u'max_columns': 5,
    u'max_rows': 150,
    u'name': u'"iris" dataset correlation',
    u'objective_field_details': { u'column_number': 4,
        u'datatype': u'string',
        u'name': u'species',
        u'optype': u'categorical',
        u'order': 4},
    u'out_of_bag': False,
    u'price': 0.0,
    u'private': True,
    u'project': None,
    u'range': [1, 150],
    u'replacement': False,
    u'resource': u'correlation/55b7c4e99841fa24f20009bf',
    u'rows': 150,
    u'sample_rate': 1.0,
    u'shared': False,
    u'size': 4609,
    u'source': u'source/55b7a6729841fa24f100036a',
    u'source_status': True,
    u'status': { u'code': 5,
        u'elapsed': 274,

```

```
        u'message': u'The correlation has been created',
        u'progress': 1.0},
u'subscription': True,
u'tags': [],
u'updated': u'2015-07-28T18:07:49.057000',
u'white_box': False}
```

Note that the output in the snippet above has been abbreviated. As you see, the `correlations` attribute contains the information about each field correlation to the objective field.

Statistical Tests

A `statisticaltest` resource contains a series of tests that compare the distribution of data in each numeric field of a dataset to certain canonical distributions, such as the [normal distribution](#) or [Benford's law](#) distribution. Statistical tests are useful in tasks such as fraud, normality, or outlier detection.

- Fraud Detection Tests:

Benford: This statistical test performs a comparison of the distribution of first significant digits (FSDs) of each value of the field to the Benford's law distribution. Benford's law applies to numerical distributions spanning several orders of magnitude, such as the values found on financial balance sheets. It states that the frequency distribution of leading, or first significant digits (FSD) in such distributions is not uniform. On the contrary, lower digits like 1 and 2 occur disproportionately often as leading significant digits. The test compares the distribution in the field to Benford's distribution using a Chi-square goodness-of-fit test, and Cho-Gaines d test. If a field has a dissimilar distribution, it may contain anomalous or fraudulent values.

- Normality tests:

These tests can be used to confirm the assumption that the data in each field of a dataset is distributed according to a normal distribution. The results are relevant because many statistical and machine learning techniques rely on this assumption. **Anderson-Darling:** The Anderson-Darling test computes a test statistic based on the difference between the observed cumulative distribution function (CDF) to that of a normal distribution. A significant result indicates that the assumption of normality is rejected. **Jarque-Bera:** The Jarque-Bera test computes a test statistic based on the third and fourth central moments (skewness and kurtosis) of the data. Again, a significant result indicates that the normality assumption is rejected. **Z-score:** For a given sample size, the maximum deviation from the mean that would be expected in a sampling of a normal distribution can be computed based on the 68-95-99.7 rule. This test simply reports this expected deviation and the actual deviation observed in the data, as a sort of sanity check.

- Outlier tests:

Grubbs: When the values of a field are normally distributed, a few values may still deviate from the mean distribution. The outlier tests reports whether at least one value in each numeric field differs significantly from the mean using Grubb's test for outliers. If an outlier is found, then its value will be returned.

The JSON structure for `statisticaltest` resources is similar to this one:

```
>>> statistical_test = api.create_statistical_test('dataset/55b7a6749841fa250000d41')
>>> api.ok(statistical_test)
```

```

True
>>> api.pprint(statistical_test['object'])
{ u'category': 0,
  u'clones': 0,
  u'code': 200,
  u'columns': 5,
  u'created': u'2015-07-28T18:16:40.582000',
  u'credits': 0.017581939697265625,
  u'dataset': u'dataset/55b7a6749841fa2500000d41',
  u'dataset_status': True,
  u'dataset_type': 0,
  u'description': u'',
  u'excluded_fields': [],
  u'fields_meta': { u'count': 5,
                   u'limit': 1000,
                   u'offset': 0,
                   u'query_total': 5,
                   u'total': 5},
  u'input_fields': [u'000000', u'000001', u'000002', u'000003'],
  u'locale': u'en_US',
  u'max_columns': 5,
  u'max_rows': 150,
  u'name': u"iris' dataset test",
  u'out_of_bag': False,
  u'price': 0.0,
  u'private': True,
  u'project': None,
  u'range': [1, 150],
  u'replacement': False,
  u'resource': u'statisticaltest/55b7c7089841fa25000010ad',
  u'rows': 150,
  u'sample_rate': 1.0,
  u'shared': False,
  u'size': 4609,
  u'source': u'source/55b7a6729841fa24f100036a',
  u'source_status': True,
  u'status': { u'code': 5,
              u'elapsed': 302,
              u'message': u'The test has been created',
              u'progress': 1.0},
  u'subscription': True,
  u'tags': [],
  u'statistical_tests': { u'ad_sample_size': 1024,
                        u'fields': { u'000000': { u'column_number': 0,
                                                  u'datatype': u'double',
                                                  u'id': 0,
                                                  u'name': u'sepal length',
                                                  u'optype': u'numeric',
                                                  u'order': 0,
                                                  u'preferred': True,
                                                  u'summary': { u'bins': [ [ 4.3,
                                                                              1],
                                                                              [ 4.

```

↪425,

```

...
[ 7.9,
  1]],

```

```

        u'kurtosis': -0.57357,
        u'maximum': 7.9,
        u'mean': 5.84333,
        u'median': 5.8,
        u'minimum': 4.3,
        u'missing_count': 0,
        u'population': 150,
        u'skewness': 0.31175,
        u'splits': [ 4.
↪51526,
        4.
↪67252,
        4.
↪81113,
        4.
↪89582,
        ...
        7.
↪20423,
        7.
↪64746],
        u'standard_deviation
↪': 0.82807,
        u'sum': 876.5,
        u'sum_squares': 5223.
↪85,
        u'variance': 0.68569}}
↪,
...
        u'000004': { u'column_number': 4,
                    u'datatype': u'string',
                    u'idx': 4,
                    u'name': u'species',
                    u'optype': u'categorical',
                    u'order': 4,
                    u'preferred': True,
                    u'summary': { u'categories': [ [ ↪
↪ u'Iris-setosa',
                    ↪
↪ 50],
                    [ ↪
↪ u'Iris-versicolor',
                    ↪
↪ 50],
                    [ ↪
↪ u'Iris-virginica',
                    ↪
↪ 50]],
                    u'missing_count': 0},
                    u'term_analysis': { u'enabled': ↪
↪True}}},
        u'fraud': [ { u'name': u'benford',
↪'chi_square_value': 506.39302,
                    u'result': { u'000000': { u'chi_square': { u
↪'p_value': 0,
                    u
↪'significant': [ True,

```



```

↪ 0,
↪ 0,
↪ 0,
↪ 0,
↪ 0],
                                     u'negatives': 0,
                                     u'zeros': 0},
↪ 'chi_square_value': 154.20728,      u'000002': { u'chi_square': { u
                                     u
↪ 'p_value': 0,
                                     u
↪ 'significant': [ True,
↪                 True,
↪                 True]],
                                     u'cho_gaines': { u
↪ 'd_statistic': 3.9229974017266054,
                                     u
↪ 'significant': [ True,
↪                 True,
↪                 True]],
                                     u'distribution': [ u
↪ 50,
↪ 0,
↪ 11,
↪ 43,
↪ 35,
↪ 11,
↪ 0,
↪ 0,
↪ 0],
                                     u'negatives': 0,
                                     u'zeros': 0},
↪ 'chi_square_value': 111.4438,      u'000003': { u'chi_square': { u
                                     u
↪ 'p_value': 0,
                                     u
↪ 'significant': [ True,
↪                 True,

```



```

→ True]]]],
                                { u'name': u'jarque_bera',
→10615,                                u'result': { u'000000': { u'p_value': 0.
                                u'significant':
→[ False,
                                u'000001': { u'p_value': 0.
→ False,
                                u'significant':
→ False]],
                                u'000002': { u'p_value': 0.
→25957,                                u'significant':
→[ False,
→ False,
→ False]],
                                u'000003': { u'p_value': 0.
→0009,                                u'significant':
→[ True,
→ True,
→ True]],
                                u'000003': { u'p_value': 0.
→00332,                                u'significant':
→[ True,
→ True,
→ True]]]],
                                { u'name': u'z_score',
→': 2.71305,                                u'result': { u'000000': { u'expected_max_z
→48369},                                u'max_z': 2.
                                u'000001': { u'expected_max_z
→': 2.71305,                                u'max_z': 3.
                                u'000002': { u'expected_max_z
→08044},                                u'max_z': 1.
                                u'000003': { u'expected_max_z
→': 2.71305,                                u'max_z': 1.
→77987},
                                u'outliers': [ { u'name': u'grubbs',
→': 2.71305,                                u'result': { u'000000': { u'p_value': 1,
→70638}}]],                                u'significant':
→[ False,
→ False,

```

```

↪ False}},
↪26555,
↪[ False,
↪ False,
↪ False]],
↪[ False,
↪ False,
↪ False]],
↪[ False,
↪ False,
↪ False]]}],
↪ u'significance_levels': [0.01, 0.05, 0.1]],
↪ u'updated': u'2015-07-28T18:17:11.829000',
↪ u'white_box': False}
↪ u'000001': { u'p_value': 0.
↪ u'significant':
↪ u'000002': { u'p_value': 1,
↪ u'significant':
↪ u'000003': { u'p_value': 1,
↪ u'significant':

```

Note that the output in the snippet above has been abbreviated. As you see, the `statistical_tests` attribute contains the `fraud``, `normality` and `outliers` sections where the information for each field's distribution is stored.

Logistic Regressions

A logistic regression is a supervised machine learning method for solving classification problems. Each of the classes in the field you want to predict, the objective field, is assigned a probability depending on the values of the input fields. The probability is computed as the value of a logistic function, whose argument is a linear combination of the predictors' values. You can create a logistic regression selecting which fields from your dataset you want to use as input fields (or predictors) and which categorical field you want to predict, the objective field. Then the created logistic regression is defined by the set of coefficients in the linear combination of the values. Categorical and text fields need some prior work to be modelled using this method. They are expanded as a set of new fields, one per category or term (respectively) where the number of occurrences of the category or term is store. Thus, the linear combination is made on the frequency of the categories or terms.

The JSON structure for a logistic regression is:

```
>>> api.pprint(logistic_regression['object'])
{  u'balance_objective': False,
   u'category': 0,
   u'code': 200,
   u'columns': 5,
   u'created': u'2015-10-09T16:11:08.444000',
   u'credits': 0.017581939697265625,
   u'credits_per_prediction': 0.0,
   u'dataset': u'dataset/561304f537203f4c930001ca',
   u'dataset_field_types': {  u'categorical': 1,
                             u'datetime': 0,
                             u'effective_fields': 5,
                             u'numeric': 4,
                             u'preferred': 5,
                             u'text': 0,
                             u'total': 5},
   u'dataset_status': True,
   u'description': u'',
   u'excluded_fields': [],
   u'fields_meta': {  u'count': 5,
                     u'limit': 1000,
                     u'offset': 0,
                     u'query_total': 5,
```

```

        u'total': 5),
u'input_fields': [u'000000', u'000001', u'000002', u'000003'],
u'locale': u'en_US',
u'logistic_regression': {  u'bias': 1,
                           u'c': 1,
                           u'coefficients': [ [ u'Iris-virginica',
                                                [ -1.7074433493289376,
                                                  -1.533662474502423,
                                                  2.47026986670851,
                                                  2.5567582221085563,
                                                  -1.2158200612711925]],
                                                [ u'Iris-setosa',
                                                  [ 0.41021712519841674,
                                                    1.464162165246765,
                                                    -2.26003266131107,
                                                    -1.0210350909174153,
                                                    0.26421852991732514]],
                                                [ u'Iris-versicolor',
                                                  [ 0.42702327817072505,
                                                    -1.611817241669904,
                                                    0.5763832839459982,
                                                    -1.4069842681625884,
                                                    1.0946877732663143]]],
                           u'eps': 1e-05,
                           u'fields': {  u'000000': {  u'column_number': 0,
                                                         u'datatype': u'double',
                                                         u'name': u'sepal length
                                                         u'optype': u'numeric',
                                                         u'order': 0,
                                                         u'preferred': True,
                                                         u'summary': {  u'bins
                                                         u'kurtosis': -0.57357,
                                                         u'maximum': 7.9,
                                                         u'mean
                                                         u'median
                                                         u'minimum': 4.3,
                                                         u'

```

```

↪ 'missing_count': 0,
↪ 'population': 150,
↪ 'skewness': 0.31175,
↪ ': [ 4.51526,
↪      4.67252,
↪      4.81113,
↪      ...
↪      6.92597,
↪      7.20423,
↪      7.64746],
↪ 'standard_deviation': 0.82807,
↪ 876.5,
↪ 'squares': 5223.85,
↪ 'variance': 0.68569}},
u'000001': { u'column_number': 1,
              u'datatype': u'double',
              u'name': u'sepal width',
              u'optype': u'numeric',
              u'order': 1,
              u'preferred': True,
              u'summary': { u'counts
↪ ': [ [ 2,
↪      1],
↪      [ 2.2,
↪      3],
↪      ...
↪      [ 4.2,
↪      1],
↪      [ 4.4,
↪      1]],
↪ 'kurtosis': 0.18098,
↪ 'maximum': 4.4,
↪ ': 3.05733,
↪ ': 3,

```

```

↪ 'minimum': 2,
↪ 'missing_count': 0,
↪ 'population': 150,
↪ 'skewness': 0.31577,
↪ 'standard_deviation': 0.43587,
↪ 458.6,
↪ squares': 1430.4,
↪ 'variance': 0.18998}},
u'000002': { u'column_number': 2,
              u'datatype': u'double',
              u'name': u'petal length
              u'optype': u'numeric',
              u'order': 2,
              u'preferred': True,
              u'summary': { u'bins
↪ ',
↪ ': [ [ 1,
↪      1],
↪      [ 1.16667,
↪      3],
...
↪      [ 6.6,
↪      1],
↪      [ 6.7,
↪      2],
↪      [ 6.9,
↪      1]],
↪ 'kurtosis': -1.39554,
↪ 'maximum': 6.9,
↪ ': 3.758,
↪ ': 4.35,
↪ 'minimum': 1,
↪ 'missing_count': 0,
↪ 'population': 150,

```

```

↪ 'skewness': -0.27213,
↪ ': [ 1.25138,
↪ 1.32426,
↪ 1.37171,
...
↪ 6.02913,
↪ 6.38125],
↪ 'standard_deviation': 1.7653,
↪ 563.7,
↪ 'squares': 2582.71,
↪ 'variance': 3.11628}},
u'000003': { u'column_number': 3,
              u'datatype': u'double',
              u'name': u'petal width',
              u'optype': u'numeric',
              u'order': 3,
              u'preferred': True,
              u'summary': { u'counts
↪ [ [ 0.1,
↪ 5],
↪ [ 0.2,
↪ 29],
...
↪ [ 2.4,
↪ 3],
↪ [ 2.5,
↪ 3]],
↪ 'kurtosis': -1.33607,
↪ 'maximum': 2.5,
↪ ': 1.19933,
↪ ': 1.3,
↪ 'minimum': 0.1,
↪ 'missing_count': 0,
↪ 'population': 150,

```

```

↪ 'skewness': -0.10193,
↪ 'standard_deviation': 0.76224,
↪ 179.9,
↪ 'squares': 302.33,
↪ 'variance': 0.58101}},
                                u'000004': {
                                    u'column_number': 4,
                                    u'datatype': u'string',
                                    u'name': u'species',
                                    u'optype': u'categorical',
                                    u'order': 4,
                                    u'preferred': True,
                                    u'summary': {
                                        u'categories': [
                                            [
                                                u'Iris-setosa',
                                                50],
                                            [
                                                u'Iris-versicolor',
                                                50],
                                            [
                                                u'Iris-virginica',
                                                50]],
                                            u'missing_count': 0},
                                            u'term_analysis': {
                                                u'normalize': False,
                                                u'regularization': u'l2'},
                                                u'max_columns': 5,
                                                u'max_rows': 150,
                                                u'name': u"iris' dataset's logistic regression",
                                                u'number_of_batchpredictions': 0,
                                                u'number_of_evaluations': 0,
                                                u'number_of_predictions': 1,
                                                u'objective_field': u'000004',
                                                u'objective_field_name': u'species',
                                                u'objective_field_type': u'categorical',
                                                u'objective_fields': [u'000004'],
                                                u'out_of_bag': False,
                                                u'private': True,
                                                u'project': u'project/561304c137203f4c9300016c',
                                                u'range': [1, 150],
                                                u'replacement': False,
                                                u'resource': u'logisticregression/5617e71c37203f506a000001',
                                                u'rows': 150,
                                                u'sample_rate': 1.0,
                                                u'shared': False,
                                                u'size': 4609,
                                                u'source': u'source/561304f437203f4c930001c3',
                                                u'source_status': True,
                                                u'status': {
                                                    u'code': 5,

```

```
        u'elapsed': 86,  
        u'message': u'The logistic regression has been created',  
        u'progress': 1.0},  
u'subscription': False,  
u'tags': [u'species'],  
u'updated': u'2015-10-09T16:14:02.336000',  
u'white_box': False}
```

Note that the output in the snippet above has been abbreviated. As you see, the `logistic_regression` attribute stores the coefficients used in the logistic function as well as the configuration parameters described in the [developers section](#) .

Association Discovery is a popular method to find out relations among values in high-dimensional datasets.

A common case where association discovery is often used is market basket analysis. This analysis seeks for customer shopping patterns across large transactional datasets. For instance, do customers who buy hamburgers and ketchup also consume bread?

Businesses use those insights to make decisions on promotions and product placements. Association Discovery can also be used for other purposes such as early incident detection, web usage analysis, or software intrusion detection.

In BigML, the Association resource object can be built from any dataset, and its results are a list of association rules between the items in the dataset. In the example case, the corresponding association rule would have hamburgers and ketchup as the items at the left hand side of the association rule and bread would be the item at the right hand side. Both sides in this association rule are related, in the sense that observing the items in the left hand side implies observing the items in the right hand side. There are some metrics to ponder the quality of these association rules:

- Support: the proportion of instances which contain an itemset.

For an association rule, it means the number of instances in the dataset which contain the rule's antecedent and rule's consequent together over the total number of instances (N) in the dataset.

It gives a measure of the importance of the rule. Association rules have to satisfy a minimum support constraint (i.e., `min_support`).

- Coverage: the support of the antecedent of an association rule.

It measures how often a rule can be applied.

- Confidence or (strength): The probability of seeing the rule's consequent

under the condition that the instances also contain the rule's antecedent. Confidence is computed using the support of the association rule over the coverage. That is, the percentage of instances which contain the consequent and antecedent together over the number of instances which only contain the antecedent.

Confidence is directed and gives different values for the association rules Antecedent \rightarrow Consequent and Consequent \rightarrow Antecedent. Association rules also need to satisfy a minimum confidence constraint (i.e., `min_confidence`).

- Leverage: the difference of the support of the association

rule (i.e., the antecedent and consequent appearing together) and what would be expected if antecedent and consequent were statistically independent. This is a value between -1 and 1. A positive value suggests a positive relationship and a negative value suggests a negative relationship. 0 indicates independence.

Lift: how many times more often antecedent and consequent occur together than expected if they were statistically independent. A value of 1 suggests that there is no relationship between the antecedent and the consequent. Higher values suggest stronger positive relationships. Lower values suggest stronger negative relationships (the presence of the antecedent reduces the likelihood of the consequent)

As to the items used in association rules, each type of field is parsed to extract items for the rules as follows:

- Categorical: each different value (class) will be considered a separate item.
- Text: each unique term will be considered a separate item.
- Items: each different item in the items summary will be considered.
- Numeric: Values will be converted into categorical by making a

segmentation of the values. For example, a numeric field with values ranging from 0 to 600 split into 3 segments: segment 1 → [0, 200), segment 2 → [200, 400), segment 3 → [400, 600]. You can refine the behavior of the transformation using [discretization](#) and [field_discretizations](#).

The JSON structure for an association resource is:

```
>>> api.pprint(association['object'])
{
  "associations":{
    "complement":false,
    "discretization":{
      "pretty":true,
      "size":5,
      "trim":0,
      "type":"width"
    },
    "items":[
      {
        "complement":false,
        "count":32,
        "field_id":"000000",
        "name":"Segment 1",
        "bin_end":5,
        "bin_start":null
      },
      {
        "complement":false,
        "count":49,
        "field_id":"000000",
        "name":"Segment 3",
        "bin_end":7,
        "bin_start":6
      },
      {
        "complement":false,
        "count":12,
        "field_id":"000000",
        "name":"Segment 4",
        "bin_end":null,
        "bin_start":7
      }
    ]
  }
}
```

```

        "complement":false,
        "count":19,
        "field_id":"000001",
        "name":"Segment 1",
        "bin_end":2.5,
        "bin_start":null
    },
    ...
    {
        "complement":false,
        "count":50,
        "field_id":"000004",
        "name":"Iris-versicolor"
    },
    {
        "complement":false,
        "count":50,
        "field_id":"000004",
        "name":"Iris-virginica"
    }
],
"max_k": 100,
"min_confidence":0,
"min_leverage":0,
"min_lift":1,
"min_support":0,
"rules":[
    {
        "confidence":1,
        "id":"000000",
        "leverage":0.22222,
        "lhs":[
            13
        ],
        "lhs_cover":[
            0.33333,
            50
        ],
        "lift":3,
        "p_value":0.000000000,
        "rhs":[
            6
        ],
        "rhs_cover":[
            0.33333,
            50
        ],
        "support":[
            0.33333,
            50
        ]
    }
],
    {
        "confidence":1,
        "id":"000001",
        "leverage":0.22222,
        "lhs":[
            6

```

```
    ],
    "lhs_cover": [
      0.33333,
      50
    ],
    ],
    "lift": 3,
    "p_value": 0.000000000,
    "rhs": [
      13
    ],
    ],
    "rhs_cover": [
      0.33333,
      50
    ],
    ],
    "support": [
      0.33333,
      50
    ]
  ]
},
...
{
  "confidence": 0.26,
  "id": "000029",
  "leverage": 0.05111,
  "lhs": [
    13
  ],
  ],
  "lhs_cover": [
    0.33333,
    50
  ],
  ],
  "lift": 2.4375,
  "p_value": 0.0000454342,
  "rhs": [
    5
  ],
  ],
  "rhs_cover": [
    0.10667,
    16
  ],
  ],
  "support": [
    0.08667,
    13
  ]
},
{
  "confidence": 0.18,
  "id": "00002a",
  "leverage": 0.04,
  "lhs": [
    15
  ],
  ],
  "lhs_cover": [
    0.33333,
    50
  ],
  ],
  "lift": 3,
  "p_value": 0.0000302052,
```

```

        "rhs": [
            9
        ],
        "rhs_cover": [
            0.06,
            9
        ],
        "support": [
            0.06,
            9
        ]
    ],
    {
        "confidence": 1,
        "id": "00002b",
        "leverage": 0.04,
        "lhs": [
            9
        ],
        "lhs_cover": [
            0.06,
            9
        ],
        "lift": 3,
        "p_value": 0.0000302052,
        "rhs": [
            15
        ],
        "rhs_cover": [
            0.33333,
            50
        ],
        "support": [
            0.06,
            9
        ]
    }
],
"rules_summary": {
    "confidence": {
        "counts": [
            [
                0.18,
                1
            ],
            [
                0.24,
                1
            ],
            [
                0.26,
                2
            ],
            ...
            [
                0.97959,
                1
            ],
        ]
    }
}

```

```

        [
            1,
            9
        ]
    ],
    "maximum":1,
    "mean":0.70986,
    "median":0.72864,
    "minimum":0.18,
    "population":44,
    "standard_deviation":0.24324,
    "sum":31.23367,
    "sum_squares":24.71548,
    "variance":0.05916
},
"k":44,
"leverage":{
    "counts":[
        [
            0.04,
            2
        ],
        [
            0.05111,
            4
        ],
        [
            0.05316,
            2
        ],
        ...
        [
            0.22222,
            2
        ]
    ],
    "maximum":0.22222,
    "mean":0.10603,
    "median":0.10156,
    "minimum":0.04,
    "population":44,
    "standard_deviation":0.0536,
    "sum":4.6651,
    "sum_squares":0.61815,
    "variance":0.00287
},
"lhs_cover":{
    "counts":[
        [
            0.06,
            2
        ],
        [
            0.08,
            2
        ],
        [
            0.10667,

```

```
        4
      ],
      [
        0.12667,
        1
      ],
      ...
      [
        0.5,
        4
      ]
    ],
    "maximum":0.5,
    "mean":0.29894,
    "median":0.33213,
    "minimum":0.06,
    "population":44,
    "standard_deviation":0.13386,
    "sum":13.15331,
    "sum_squares":4.70252,
    "variance":0.01792
  },
  "lift":{
    "counts":[
      [
        1.40625,
        2
      ],
      [
        1.5067,
        2
      ],
      ...
      [
        2.63158,
        4
      ],
      [
        3,
        10
      ],
      [
        4.93421,
        2
      ],
      [
        12.5,
        2
      ]
    ],
    "maximum":12.5,
    "mean":2.91963,
    "median":2.58068,
    "minimum":1.40625,
    "population":44,
    "standard_deviation":2.24641,
    "sum":128.46352,
    "sum_squares":592.05855,
```

```
    "variance":5.04635
  },
  "p_value":{
    "counts":[
      [
        0.000000000,
        2
      ],
      [
        0.000000000,
        4
      ],
      [
        0.000000000,
        2
      ],
      ...
      [
        0.0000910873,
        2
      ]
    ],
    "maximum":0.0000910873,
    "mean":0.0000106114,
    "median":0.000000000,
    "minimum":0.000000000,
    "population":44,
    "standard_deviation":0.0000227364,
    "sum":0.000466903,
    "sum_squares":0.0000000,
    "variance":0.000000001
  },
  "rhs_cover":{
    "counts":[
      [
        0.06,
        2
      ],
      [
        0.08,
        2
      ],
      ...
      [
        0.42667,
        2
      ],
      [
        0.46667,
        3
      ],
      [
        0.5,
        4
      ]
    ],
    "maximum":0.5,
    "mean":0.29894,
```



```
    "median":0.33213,
    "minimum":0.06,
    "population":44,
    "standard_deviation":0.13386,
    "sum":13.15331,
    "sum_squares":4.70252,
    "variance":0.01792
  },
  "support":{
    "counts":[
      [
        0.06,
        4
      ],
      [
        0.06667,
        2
      ],
      [
        0.08,
        2
      ],
      [
        0.08667,
        4
      ],
      [
        0.10667,
        4
      ],
      [
        0.15333,
        2
      ],
      [
        0.18667,
        4
      ],
      [
        0.19333,
        2
      ],
      [
        0.20667,
        2
      ],
      [
        0.27333,
        2
      ],
      [
        0.28667,
        2
      ],
      [
        0.3,
        4
      ],
    ],
```

```
        [
          0.32,
          2
        ],
        [
          0.33333,
          6
        ],
        [
          0.37333,
          2
        ]
      ],
      "maximum":0.37333,
      "mean":0.20152,
      "median":0.19057,
      "minimum":0.06,
      "population":44,
      "standard_deviation":0.10734,
      "sum":8.86668,
      "sum_squares":2.28221,
      "variance":0.01152
    }
  },
  "search_strategy":"leverage",
  "significance_level":0.05
},
"category":0,
"clones":0,
"code":200,
"columns":5,
"created":"2015-11-05T08:06:08.184000",
"credits":0.017581939697265625,
"dataset":"dataset/562fae3f4e1727141d00004e",
"dataset_status":true,
"dataset_type":0,
"description:"",
"excluded_fields":[ ],
"fields_meta":{
  "count":5,
  "limit":1000,
  "offset":0,
  "query_total":5,
  "total":5
},
"input_fields":[
  "000000",
  "000001",
  "000002",
  "000003",
  "000004"
],
"locale":"en_US",
"max_columns":5,
"max_rows":150,
"name":"iris' dataset's association",
"out_of_bag":false,
"price":0,
```

```
"private":true,
"project":null,
"range":[
  1,
  150
],
"replacement":false,
"resource":"association/5621b70910cb86ae4c000000",
"rows":150,
"sample_rate":1,
"shared":false,
"size":4609,
"source":"source/562fae3a4e1727141d000048",
"source_status":true,
"status":{
  "code":5,
  "elapsed":1072,
  "message":"The association has been created",
  "progress":1
},
"subscription":false,
"tags":[ ],
"updated":"2015-11-05T08:06:20.403000",
"white_box":false
}
```

Note that the output in the snippet above has been abbreviated. As you see, the `associations` attribute stores items, rules and metrics extracted from the datasets as well as the configuration parameters described in the [developers section](#).

A topic model is an unsupervised machine learning method for unveiling all the different topics underlying a collection of documents. BigML uses Latent Dirichlet Allocation (LDA), one of the most popular probabilistic methods for topic modeling. In BigML, each instance (i.e. each row in your dataset) will be considered a document and the contents of all the text fields given as inputs will be automatically concatenated and considered the document bag of words.

Topic model is based on the assumption that any document exhibits a mixture of topics. Each topic is composed of a set of words which are thematically related. The words from a given topic have different probabilities for that topic. At the same time, each word can be attributable to one or several topics. So for example the word “sea” may be found in a topic related with sea transport but also in a topic related to holidays. Topic model automatically discards stop words and high frequency words.

Topic model’s main applications include browsing, organizing and understanding large archives of documents. It can be applied for information retrieval, collaborative filtering, assessing document similarity among others. The topics found in the dataset can also be very useful new features before applying other models like classification, clustering, or anomaly detection.

The JSON structure for a topic model is:

```
>>> api.pprint(topic['object'])
{  u'category': 0,
   u'code': 200,
   u'columns': 1,
   u'configuration': None,
   u'configuration_status': False,
   u'created': u'2016-11-23T23:47:54.703000',
   u'credits': 0.0,
   u'credits_per_prediction': 0.0,
   u'dataset': u'dataset/58362aa0983efc45a0000005',
   u'dataset_field_types': {  u'categorical': 1,
                             u'datetime': 0,
                             u'effective_fields': 672,
                             u'items': 0,
                             u'numeric': 0,
                             u'preferred': 2,
                             u'text': 1,
```

```

        u'total': 2},
    u'dataset_status': True,
    u'dataset_type': 0,
    u'description': u'',
    u'excluded_fields': [],
    u'fields_meta': {
        u'count': 1,
        u'limit': 1000,
        u'offset': 0,
        u'query_total': 1,
        u'total': 1},
    u'input_fields': [u'000001'],
    u'locale': u'en_US',
    u'max_columns': 2,
    u'max_rows': 656,
    u'name': u"spam dataset's Topic Model ",
    u'number_of_batchtopicdistributions': 0,
    u'number_of_public_topicdistributions': 0,
    u'number_of_topicdistributions': 0,
    u'ordering': 0,
    u'out_of_bag': False,
    u'price': 0.0,
    u'private': True,
    u'project': None,
    u'range': [1, 656],
    u'replacement': False,
    u'resource': u'topicmodel/58362aaa983efc45a1000007',
    u'rows': 656,
    u'sample_rate': 1.0,
    u'shared': False,
    u'size': 54740,
    u'source': u'source/58362a69983efc459f000001',
    u'source_status': True,
    u'status': {
        u'code': 5,
        u'elapsed': 3222,
        u'message': u'The topic model has been created',
        u'progress': 1.0},
    u'subscription': True,
    u'tags': [],
    u'topic_model': {
        u'alpha': 4.166666666666667,
        u'beta': 0.1,
        u'bigrams': False,
        u'case_sensitive': False,
        u'fields': {
            u'000001': {
                u'column_number': 1,
                u'datatype': u'string',
                u'name': u'Message',
                u'optype': u'text',
                u'order': 0,
                u'preferred': True,
                u'summary': {
                    u'average_length
↪': 78.14787,
                    u'missing_count
↪': 0,
                    u'tag_cloud': [
↪ [ u'call',
↪     72],
↪ [ u'ok',

```

```

↪      36],
↪ [   u'gt',
↪      34],
↪ ...
↪ [   u'worse',
↪      2],
↪ [   u'worth',
↪      2],
↪ [   u'write',
↪      2],
↪ [   u'yest',
↪      2],
↪ [   u'yijue',
↪      2]],
↪{   }},
↪sensitive': False,
↪': True,
↪': u'en',
↪words': False,
↪mode': u'all',
↪stopwords': False}}},
    u'hashed_seed': 62146850,
    u'language': u'en',
    u'number_of_topics': 12,
    u'term_limit': 4096,
    u'term_topic_assignments': [ [ 0,
                                  5,
                                  0,
                                  1,
                                  0,
                                  19,
                                  0,
                                  0,
                                  19,
                                  0,
                                  1,
                                  0],
                                  [ 0,

```

```

0,
0,
13,
0,
0,
0,
0,
0,
5,
0,
0,
0,
0],
...
[ 0,
7,
27,
0,
112,
0,
0,
0,
0,
0,
0,
14,
2]],
u'termset': [ u'000',
              u'03',
              u'04',
              u'06',
              u'08000839402',
              u'08712460324',
              u'yes',
              u'yest',
              u'yesterday',
              u'yijue',
              u'yo',
              u'yr',
              u'yup',
              u'\xfc'],
u'top_n_terms': 10,
u'topicmodel_seed': u'26c386d781963calea5c90dab8a6b023b5e1d180
→',
u'topics': [ { u'id': u'000000',
               u'name': u'Topic 00',
               u'probability': 0.09375,
               u'top_terms': [ [ u'im',
                                0.04849],
                              [ u'hi',
                                0.04717],
                              [ u'love',
                                0.04585],
                              [ u'please',
                                0.02867],
                              [ u'tomorrow',
                                0.02867],
                              [ u'cos',
                                0.02823],

```



```

        [ u'sent',
          0.02647],
        [ u'da',
          0.02383],
        [ u'meet',
          0.02207],
        [ u'dinner',
          0.01898]]},
    { u'id': u'000001',
      u'name': u'Topic 01',
      u'probability': 0.08215,
      u'top_terms': [ [ u'lt',
                        0.1015],
                      [ u'gt',
                        0.1007],
                      [ u'wish',
                        0.03958],
                      [ u'feel',
                        0.0272],
                      [ u'shit',
                        0.02361],
                      [ u'waiting',
                        0.02281],
                      [ u'stuff',
                        0.02001],
                      [ u'name',
                        0.01921],
                      [ u'comp',
                        0.01522],
                      [ u'forgot',
                        0.01482]]}],
    ...
    { u'id': u'00000b',
      u'name': u'Topic 11',
      u'probability': 0.0826,
      u'top_terms': [ [ u'call',
                        0.15084],
                      [ u'min',
                        0.05003],
                      [ u'msg',
                        0.03185],
                      [ u'home',
                        0.02648],
                      [ u'mind',
                        0.02152],
                      [ u'lt',
                        0.01987],
                      [ u'bring',
                        0.01946],
                      [ u'camera',
                        0.01905],
                      [ u'set',
                        0.01905],
                      [ u'contact',
                        0.01781]]}],
      u'use_stopwords': False},
    u'updated': u'2016-11-23T23:48:03.336000',
    u'white_box': False}

```

Note that the output in the snippet above has been abbreviated.

The topic model returns a list of top terms for each topic found in the data. Note that topics are not labeled, so you have to infer their meaning according to the words they are composed of.

Once you build the topic model you can calculate each topic probability for a given document by using Topic Distribution. This information can be useful to find documents similarities based on their thematic.

As you see, the `topic_model` attribute stores the topics and termset and term to topic assignment, as well as the configuration parameters described in the [developers section](#) .

Whizzml Resources

Whizzml is a Domain Specific Language that allows the definition and execution of ML-centric workflows. Its objective is allowing BigML users to define their own composite tasks, using as building blocks the basic resources provided by BigML itself. Using Whizzml they can be glued together using a higher order, functional, Turing-complete language. The Whizzml code can be stored and executed in BigML using three kinds of resources: *Scripts*, *Libraries* and *Executions*.

Whizzml *Scripts* can be executed in BigML's servers, that is, in a controlled, fully-scalable environment which takes care of their parallelization and fail-safe operation. Each execution uses an *Execution* resource to store the arguments and results of the process. Whizzml *Libraries* store generic code to be shared or reused in other Whizzml *Scripts*.

In BigML a `Script` resource stores Whizzml source code, and the results of its compilation. Once a Whizzml script is created, it's automatically compiled; if compilation succeeds, the script can be run, that is, used as the input for a Whizzml execution resource.

An example of a script that would create a source in BigML using the contents of a remote file is:

```
>>> from bigml.api import BigML
>>> api = BigML()
# creating a script directly from the source code. This script creates
# a source uploading data from an s3 repo. You could also create a
# a script by using as first argument the path to a .whizzml file which
# contains your source code.
>>> script = api.create_script( \
    "(create-source {\\"remote\\" \\"s3://bigml-public/csv/iris.csv\\"})")
>>> api.ok(script) # waiting for the script compilation to finish
>>> api.pprint(script['object'])
{  u'approval_status': 0,
   u'category': 0,
   u'code': 200,
   u'created': u'2016-05-18T16:54:05.666000',
   u'description': u'',
   u'imports': [],
   u'inputs': None,
   u'line_count': 1,
   u'locale': u'en-US',
   u'name': u'Script',
   u'number_of_executions': 0,
   u'outputs': None,
   u'price': 0.0,
   u'private': True,
   u'project': None,
   u'provider': None,
   u'resource': u'script/573c9e2db85eee23cd000489',
   u'shared': False,
   u'size': 59,
```

```
u'source_code': u'(create-source {"remote" "s3://bigml-public/csv/iris.csv"})',
u'status': { u'code': 5,
            u'elapsed': 4,
            u'message': u'The script has been created',
            u'progress': 1.0},
u'subscription': True,
u'tags': [],
u'updated': u'2016-05-18T16:54:05.850000',
u'white_box': False}
```

A script allows to define some variables as inputs. In the previous example, no input has been defined, but we could modify our code to allow the user to set the remote file name as input:

```
>>> from bigml.api import BigML
>>> api = BigML()
>>> script = api.create_script( \
    "(create-source {\\"remote\\" my_remote_data})",
    {"inputs": [{"name": "my_remote_data",
                 "type": "string",
                 "default": "s3://bigml-public/csv/iris.csv",
                 "description": "Location of the remote data"}]})
```

The script can also use a library resource (please, see the [Libraries](#) section below for more details) by including its id in the `imports` attribute. Other attributes can be checked at the [API Developers documentation for Scripts](#).

Executions

To execute in BigML a compiled Whizzml script you need to create an execution resource. It's also possible to execute a pipeline of many compiled scripts in one request.

Each execution is run under its associated user credentials and its particular environment constraints. As scripts can be shared, you can execute the same script several times under different usernames by creating different executions.

As an example of execution resource, let's create one for the script in the previous section:

```
>>> from bigml.api import BigML
>>> api = BigML()
>>> execution = api.create_execution('script/573c9e2db85eee23cd000489')
>>> api.ok(execution) # waiting for the execution to finish
>>> api.pprint(execution['object'])
{  u'category': 0,
   u'code': 200,
   u'created': u'2016-05-18T16:58:01.613000',
   u'creation_defaults': {  },
   u'description': u'',
   u'execution': {  u'output_resources': [  {  u'code': 1,
                                             u'id': u'source/
↪573c9f19b85eee23c600024a',
                                             u'last_update': 1463590681854,
                                             u'progress': 0.0,
                                             u'state': u'queued',
                                             u'task': u'Queuing job',
                                             u'variable': u''}],
                   u'outputs': [],
                   u'result': u'source/573c9f19b85eee23c600024a',
                   u'results': [u'source/573c9f19b85eee23c600024a'],
                   u'sources': [[  u'script/573c9e2db85eee23cd000489',
                                   u'']],
                   u'steps': 16},
   u'inputs': None,
   u'locale': u'en-US',
```

```
u'name': u"Script's Execution",
u'project': None,
u'resource': u'execution/573c9f19b85eee23bd000125',
u'script': u'script/573c9e2db85eee23cd000489',
u'script_status': True,
u'shared': False,
u'status': { u'code': 5,
             u'elapsed': 249,
             u'elapsed_times': { u'in-progress': 247,
                                  u'queued': 62,
                                  u'started': 2},
             u'message': u'The execution has been created',
             u'progress': 1.0},
u'subscription': True,
u'tags': [],
u'updated': u'2016-05-18T16:58:02.035000'}
```

An execution receives inputs, the ones defined in the script chosen to be executed, and generates a result. It can also generate outputs. As you can see, the execution resource contains information about the result of the execution, the resources that have been generated while executing and users can define some variables in the code to be exported as outputs. Please refer to the **[‘Developers documentation for Executions<https://bigml.com/api/executions#we_execution_arguments>’](https://bigml.com/api/executions#we_execution_arguments)** for details on how to define execution outputs.

The library resource in BigML stores a special kind of compiled Whizzml source code that only defines functions and constants. The library is intended as an import for executable scripts. Thus, a compiled library cannot be executed, just used as an import in other libraries and scripts (which then have access to all identifiers defined in the library).

As an example, we build a library to store the definition of two functions: `mu` and `g`. The first one adds one to the value set as argument and the second one adds two variables and increments the result by one.

```
>>> from bigml.api import BigML
>>> api = BigML()
>>> library = api.create_library( \
    "(define (mu x) (+ x 1)) (define (g z y) (mu (+ y z)))")
>>> api.ok(library) # waiting for the library compilation to finish
>>> api.pprint(library['object'])
{ u'approval_status': 0,
  u'category': 0,
  u'code': 200,
  u'created': u'2016-05-18T18:58:50.838000',
  u'description': u'',
  u'exports': [ { u'name': u'mu', u'signature': [u'x']},
                { u'name': u'g', u'signature': [u'z', u'y']}],
  u'imports': [],
  u'line_count': 1,
  u'name': u'Library',
  u'price': 0.0,
  u'private': True,
  u'project': None,
  u'provider': None,
  u'resource': u'library/573cbb6ab85eee23c300018e',
  u'shared': False,
  u'size': 53,
  u'source_code': u'(define (mu x) (+ x 1)) (define (g z y) (mu (+ y z)))',
  u'status': { u'code': 5,
              u'elapsed': 2,
              u'message': u'The library has been created',
```

```
        u'progress': 1.0},
    u'subscription': True,
    u'tags': [],
    u'updated': u'2016-05-18T18:58:52.432000',
    u'white_box': False}
```

Libraries can be imported in scripts. The `imports` attribute of a script can contain a list of library IDs whose defined functions and constants will be ready to be used throughout the script. Please, refer to the [API Developers documentation for Libraries](#) for more details.

Creating Resources

Newly-created resources are returned in a dictionary with the following keys:

- **code**: If the request is successful you will get a `bigml.api.HTTP_CREATED` (201) status code. In asynchronous file uploading `api.create_source` calls, it will contain `bigml.api.HTTP_ACCEPTED` (202) status code. Otherwise, it will be one of the standard HTTP error codes [detailed in the documentation](#).
- **resource**: The identifier of the new resource.
- **location**: The location of the new resource.
- **object**: The resource itself, as computed by BigML.
- **error**: If an error occurs and the resource cannot be created, it will contain an additional code and a description of the error. In this case, **location**, and **resource** will be `None`.

Statuses

Please, bear in mind that resource creation is almost always asynchronous (**predictions** are the only exception). Therefore, when you create a new source, a new dataset or a new model, even if you receive an immediate response from the BigML servers, the full creation of the resource can take from a few seconds to a few days, depending on the size of the resource and BigML's load. A resource is not fully created until its status is `bigml.api.FINISHED`. See the [documentation on status codes](#) for the listing of potential states and their semantics. So depending on your application you might need to import the following constants:

```
from bigml.api import WAITING
from bigml.api import QUEUED
from bigml.api import STARTED
from bigml.api import IN_PROGRESS
from bigml.api import SUMMARIZED
from bigml.api import FINISHED
from bigml.api import UPLOADING
from bigml.api import FAULTY
from bigml.api import UNKNOWN
from bigml.api import RUNNABLE
```

Usually, you will simply need to wait until the resource is in the `bigml.api.FINISHED` state for further processing. If that's the case, the easiest way is calling the `api.ok` method and passing as first argument the object that contains your resource:

```
from bigml.api import BigML
api = BigML() # creates a connection to BigML's API
source = api.create_source('my_file.csv') # creates a source object
api.ok(source) # checks that the source is finished and updates ``source``
```

In this code, `api.create_source` will probably return a non-finished source object. Then, `api.ok` will query its status and update the contents of the `source` variable with the retrieved information until it reaches a `bigml.api.FINISHED` or `bigml.api.FAILED` status.

If you don't want the contents of the variable to be updated, you can also use the `check_resource` function:

```
check_resource(resource, api.get_source)
```

that will constantly query the API until the resource gets to a `FINISHED` or `FAULTY` state, or can also be used with `wait_time` (in seconds) and `retries` arguments to control the polling:

```
check_resource(resource, api.get_source, wait_time=2, retries=20)
```

The `wait_time` value is used as seed to a wait interval that grows exponentially with the number of retries up to the given `retries` limit.

However, in other scenarios you might need to control the complete evolution of the resource, not only its final states. There, you can query the status of any resource with the `status` method, which simply returns its value and does not update the contents of the associated variable:

```
api.status(source)
api.status(dataset)
api.status(model)
api.status(prediction)
api.status(evaluation)
api.status(ensemble)
api.status(batch_prediction)
api.status(cluster)
api.status(centroid)
api.status(batch_centroid)
api.status(anomaly)
api.status(anomaly_score)
api.status(batch_anomaly_score)
api.status(sample)
api.status(correlation)
api.status(statistical_test)
api.status(logistic_regression)
api.status(association)
api.status(association_set)
api.status(topic_model)
api.status(topic_distribution)
api.status(batch_topic_distribution)
api.status(script)
api.status(execution)
api.status(library)
```

Remember that, consequently, you will need to retrieve the resources explicitly in your code to get the updated information.

Projects

A special kind of resource is `project`. Projects are repositories for resources, intended to fulfill organizational purposes. Each project can contain any other kind of resource, but the project that a certain resource belongs to is determined by the one used in the `source` they are generated from. Thus, when a source is created and assigned a certain `project_id`, the rest of resources generated from this source will remain in this project.

The REST calls to manage the `project` resemble the ones used to manage the rest of resources. When you create a `project`:

```
from bigml.api import BigML
api = BigML()

project = api.create_project({'name': 'my first project'})
```

the resulting resource is similar to the rest of resources, although shorter:

```
{'code': 201,
 'resource': u'project/54a1bd0958a27e3c4c0002f0',
 'location': 'http://bigml.io/andromeda/project/54a1bd0958a27e3c4c0002f0',
 'object': {'category': 0,
            u'updated': u'2014-12-29T20:43:53.060045',
            u'resource': u'project/54a1bd0958a27e3c4c0002f0',
            u'name': u'my first project',
            u'created': u'2014-12-29T20:43:53.060013',
            u'tags': [],
            u'private': True,
            u'dev': None,
            u'description': u''},
 'error': None}
```

and you can use its project id to get, update or delete it:

```
project = api.get_project('project/54a1bd0958a27e3c4c0002f0')
api.update_project(project['resource'],
                  {'description': 'This is my first project'})

api.delete_project(project['resource'])
```

Important: Deleting a non-empty project will also delete **all resources** assigned to it, so please be extra-careful when using the `api.delete_project` call.

Creating sources

To create a source from a local data file, you can use the `create_source` method. The only required parameter is the path to the data file (or file-like object). You can use a second optional parameter to specify any of the options for source creation described in the [BigML API documentation](#).

Here's a sample invocation:

```
from bigml.api import BigML
api = BigML()

source = api.create_source('./data/iris.csv',
                          {'name': 'my source', 'source_parser': {'missing_tokens': ['?']}})
```

or you may want to create a source from a file in a remote location:

```
source = api.create_source('s3://bigml-public/csv/iris.csv',
    {'name': 'my remote source', 'source_parser': {'missing_tokens': ['?']}})
```

or maybe reading the content from stdin:

```
content = StringIO.StringIO(sys.stdin.read())
source = api.create_source(content,
    {'name': 'my stdin source', 'source_parser': {'missing_tokens': ['?']}})
```

or using data stored in a local python variable. The following example shows the two accepted formats:

```
local = [['a', 'b', 'c'], [1, 2, 3], [4, 5, 6]]
local2 = [{'a': 1, 'b': 2, 'c': 3}, {'a': 4, 'b': 5, 'c': 6}]
source = api.create_source(local, {'name': 'inline source'})
```

As already mentioned, source creation is asynchronous. In both these examples, the `api.create_source` call returns once the file is uploaded. Then `source` will contain a resource whose status code will be either `WAITING` or `QUEUED`.

For local data files you can go one step further and use asynchronous uploading:

```
source = api.create_source('./data/iris.csv',
    {'name': 'my source', 'source_parser': {'missing_tokens': ['?']}},
    async=True)
```

In this case, the call fills `source` immediately with a primary resource like:

```
{'code': 202,
 'resource': None,
 'location': None,
 'object': {'status':
             {'progress': 0.99,
              'message': 'The upload is in progress',
              'code': 6}},
 'error': None}
```

where the `source['object']` status is set to `UPLOADING` and its `progress` is periodically updated with the current uploading progress ranging from 0 to 1. When upload completes, this structure will be replaced by the real resource info as computed by BigML. Therefore `source`'s status will eventually be (as it is in the synchronous upload case) `WAITING` or `QUEUED`.

You can retrieve the updated status at any time using the corresponding get method. For example, to get the status of our source we would use:

```
api.status(source)
```

Creating datasets

Once you have created a source, you can create a dataset. The only required argument to create a dataset is a source id. You can add all the additional arguments accepted by BigML and documented in the [Datasets](#) section of the [Developer's documentation](#).

For example, to create a dataset named “my dataset” with the first 1024 bytes of a source, you can submit the following request:

```
dataset = api.create_dataset(source, {"name": "my dataset", "size": 1024})
```

Upon success, the dataset creation job will be queued for execution, and you can follow its evolution using `api.status(dataset)`.

As for the rest of resources, the create method will return an incomplete object, that can be updated by issuing the corresponding `api.get_dataset` call until it reaches a `FINISHED` status. Then you can export the dataset data to a CSV file using:

```
api.download_dataset('dataset/526fc344035d071ea3031d75',
    filename='my_dir/my_dataset.csv')
```

You can also extract samples from an existing dataset and generate a new one with them using the `api.create_dataset` method. The first argument should be the origin dataset and the rest of arguments that set the range or the sampling rate should be passed as a dictionary. For instance, to create a new dataset extracting the 80% of instances from an existing one, you could use:

```
dataset = api.create_dataset(origin_dataset, {"sample_rate": 0.8})
```

Similarly, if you want to split your source into training and test datasets, you can set the `sample_rate` as before to create the training dataset and use the `out_of_bag` option to assign the complementary subset of data to the test dataset. If you set the `seed` argument to a value of your choice, you will ensure a determinist sampling, so that each time you execute this call you will get the same datasets as a result and they will be complementary:

```
origin_dataset = api.create_dataset(source)
train_dataset = api.create_dataset(
    origin_dataset, {"name": "Dataset Name | Training",
                    "sample_rate": 0.8, "seed": "my seed"})
test_dataset = api.create_dataset(
    origin_dataset, {"name": "Dataset Name | Test",
                    "sample_rate": 0.8, "seed": "my seed",
                    "out_of_bag": True})
```

It is also possible to generate a dataset from a list of datasets (multidataset):

```
dataset1 = api.create_dataset(source1)
dataset2 = api.create_dataset(source2)
multidataset = api.create_dataset([dataset1, dataset2])
```

Clusters can also be used to generate datasets containing the instances grouped around each centroid. You will need the cluster id and the centroid id to reference the dataset to be created. For instance,

```
cluster = api.create_cluster(dataset)
cluster_dataset_1 = api.create_dataset(cluster,
    args={'centroid': '000000'})
```

would generate a new dataset containing the subset of instances in the cluster associated to the centroid id 000000.

Creating models

Once you have created a dataset you can create a model from it. If you don't select one, the model will use the last field of the dataset as objective field. The only required argument to create a model is a dataset id. You can also include in the request all the additional arguments accepted by BigML and documented in the [Models section of the Developer's documentation](#).

For example, to create a model only including the first two fields and the first 10 instances in the dataset, you can use the following invocation:

```
model = api.create_model(dataset, {
    "name": "my model", "input_fields": ["000000", "000001"], "range": [1, 10]})
```

Again, the model is scheduled for creation, and you can retrieve its status at any time by means of `api.status(model)`.

Models can also be created from lists of datasets. Just use the list of ids as the first argument in the api call

```
model = api.create_model([dataset1, dataset2], {
    "name": "my model", "input_fields": ["000000", "000001"], "range": [1, 10]})
```

And they can also be generated as the result of a clustering procedure. When a cluster is created, a model that predicts if a certain instance belongs to a concrete centroid can be built by providing the cluster and centroid ids:

```
model = api.create_model(cluster, {
    "name": "model for centroid 000001", "centroid": "000001"})
```

if no centroid id is provided, the first one appearing in the cluster is used.

Creating clusters

If your dataset has no fields showing the objective information to predict for the training data, you can still build a cluster that will group similar data around some automatically chosen points (centroids). Again, the only required argument to create a cluster is the dataset id. You can also include in the request all the additional arguments accepted by BigML and documented in the [Clusters](#) section of the [Developer's documentation](#).

Let's create a cluster from a given dataset:

```
cluster = api.create_cluster(dataset, {"name": "my cluster",
                                       "k": 5})
```

that will create a cluster with 5 centroids.

Creating anomaly detectors

If your problem is finding the anomalous data in your dataset, you can build an anomaly detector, that will use iforest to single out the anomalous records. Again, the only required argument to create an anomaly detector is the dataset id. You can also include in the request all the additional arguments accepted by BigML and documented in the [Anomaly detectors](#) section of the [Developer's documentation](#).

Let's create an anomaly detector from a given dataset:

```
anomaly = api.create_anomaly(dataset, {"name": "my anomaly"})
```

that will create an anomaly resource with a `top_anomalies` block of the most anomalous points.

Creating associations

To find relations between the field values you can create an association discovery resource. The only required argument to create an association is a dataset id. You can also include in the request all the additional arguments accepted by

BigML and documented in the [Association](#) section of the Developer's documentation.

For example, to create an association only including the first two fields and the first 10 instances in the dataset, you can use the following invocation:

```
association = api.create_association(dataset, { \
    "name": "my association", "input_fields": ["000000", "000001"], \
    "range": [1, 10]})
```

Again, the association is scheduled for creation, and you can retrieve its status at any time by means of `api.status(association)`.

Associations can also be created from lists of datasets. Just use the list of ids as the first argument in the api call

```
association = api.create_association([dataset1, dataset2], { \
    "name": "my association", "input_fields": ["000000", "000001"], \
    "range": [1, 10]})
```

Creating topic models

To find which topics do your documents refer to you can create a topic model. The only required argument to create a topic model is a dataset id. You can also include in the request all the additional arguments accepted by BigML and documented in the [Topic Model](#) section of the Developer's documentation.

For example, to create a topic model including exactly 32 topics you can use the following invocation:

```
topic_model = api.create_topic_model(dataset, { \
    "name": "my topics", "number_of_topics": 32})
```

Again, the topic model is scheduled for creation, and you can retrieve its status at any time by means of `api.status(topic_model)`.

Topic models can also be created from lists of datasets. Just use the list of ids as the first argument in the api call

```
topic_model = api.create_topic_model([dataset1, dataset2], { \
    "name": "my topics", "number_of_topics": 32})
```

Creating predictions

You can now use the model resource identifier together with some input parameters to ask for predictions, using the `create_prediction` method. You can also give the prediction a name:

```
prediction = api.create_prediction(model,
    {"sepal length": 5,
     "sepal width": 2.5},
    {"name": "my prediction"})
```

To see the prediction you can use `pprint`:

```
api.pprint(prediction)
```

Creating centroids

To obtain the centroid associated to new input data, you can now use the `create_centroid` method. Give the method a cluster identifier and the input data to obtain the centroid. You can also give the centroid prediction a name:

```
centroid = api.create_centroid(cluster,
                               {"pregnancies": 0,
                                "plasma glucose": 118,
                                "blood pressure": 84,
                                "triceps skin thickness": 47,
                                "insulin": 230,
                                "bmi": 45.8,
                                "diabetes pedigree": 0.551,
                                "age": 31,
                                "diabetes": "true"},
                               {"name": "my centroid"})
```

Creating anomaly scores

To obtain the anomaly score associated to new input data, you can now use the `create_anomaly_score` method. Give the method an anomaly detector identifier and the input data to obtain the score:

```
anomaly_score = api.create_anomaly_score(anomaly, {"src_bytes": 350},
                                           args={"name": "my score"})
```

Creating association sets

Using the association resource, you can obtain the consequent items associated by its rules to your input data. These association sets can be obtained calling the `create_association_set` method. The first argument is the association ID or object and the next one is the input data.

```
association_set = api.create_association_set( \
    association, {"genres": "Action$Adventure"}, \
    args={"name": "my association set"})
```

Creating topic distributions

To obtain the topic distributions associated to new input data, you can now use the `create_topic_distribution` method. Give the method a topic model identifier and the input data to obtain the score:

```
anomaly_score = api.create_topic_distribution( \
    topic_model,
    {"Message": "The bubble exploded in 2007."},
    args={"name": "my topic distribution"})
```

Creating evaluations

Once you have created a model, you can measure its performance by running a dataset of test data through it and comparing its predictions to the objective field real values. Thus, the required arguments to create an evaluation are model id and a dataset id. You can also include in the request all the additional arguments accepted by BigML and documented in the [Evaluations](#) section of the [Developer's documentation](#).

For instance, to evaluate a previously created model using an existing dataset you can use the following call:

```
evaluation = api.create_evaluation(model, dataset, {
    "name": "my model"})
```

Again, the evaluation is scheduled for creation and `api.status(evaluation)` will show its state.

Evaluations can also check the ensembles' performance. To evaluate an ensemble you can do exactly what we just did for the model case, using the ensemble object instead of the model as first argument:

```
evaluation = api.create_evaluation(ensemble, dataset)
```

Creating ensembles

To improve the performance of your predictions, you can create an ensemble of models and combine their individual predictions. The only required argument to create an ensemble is the dataset id:

```
ensemble = api.create_ensemble('dataset/5143a51a37203f2cf7000972')
```

BigML offers three kinds of ensembles. Two of them are known as `Decision Forests` because they are built as collections of `Decision trees` whose predictions are aggregated using different combiners (`plurality`, `confidence weighted`, `probability weighted`) or setting a `threshold` to issue the ensemble's prediction. All `Decision Forests` use `bagging` to sample the data used to build the underlying models.

As an example of how to create a `Decision Forest` with 20 models, you only need to provide the dataset ID that you want to build the ensemble from and the number of models:

```
args = {'number_of_models': 20}
ensemble = api.create_ensemble('dataset/5143a51a37203f2cf7000972', args)
```

If no `number_of_models` is provided, the ensemble will contain 10 models.

`Random Decision Forests` fall also into the `Decision Forest` category, but they only use a subset of the fields chosen at random at each split. To create this kind of ensemble, just use the `randomize` option:

```
args = {'number_of_models': 20, 'randomize': True}
ensemble = api.create_ensemble('dataset/5143a51a37203f2cf7000972', args)
```

The third kind of ensemble is `Boosted Trees`. This type of ensemble uses quite a different algorithm. The trees used in the ensemble don't have as objective field the one you want to predict, and they don't aggregate the underlying models' votes. Instead, the goal is adjusting the coefficients of a function that will be used to predict. The models' objective is, therefore, the gradient that minimizes the error of the predicting function (when comparing its output with the real values). The process starts with some initial values and computes these gradients. Next step uses the previous fields plus the last computed gradient field as the new initial state for the next iteration. Finally, it stops when the error is smaller than a certain threshold or iterations reach a user-defined limit. In classification problems, every category in the ensemble's objective field would be associated with a subset of the `Boosted Trees`. The objective of each subset of trees is adjusting the function to the probability of belonging to this particular category.

In order to build an ensemble of `Boosted Trees` you need to provide the `boosting` attributes. You can learn about the existing attributes in the `ensembles`' section of the [API documentation](#), but a typical attribute to be set would be the maximum number of iterations:

```
args = {'boosting': {'iterations': 20}}
ensemble = api.create_ensemble('dataset/5143a51a37203f2cf7000972', args)
```

Creating logistic regressions

For classification problems, you can choose also logistic regressions to model your data. Logistic regressions compute a probability associated to each class in the objective field. The probability is obtained using a logistic function, whose argument is a linear combination of the field values.

As the rest of models, logistic regressions can be created from a dataset by calling the corresponding create method:

```
logistic_regression = api.create_logistic_regression( \
    'dataset/5143a51a37203f2cf7000972',
    {"name": "my logistic regression",
     "objective_field": "my_objective_field"})
```

In this example, we created a logistic regression named `my logistic regression` and set the objective field to be `my_objective_field`. Other arguments, like `bias`, `missing_numerics` and `c` can also be specified as attributes in arguments dictionary at creation time. Particularly for categorical fields, there are four different available `field_codings`' options (`dummy`, `contrast`, `other` or the `one-hot` default coding). For a more detailed description of the `field_codings` attribute and its syntax, please see the [Developers API Documentation](#).

Creating batch predictions

We have shown how to create predictions individually, but when the amount of predictions to make increases, this procedure is far from optimal. In this case, the more efficient way of predicting remotely is to create a dataset containing the input data you want your model to predict from and to give its id and the one of the model to the `create_batch_prediction` api call:

```
batch_prediction = api.create_batch_prediction(model, dataset, {
    "name": "my batch prediction", "all_fields": True,
    "header": True,
    "confidence": True})
```

In this example, setting `all_fields` to `true` causes the input data to be included in the prediction output, `header` controls whether a headers line is included in the file or not and `confidence` set to `true` causes the confidence of the prediction to be appended. If none of these arguments is given, the resulting file will contain the name of the objective field as a header row followed by the predictions.

As for the rest of resources, the create method will return an incomplete object, that can be updated by issuing the corresponding `api.get_batch_prediction` call until it reaches a `FINISHED` status. Then you can download the created predictions file using:

```
api.download_batch_prediction('batchprediction/526fc344035d071ea3031d70',
    filename='my_dir/my_predictions.csv')
```

that will copy the output predictions to the local file given in `filename`. If no `filename` is provided, the method returns a file-like object that can be read as a stream:

```
CHUNK_SIZE = 1024
response = api.download_batch_prediction(
    'batchprediction/526fc344035d071ea3031d70')
chunk = response.read(CHUNK_SIZE)
if chunk:
    print chunk
```

The output of a batch prediction can also be transformed to a source object using the `source_from_batch_prediction` method in the api:

```
api.source_from_batch_prediction(
    'batchprediction/526fc344035d071ea3031d70',
    args={'name': 'my_batch_prediction_source'})
```

This code will create a new source object, that can be used again as starting point to generate datasets.

Creating batch centroids

As described in the previous section, it is also possible to make centroids' predictions in batch. First you create a dataset containing the input data you want your cluster to relate to a centroid. The `create_batch_centroid` call will need the id of the input data dataset and the cluster used to assign a centroid to each instance:

```
batch_centroid = api.create_batch_centroid(cluster, dataset, {
    "name": "my batch centroid", "all_fields": True,
    "header": True})
```

Creating batch anomaly scores

Input data can also be assigned an anomaly score in batch. You train an anomaly detector with your training data and then build a dataset from your input data. The `create_batch_anomaly_score` call will need the id of the dataset and of the anomaly detector to assign an anomaly score to each input data instance:

```
batch_anomaly_score = api.create_batch_anomaly_score(anomaly, dataset, {
    "name": "my batch anomaly score", "all_fields": True,
    "header": True})
```

Creating batch topic distributions

Input data can also be assigned a topic distribution in batch. You train a topic model with your training data and then build a dataset from your input data. The `create_batch_topic_distribution` call will need the id of the dataset and of the topic model to assign a topic distribution to each input data instance:

```
batch_topic_distribution = api.create_batch_topic_distribution( \
    topic_model, dataset, {
    "name": "my batch topic distribution", "all_fields": True,
    "header": True})
```


CHAPTER 24

Reading Resources

When retrieved individually, resources are returned as a dictionary identical to the one you get when you create a new resource. However, the status code will be `bigml.api.HTTP_OK` if the resource can be retrieved without problems, or one of the HTTP standard error codes otherwise.

Listing Resources

You can list resources with the appropriate api method:

```
api.list_sources()
api.list_datasets()
api.list_models()
api.list_predictions()
api.list_evaluations()
api.list_ensembles()
api.list_batch_predictions()
api.list_clusters()
api.list_centroids()
api.list_batch_centroids()
api.list_anomalies()
api.list_anomaly_scores()
api.list_batch_anomaly_scores()
api.list_projects()
api.list_samples()
api.list_correlations()
api.list_statistical_tests()
api.list_logistic_regressions()
api.list_associations()
api.list_association_sets()
api.list_topic_models()
api.list_topic_distributions()
api.list_batch_topic_distributions()
api.list_scripts()
api.list_libraries()
api.list_executions()
```

you will receive a dictionary with the following keys:

- **code:** If the request is successful you will get a `bigml.api.HTTP_OK (200)` status code. Otherwise, it will be one of the standard HTTP error codes. See [BigML documentation on status codes](#) for more info.
- **meta:** A dictionary including the following keys that can help you paginate listings:

- **previous**: Path to get the previous page or `None` if there is no previous page.
- **next**: Path to get the next page or `None` if there is no next page.
- **offset**: How far off from the first entry in the resources is the first one listed in the resources key.
- **limit**: Maximum number of resources that you will get listed in the resources key.
- **total_count**: The total number of resources in BigML.
- **objects**: A list of resources as returned by BigML.
- **error**: If an error occurs and the resource cannot be created, it will contain an additional code and a description of the error. In this case, **meta**, and **resources** will be `None`.

Filtering Resources

You can filter resources in listings using the syntax and fields labeled as *filterable* in the [BigML documentation](#) for each resource.

A few examples:

Ids of the first 5 sources created before April 1st, 2012

```
[source['resource'] for source in
 api.list_sources("limit=5;created__lt=2012-04-1") ['objects']]
```

Name of the first 10 datasets bigger than 1MB

```
[dataset['name'] for dataset in
 api.list_datasets("limit=10;size__gt=1048576") ['objects']]
```

Name of models with more than 5 fields (columns)

```
[model['name'] for model in api.list_models("columns__gt=5") ['objects']]
```

Ids of predictions whose model has not been deleted

```
[prediction['resource'] for prediction in
 api.list_predictions("model_status=true") ['objects']]
```

Ordering Resources

You can order resources in listings using the syntax and fields labeled as *sortable* in the [BigML documentation](#) for each resource.

A few examples:

Name of sources ordered by size

```
[source['name'] for source in api.list_sources("order_by=size")['objects']]
```

Number of instances in datasets created before April 1st, 2012 ordered by size

```
[dataset['rows'] for dataset in  
api.list_datasets("created__lt=2012-04-1;order_by=size")['objects']]
```

Model ids ordered by number of predictions (in descending order).

```
[model['resource'] for model in  
api.list_models("order_by=-number_of_predictions")['objects']]
```

Name of predictions ordered by name.

```
[prediction['name'] for prediction in  
api.list_predictions("order_by=name")['objects']]
```

Updating Resources

When you update a resource, it is returned in a dictionary exactly like the one you get when you create a new one. However the status code will be `bigml.api.HTTP_ACCEPTED` if the resource can be updated without problems or one of the HTTP standard error codes otherwise.

```
api.update_source(source, {"name": "new name"})
api.update_dataset(dataset, {"name": "new name"})
api.update_model(model, {"name": "new name"})
api.update_prediction(prediction, {"name": "new name"})
api.update_evaluation(evaluation, {"name": "new name"})
api.update_ensemble(ensemble, {"name": "new name"})
api.update_batch_prediction(batch_prediction, {"name": "new name"})
api.update_cluster(cluster, {"name": "new name"})
api.update_centroid(centroid, {"name": "new name"})
api.update_batch_centroid(batch_centroid, {"name": "new name"})
api.update_anomaly(anomaly, {"name": "new name"})
api.update_anomaly_score(anomaly_score, {"name": "new name"})
api.update_batch_anomaly_score(batch_anomaly_score, {"name": "new name"})
api.update_project(project, {"name": "new name"})
api.update_correlation(correlation, {"name": "new name"})
api.update_statistical_test(statistical_test, {"name": "new name"})
api.update_logistic_regression(logistic_regression, {"name": "new name"})
api.update_association(association, {"name": "new name"})
api.update_association_set(association_set, {"name": "new name"})
api.update_topic_model(topic_model, {"name": "new name"})
api.update_topic_distribution(topic_distribution, {"name": "new name"})
api.update_batch_topic_distribution(\
    batch_topic_distribution, {"name": "new name"})
api.update_script(script, {"name": "new name"})
api.update_library(library, {"name": "new name"})
api.update_execution(execution, {"name": "new name"})
```

Updates can change resource general properties, such as the name or description attributes of a dataset, or specific properties, like the missing tokens (strings considered as missing values). As an example, let's say that your source has a certain field whose contents are numeric integers. BigML will assign a numeric type to the field, but you might want it to be used as a categorical field. You could change its type to `categorical` by calling:

```
api.update_source(source, \
    {"fields": {"000001": {"optype": "categorical"}}})
```

where 000001 is the field id that corresponds to the updated field.

Another usually needed update is changing a fields' non-preferred attribute, so that it can be used in the modeling process:

```
api.update_dataset(dataset, {"fields": {"000001": {"preferred": True}}})
```

where you would be setting as preferred the field whose id is 000001.

You may also want to change the name of one of the clusters found in your clustering:

```
api.update_cluster(cluster, \
    {"clusters": {"000001": {"name": "my_cluster"}}})
```

which is changing the name of the cluster whose centroid id is 000001 to `my_cluster`. Or, similarly, changing the name of one detected topic:

```
api.update_topic_model(topic_model, \
    {"topics": {"000001": {"name": "my_topic"}}})
```

You will find detailed information about the updatable attributes of each resource in [BigML developer's documentation](#).

Deleting Resources

Resources can be deleted individually using the corresponding method for each type of resource.

```
api.delete_source(source)
api.delete_dataset(dataset)
api.delete_model(model)
api.delete_prediction(prediction)
api.delete_evaluation(evaluation)
api.delete_ensemble(ensemble)
api.delete_batch_prediction(batch_prediction)
api.delete_cluster(cluster)
api.delete_centroid(centroid)
api.delete_batch_centroid(batch_centroid)
api.delete_anomaly(anomaly)
api.delete_anomaly_score(anomaly_score)
api.delete_batch_anomaly_score(batch_anomaly_score)
api.delete_sample(sample)
api.delete_correlation(correlation)
api.delete_statistical_test(statistical_test)
api.delete_logistic_regression(logistic_regression)
api.delete_association(association)
api.delete_association_set(association_set)
api.delete_topic_model(topic_model)
api.delete_topic_distribution(topic_distribution)
api.delete_batch_topic_distribution(batch_topic_distribution)
api.delete_project(project)
api.delete_script(script)
api.delete_library(library)
api.delete_execution(execution)
```

Each of the calls above will return a dictionary with the following keys:

- **code** If the request is successful, the code will be a `bigml.api.HTTP_NO_CONTENT (204)` status code. Otherwise, it will be one of the standard HTTP error codes. See the [documentation on status codes](#) for more info.

- **error** If the request does not succeed, it will contain a dictionary with an error code and a message. It will be `None` otherwise.

Public and shared resources

The previous examples use resources that were created by the same user that asks for their retrieval or modification. If a user wants to share one of her resources, she can make them public or share them. Declaring a resource public means that anyone can see the resource. This can be applied to datasets and models. To turn a dataset public, just update its `private` property:

```
api.update_dataset('dataset/5143a51a37203f2cf7000972', {'private': false})
```

and any user will be able to download it using its id prepended by `public`:

```
api.get_dataset('public/dataset/5143a51a37203f2cf7000972')
```

In the models' case, you can also choose if you want the model to be fully downloadable or just accessible to make predictions. This is controlled with the `white_box` property. If you want to publish your model completely, just use:

```
api.update_model('model/5143a51a37203f2cf7000956', {'private': false,
                                                    'white_box': true})
```

Both public models and datasets, will be openly accessible for anyone, registered or not, from the web gallery.

Still, you may want to share your models with other users, but without making them public for everyone. This can be achieved by setting the `shared` property:

```
api.update_model('model/5143a51a37203f2cf7000956', {'shared': true})
```

Shared models can be accessed using their share hash (property `shared_hash` in the original model):

```
api.get_model('shared/model/d53iw39euTdjsgesj7382ufhwnD')
```

or by using their original id with the creator user as username and a specific sharing `api_key` you will find as property `sharing_api_key` in the updated model:

```
api.get_model('model/5143a51a37203f2cf7000956', shared_username='creator',
              shared_api_key='c972018dc5f2789e65c74ba3170fda31d02e00c3')
```

Only users with the share link or credentials information will be able to access your shared models.

Local Models

You can instantiate a local version of a remote model.

```
from bigml.model import Model
local_model = Model('model/502fdbff15526876610002615')
```

This will retrieve the remote model information, using an implicitly built `BigML()` connection object (see the Authentication section for more details on how to set your credentials) and return a `Model` object that you can use to make local predictions. If you want to use a specific connection object for the remote retrieval, you can set it as second parameter:

```
from bigml.model import Model
from bigml.api import BigML

local_model = Model('model/502fdbff15526876610002615',
                    api=BigML(my_username,
                               my_api_key))
```

or even use the remote model information previously retrieved to build the local model object:

```
from bigml.model import Model
from bigml.api import BigML
api = BigML()
model = api.get_model('model/502fdbff15526876610002615',
                     query_string='only_model=true;limit=-1')

local_model = Model(model)
```

As you can see, the `query_string` used to retrieve the model has two parts. They both act on the `fields` information that is added to the JSON response. First `only_model=true` is used to restrict the fields described in the `fields` structure of the response to those used as predictors in the model. Also `limit=-1` avoids the pagination of fields which is used by default and includes them all at once. These details are already taken care of in the two previous examples, where the model ID is used as argument.

Any of these methods will return a `Model` object that you can use to make local predictions, generate IF-THEN rules, Tableau rules or a Python function that implements the model.

You can also build a local model from a model previously retrieved and stored in a JSON file:

```
from bigml.model import Model
local_model = Model('./my_model.json')
```

Local Predictions

Once you have a local model you can use to generate predictions locally.

```
local_model.predict({"petal length": 3, "petal width": 1})
petal length > 2.45 AND petal width <= 1.65 AND petal length <= 4.95 =>
Iris-versicolor
```

Local predictions have three clear advantages:

- Removing the dependency from BigML to make new predictions.
- No cost (i.e., you do not spend BigML credits).
- Extremely low latency to generate predictions for huge volumes of data.

The default output for local predictions is the prediction itself, but you can also add the associated confidence, the distribution, and the number of instances in the final node by using some additional arguments. To obtain a dictionary with the prediction, confidence and rules:

```
local_model.predict({"petal length": 3, "petal width": 1},
                    add_confidence=True,
                    add_path=True)
```

that will return:

```
{'path': [u'petal length > 2.35',
          u'petal width <= 1.75',
          u'petal length <= 4.95',
          u'petal width <= 1.65'],
 'confidence': 0.91033,
 'prediction': 'Iris-versicolor'}
```

Note that the `add_path` argument for the `proportional` missing strategy shows the path leading to a final unique node, that gives the prediction, or to the first split where a missing value is found. Other options are `add_next` which includes the field that determines the next split after the prediction node and `add_distribution` that adds the distribution that leads to the prediction. For regression models, `add_min` and `add_max` will add the limit values for the data that supports the prediction.

In classification models, the prediction is always the most frequent category amongst the ones that form the distribution in the predicted node. However, you might want to get the complete list of the categories in the predicted node, together with their confidence. Using the `multiple` argument you will get the list of categories with their associated information.

```
local_model.predict({"petal length": 3}, multiple='all')
```

will result in

```
[{'count': 50,
  'confidence': 0.2628864565745068,
  'prediction': u'Iris-setosa',
  'probability': 0.3333333333333333},
 {'count': 50,
  'confidence': 0.2628864565745068,
  'prediction': u'Iris-versicolor',
  'probability': 0.3333333333333333},
 {'count': 50,
  'confidence': 0.2628864565745068,
  'prediction': u'Iris-virginica',
  'probability': 0.3333333333333333}]
```

The argument can be set to `all` to obtain the complete list or to an integer ‘`n`’, in which case you will obtain the top `n` predictions. **Note importantly that the `multiple` argument is scheduled for deprecation in a future version. Similar functionality is available using the `predict_probability` and `predict_confidence` functions described below.**

When your test data has missing values, you can choose between `last prediction` or `proportional` strategy to compute the prediction. The `last prediction` strategy is the one used by default. To compute a prediction, the algorithm goes down the model’s decision tree and checks the condition it finds at each node (e.g.: ‘sepal length’ > 2). If the field checked is missing in your input data you have two options: by default (`last prediction` strategy) the algorithm will stop and issue the last prediction it computed in the previous node. If you chose `proportional` strategy instead, the algorithm will continue to go down the tree considering both branches from that node on. Thus, it will store a list of possible predictions from then on, one per valid node. In this case, the final prediction will be the majority (for categorical models) or the average (for regressions) of values predicted by the list of predicted values.

You can set this strategy by using the `missing_strategy` argument with code 0 to use `last prediction` and 1 for `proportional`.

```
from bigml.model import LAST_PREDICTION, PROPORTIONAL
# LAST_PREDICTION = 0; PROPORTIONAL = 1
local_model.predict({"petal length": 3, "petal width": 1},
                    missing_strategy=PROPORTIONAL)
```

For classification models, it is sometimes useful to obtain a probability or confidence prediction for each possible class of the objective field. To do this, you can use the `predict_probability` and `predict_confidence` methods respectively. The former gives a prediction based on the distribution of instances at the appropriate leaf node, with a Laplace correction based on the root node distribution. The latter returns a lower confidence bound on the leaf node probability based on the Wilson score interval.

Each of these methods take the `by_name` and `missing_strategy` arguments that function as they do in `predict`, and one additional argument, `compact`. If `compact` is `False` (the default), the output of these functions is a list of maps, each with the keys `prediction` and `probability` (or `confidence`) mapped to the class name and its associated probability (or confidence).

So, for example, the following:

```
local_model.predict_probability({"petal length": 3})
```

would result in

```
[{'prediction': u'Iris-setosa',  
  'probability': 0.0033003300330033},  
 {'prediction': u'Iris-versicolor',  
  'probability': 0.4983498349834984},  
 {'prediction': u'Iris-virginica',  
  'probability': 0.4983498349834984}]
```

If `compact` is `True`, only the probabilities themselves are returned, as a list in class name order. Note that, for reference, the attribute `Model.class_names` contains the class names in the appropriate ordering.

To illustrate, the following:

```
local_model.predict_probability({"petal length": 3}, compact=True)
```

would result in

```
[0.0033003300330033, 0.4983498349834984, 0.4983498349834984]
```

The output of `predict_confidence` is the same, except that the output maps are keyed with `confidence` instead of `probability`.

Local Clusters

You can also instantiate a local version of a remote cluster.

```
from bigml.cluster import Cluster
local_cluster = Cluster('cluster/502fdbff15526876610002435')
```

This will retrieve the remote cluster information, using an implicitly built `BigML()` connection object (see the [Authentication](#) section for more details on how to set your credentials) and return a `Cluster` object that you can use to make local centroid predictions. If you want to use a specific connection object for the remote retrieval, you can set it as second parameter:

```
from bigml.cluster import Cluster
from bigml.api import BigML

local_cluster = Cluster('cluster/502fdbff15526876610002435',
                        api=BigML(my_username,
                                  my_api_key))
```

or even use the remote cluster information previously retrieved to build the local cluster object:

```
from bigml.cluster import Cluster
from bigml.api import BigML
api = BigML()
cluster = api.get_cluster('cluster/502fdbff15526876610002435',
                          query_string='limit=-1')

local_cluster = Cluster(cluster)
```

Note that in this example we used a `limit=-1` query string for the cluster retrieval. This ensures that all fields are retrieved by the `get` method in the same call (unlike in the standard calls where the number of fields returned is limited).

Local clusters provide also methods for the significant operations that can be done using clusters: finding the centroid assigned to a certain data point, sorting centroids according to their distance to a data point, summarizing the centroids intra-distances and inter-distances and also finding the closest points to a given one. The *Local Centroids* and *Summary generation* sections will explain these methods.

Local Centroids

Using the local cluster object, you can predict the centroid associated to an input data set:

```
local_cluster.centroid({"pregnancies": 0, "plasma glucose": 118,
                       "blood pressure": 84, "triceps skin thickness": 47,
                       "insulin": 230, "bmi": 45.8,
                       "diabetes pedigree": 0.551, "age": 31,
                       "diabetes": "true"})
{'distance': 0.454110207355, 'centroid_name': 'Cluster 4',
 'centroid_id': '000004'}
```

You must keep in mind, though, that to obtain a centroid prediction, input data must have values for all the numeric fields. No missing values for the numeric fields are allowed unless you provided a `default_numeric_value` in the cluster construction configuration. If so, this value will be used to fill the missing numeric fields.

As in the local model predictions, producing local centroids can be done independently of BigML servers, so no cost or connection latencies are involved.

Another interesting method in the cluster object is `local_cluster.closests_in_cluster`, which given a reference data point will provide the rest of points that fall into the same cluster sorted in an ascending order according to their distance to this point. You can limit the maximum number of points returned by setting the `number_of_points` argument to any positive integer.

```
local_cluster.closests_in_cluster( \
    {"pregnancies": 0, "plasma glucose": 118,
     "blood pressure": 84, "triceps skin thickness": 47,
     "insulin": 230, "bmi": 45.8,
     "diabetes pedigree": 0.551, "age": 31,
     "diabetes": "true"}, number_of_points=2)
```

The response will be a dictionary with the centroid id of the cluster and the list of closest points and their distances to the reference point.

```
{'closest': [ \
    {'distance': 0.06912270988567025,
     'data': {'plasma glucose': '115', 'blood pressure': '70',
```

```

        'triceps skin thickness': '30', 'pregnancies': '1',
        'bmi': '34.6', 'diabetes pedigree': '0.529',
        'insulin': '96', 'age': '32', 'diabetes': 'true'}},
    {'distance': 0.10396456577958413,
     'data': {'plasma glucose': '167', 'blood pressure': '74',
              'triceps skin thickness': '17', 'pregnancies': '1', 'bmi': '23.4',
              'diabetes pedigree': '0.447', 'insulin': '144', 'age': '33',
              'diabetes': 'true'}}],
  'reference': {'age': 31, 'bmi': 45.8, 'plasma glucose': 118,
               'insulin': 230, 'blood pressure': 84,
               'pregnancies': 0, 'triceps skin thickness': 47,
               'diabetes pedigree': 0.551, 'diabetes': 'true'},
  'centroid_id': u'000000'}

```

No missing numeric values are allowed either in the reference data point. If you want the data points to belong to a different cluster, you can provide the `centroid_id` for the cluster as an additional argument.

Other utility methods are `local_cluster.sorted_centroids` which given a reference data point will provide the list of centroids sorted according to the distance to it

```

local_cluster.sorted_centroids( \
{'plasma glucose': '115', 'blood pressure': '70',
 'triceps skin thickness': '30', 'pregnancies': '1',
 'bmi': '34.6', 'diabetes pedigree': '0.529',
 'insulin': '96', 'age': '32', 'diabetes': 'true'})
{'centroids': [{'distance': 0.31656890408929705,
                'data': {u'000006': 0.34571, u'000007': 30.7619,
                        u'000000': 3.79592, u'000008': u'false'},
                'centroid_id': u'000000'},
               {'distance': 0.4424198506958207,
                'data': {u'000006': 0.77087, u'000007': 45.50943,
                        u'000000': 5.90566, u'000008': u'true'},
                'centroid_id': u'000001'}],
 'reference': {'age': '32', 'bmi': '34.6', 'plasma glucose': '115',
               'insulin': '96', 'blood pressure': '70',
               'pregnancies': '1', 'triceps skin thickness': '30',
               'diabetes pedigree': '0.529', 'diabetes': 'true'}}

```

or `points_in_cluster` that returns the list of data points assigned to a certain cluster, given its `centroid_id`.

```

centroid_id = "000000"
local_cluster.points_in_cluster(centroid_id)

```

Local Anomaly Detector

You can also instantiate a local version of a remote anomaly.

```
from bigml.anomaly import Anomaly
local_anomaly = Anomaly('anomaly/502fcbff15526876610002435')
```

This will retrieve the remote anomaly detector information, using an implicitly built `BigML()` connection object (see the `Authentication` section for more details on how to set your credentials) and return an `Anomaly` object that you can use to make local anomaly scores. If you want to use a specific connection object for the remote retrieval, you can set it as second parameter:

```
from bigml.anomaly import Anomaly
from bigml.api import BigML

local_anomaly = Anomaly('anomaly/502fcbff15526876610002435',
                        api=BigML(my_username,
                                  my_api_key))
```

or even use the remote anomaly information retrieved previously to build the local anomaly detector object:

```
from bigml.anomaly import Anomaly
from bigml.api import BigML
api = BigML()
anomaly = api.get_anomaly('anomaly/502fcbff15526876610002435',
                          query_string='limit=-1')

local_anomaly = Anomaly(anomaly)
```

Note that in this example we used a `limit=-1` query string for the anomaly retrieval. This ensures that all fields are retrieved by the `get` method in the same call (unlike in the standard calls where the number of fields returned is limited).

The anomaly detector object has also the method `anomalies_filter` that will build the LISP filter you would need to filter the original dataset and create a new one excluding the top anomalies. Setting the `include` parameter to `True` you can do the inverse and create a dataset with only the most anomalous data points.

Local Anomaly Scores

Using the local anomaly detector object, you can predict the anomaly score associated to an input data set:

```
local_anomaly.anomaly_score({"src_bytes": 350})  
0.9268527808726705
```

As in the local model predictions, producing local anomaly scores can be done independently of BigML servers, so no cost or connection latencies are involved.

Local Logistic Regression

You can also instantiate a local version of a remote logistic regression.

```
from bigml.logistic import LogisticRegression
local_log_regression = LogisticRegression(
    'logisticregression/502fdbff15526876610042435')
```

This will retrieve the remote logistic regression information, using an implicitly built `BigML()` connection object (see the Authentication section for more details on how to set your credentials) and return a `LogisticRegression` object that you can use to make local predictions. If you want to use a specific connection object for the remote retrieval, you can set it as second parameter:

```
from bigml.logistic import LogisticRegression
from bigml.api import BigML

local_log_regression = LogisticRegression(
    'logisticregression/502fdbff15526876610602435',
    api=BigML(my_username, my_api_key))
```

You can also reuse a remote logistic regression JSON structure as previously retrieved to build the local logistic regression object:

```
from bigml.logistic import LogisticRegression
from bigml.api import BigML
api = BigML()
logistic_regression = api.get_logistic_regression(
    'logisticregression/502fdbff15526876610002435',
    query_string='limit=-1')

local_log_regression = LogisticRegression(logistic_regression)
```

Note that in this example we used a `limit=-1` query string for the logistic regression retrieval. This ensures that all fields are retrieved by the `get` method in the same call (unlike in the standard calls where the number of fields returned is limited).

Local Logistic Regression Predictions

Using the local logistic regression object, you can predict the prediction for an input data set:

```
local_log_regression.predict({"petal length": 2, "sepal length": 1.5,
                             "petal width": 0.5, "sepal width": 0.7})
{'distribution': [
  {'category': u'Iris-virginica', 'probability': 0.5041444478857267},
  {'category': u'Iris-versicolor', 'probability': 0.46926542042788333},
  {'category': u'Iris-setosa', 'probability': 0.02659013168639014}],
 'prediction': u'Iris-virginica', 'probability': 0.5041444478857267}
```

As you can see, the prediction contains the predicted category and the associated probability. It also shows the distribution of probabilities for all the possible categories in the objective field.

You must keep in mind, though, that to obtain a logistic regression prediction, input data must have values for all the numeric fields. No missing values for the numeric fields are allowed.

For consistency of interface with the `Model` class, logistic regressions again have a `predict_probability` method, which takes two of the same arguments as `Model.predict`: `by_name` and `compact`. As stated above, missing values are not allowed, and so there is no `missing_strategy` argument.

As with local Models, if `compact` is `False` (the default), the output is a list of maps, each with the keys `prediction` and `probability` mapped to the class name and its associated probability.

So, for example

```
local_log_regression.predict_probability({"petal length": 2, "sepal length": 1.5,
                                         "petal width": 0.5, "sepal width": 0.7})

[{'prediction': u'Iris-setosa', 'probability': 0.02659013168639014},
 {'prediction': u'Iris-versicolor', 'probability': 0.46926542042788333},
 {'prediction': u'Iris-virginica', 'probability': 0.5041444478857267}]
```

If `compact` is `True`, only the probabilities themselves are returned, as a list in class name order, again, as is the case with local Models.

Local Association

You can also instantiate a local version of a remote association resource.

```
from bigml.association import Association
local_association = Association('association/502fdcff15526876610002435')
```

This will retrieve the remote association information, using an implicitly built `BigML()` connection object (see the Authentication section for more details on how to set your credentials) and return an `Association` object that you can use to extract the rules found in the original dataset. If you want to use a specific connection object for the remote retrieval, you can set it as second parameter:

```
from bigml.association import Association
from bigml.api import BigML

local_association = Association('association/502fdcff15526876610002435',
                               api=BigML(my_username,
                                          my_api_key))
```

or even use the remote association information retrieved previously to build the local association object:

```
from bigml.association import Association
from bigml.api import BigML
api = BigML()
association = api.get_association('association/502fdcff15526876610002435',
                                 query_string='limit=-1')

local_association = Association(association)
```

Note that in this example we used a `limit=-1` query string for the association retrieval. This ensures that all fields are retrieved by the `get` method in the same call (unlike in the standard calls where the number of fields returned is limited).

The created `Association` object has some methods to help retrieving the association rules found in the original data. The `get_rules` method will return the association rules. Arguments can be set to filter the rules returned according to its leverage, strength, support, `p_value`, a list of items involved in the rule or a user-given filter function.

```
from bigml.association import Association
local_association = Association('association/502fdcff15526876610002435')
local_association.get_rules(item_list=["Edible"], min_p_value=0.3)
```

In this example, the only rules that will be returned by the `get_rules` method will be the ones that mention `Edible` and their `p_value` is greater or equal to `0.3`.

The rules can also be stored in a CSV file using `rules_CSV`:

```
from bigml.association import Association
local_association = Association('association/502fdcff15526876610002435')
local_association.rules_CSV(file_name='/tmp/my_rules.csv',
                             min_strength=0.1)
```

This example will store the rules whose strength is bigger or equal to `0.1` in the `/tmp/my_rules.csv` file.

You can also obtain the list of items parsed in the dataset using the `get_items` method. You can also filter the results by field name, by item names and by a user-given function:

```
from bigml.association import Association
local_association = Association('association/502fdcff15526876610002435')
local_association.get_items(field="Cap Color",
                             names=["Brown cap", "White cap", "Yellow cap"])
```

This will recover the `Item` objects found in the `Cap Color` field for the names in the list, with their properties as described in the [developers section](#)

Local Association Sets

Using the local association object, you can predict the association sets related to an input data set:

```
local_association.association_set( \
    {"gender": "Female", "genres": "Adventure$Action", \
     "timestamp": 993906291, "occupation": "K-12 student", \
     "zipcode": 59583, "rating": 3})
[{'item': {'complement': False,
           'count': 70,
           'field_id': u'000002',
           'name': u'Under 18'},
  'rules': ['000000'],
  'score': 0.0969181441561211},
 {'item': {'complement': False,
           'count': 216,
           'field_id': u'000007',
           'name': u'Drama'},
  'score': 0.0250501115102862636},
 {'item': {'complement': False,
           'count': 108,
           'field_id': u'000007',
           'name': u'Sci-Fi'},
  'rules': ['000003'],
  'score': 0.02384578264599424},
 {'item': {'complement': False,
           'count': 40,
           'field_id': u'000002',
           'name': u'56+'},
  'rules': ['000008',
           '000020'],
  'score': 0.021845366022721312},
 {'item': {'complement': False,
           'count': 66,
           'field_id': u'000002',
           'name': u'45-49'},
  'rules': ['00000e'],
```

```
'score': 0.019657155185835006}]
```

As in the local model predictions, producing local association sets can be done independently of BigML servers, so no cost or connection latencies are involved.

Local Topic Model

You can also instantiate a local version of a remote topic model.

```
from bigml.topicmodel import TopicModel
local_topic_model = TopicModel(
    'topicmodel/502fdbcf15526876210042435')
```

This will retrieve the remote topic model information, using an implicitly built `BigML()` connection object (see the Authentication section for more details on how to set your credentials) and return a `TopicModel` object that you can use to obtain local topic distributions. If you want to use a specific connection object for the remote retrieval, you can set it as second parameter:

```
from bigml.topicmodel import TopicModel
from bigml.api import BigML

local_topic_model = TopicModel(
    'topicmodel/502fdbcf15526876210042435',
    api=BigML(my_username, my_api_key))
```

You can also reuse a remote topic model JSON structure as previously retrieved to build the local topic model object:

```
from bigml.topicmodel import TopicModel
from bigml.api import BigML
api = BigML()
topic_model = api.get_topic_model(
    'topicmodel/502fdbcf15526876210042435',
    query_string='limit=-1')

local_topic_model = TopicModel(topic_model)
```

Note that in this example we used a `limit=-1` query string for the topic model retrieval. This ensures that all fields are retrieved by the get method in the same call (unlike in the standard calls where the number of fields returned is limited).

Local Topic Distributions

Using the local topic model object, you can predict the local topic distribution for an input data set:

```
local_topic_model.distribution({"Message": "Our mobile phone is free"})
[  { 'name': u'Topic 00', 'probability': 0.002627154266498529},
    { 'name': u'Topic 01', 'probability': 0.003257671290458176},
    { 'name': u'Topic 02', 'probability': 0.002627154266498529},
    { 'name': u'Topic 03', 'probability': 0.1968263976460698},
    { 'name': u'Topic 04', 'probability': 0.002627154266498529},
    { 'name': u'Topic 05', 'probability': 0.002627154266498529},
    { 'name': u'Topic 06', 'probability': 0.13692728036990331},
    { 'name': u'Topic 07', 'probability': 0.6419714165615805},
    { 'name': u'Topic 08', 'probability': 0.002627154266498529},
    { 'name': u'Topic 09', 'probability': 0.002627154266498529},
    { 'name': u'Topic 10', 'probability': 0.002627154266498529},
    { 'name': u'Topic 11', 'probability': 0.002627154266498529}]
```

As you can see, the topic distribution contains the name of the possible topics in the model and the associated probabilities.

Multi Models

Multi Models use a numbers of BigML remote models to build a local version that can be used to generate predictions locally. Predictions are generated combining the outputs of each model.

```
from bigml.api import BigML
from bigml.multimodel import MultiModel

api = BigML()

model = MultiModel([api.get_model(model['resource']) for model in
                    api.list_models(query_string="tags__in=my_tag")
                    ['objects']])

model.predict({"petal length": 3, "petal width": 1})
```

This will create a multi model using all the models that have been previously tagged with `my_tag` and predict by combining each model's prediction. The combination method used by default is `plurality` for categorical predictions and mean value for numerical ones. You can also use `confidence weighted`:

```
model.predict({"petal length": 3, "petal width": 1}, method=1)
```

that will weight each vote using the confidence/error given by the model to each prediction, or even `probability weighted`:

```
model.predict({"petal length": 3, "petal width": 1}, method=2)
```

that weights each vote by using the probability associated to the training distribution at the prediction node.

There's also a `threshold` method that uses an additional set of options: `threshold` and `category`. The category is predicted if and only if the number of predictions for that category is at least the threshold value. Otherwise, the prediction is `plurality` for the rest of predicted values.

An example of `threshold` combination method would be:

```
model.predict({'petal length': 0.9, 'petal width': 3.0}, method=3,
            options={'threshold': 3, 'category': 'Iris-virginica'})
```

When making predictions on a test set with a large number of models, `batch_predict` can be useful to log each model's predictions in a separated file. It expects a list of input data values and the directory path to save the prediction files in.

```
model.batch_predict([{"petal length": 3, "petal width": 1},
                    {"petal length": 1, "petal width": 5.1}],
                  "data/predictions")
```

The predictions generated for each model will be stored in an output file in `data/predictions` using the syntax `model_[id of the model]_predictions.csv`. For instance, when using `model/50c0de043b563519830001c2` to predict, the output file name will be `model_50c0de043b563519830001c2_predictions.csv`. An additional feature is that using `reuse=True` as argument will force the function to skip the creation of the file if it already exists. This can be helpful when using repeatedly a bunch of models on the same test set.

```
model.batch_predict([{"petal length": 3, "petal width": 1},
                    {"petal length": 1, "petal width": 5.1}],
                  "data/predictions", reuse=True)
```

Prediction files can be subsequently retrieved and converted into a votes list using `batch_votes`:

```
model.batch_votes("data/predictions")
```

which will return a list of `MultiVote` objects. Each `MultiVote` contains a list of predictions (e.g. `[{'prediction': u'Iris-versicolor', 'confidence': 0.34, 'order': 0}, {'prediction': u'Iris-setosa', 'confidence': 0.25, 'order': 1}]`). These votes can be further combined to issue a final prediction for each input data element using the method `combine`

```
for multivote in model.batch_votes("data/predictions"):
    prediction = multivote.combine()
```

Again, the default method of combination is `plurality` for categorical predictions and `mean value` for numerical ones. You can also use `confidence weighted`:

```
prediction = multivote.combine(1)
```

or `probability weighted`:

```
prediction = multivote.combine(2)
```

You can also get a confidence measure for the combined prediction:

```
prediction = multivote.combine(0, with_confidence=True)
```

For classification, the confidence associated to the combined prediction is derived by first selecting the model's predictions that voted for the resulting prediction and computing the weighted average of their individual confidence. Nevertheless, when `probability weighted` is used, the confidence is obtained by using each model's distribution at the prediction node to build a probability distribution and combining them. The confidence is then computed as the wilson score interval of the combined distribution (using as total number of instances the sum of all the model's distributions original instances at the prediction node)

In regression, all the models predictions' confidences contribute to the weighted average confidence.

Local Ensembles

Remote ensembles can also be used locally through the `Ensemble` class. The simplest way to access an existing ensemble and using it to predict locally is:

```
from bigml.ensemble import Ensemble
ensemble = Ensemble('ensemble/5143a51a37203f2cf7020351')
ensemble.predict({"petal length": 3, "petal width": 1})
```

This call will download all the ensemble related info and store it in a `./storage` directory ready to be used to predict, but you can choose another storage directory or even avoid storing at all.

The local ensemble object can be used to manage the three types of ensembles: Decision Forests (bagging or random) and the ones using Boosted Trees. However, arguments like the predictions combiner (method argument) will only apply to Decision Forests. As in `MultipleModel`, several prediction combination methods are available, for instance:

```
from bigml.api import BigML
from bigml.ensemble import Ensemble

# api connection using a user-selected storage
api = BigML(storage='./my_storage')

# creating ensemble
ensemble = api.create_ensemble('dataset/5143a51a37203f2cf7000972')

# Ensemble object to predict
ensemble = Ensemble(ensemble, api)
ensemble.predict({"petal length": 3, "petal width": 1}, method=1)
```

creates a new ensemble and stores its information in `./my_storage` folder. Then this information is used to predict locally using the confidence weighted method.

Similarly, local ensembles can also be created by giving a list of models to be combined to issue the final prediction (note: only random decision forests and bagging ensembles can be built using this method):

```
from bigml.ensemble import Ensemble
ensemble = Ensemble(['model/50c0de043b563519830001c2', \
                    'model/50c0de043b5635198300031b'])
ensemble.predict({"petal length": 3, "petal width": 1})
```

or even a JSON file that contains the ensemble resource:

```
import json
from bigml.ensemble import Ensemble
from bigml.api import BigML
api = api.BigML()
ensemble_info = api.get_ensemble('ensemble/50c0de043b5635198300033c')
with open("./my_ensemble", "w") as ensemble_file:
    ensemble_file.write(json.dumps(ensemble_info))
local_ensemble = Ensemble("./my_ensemble")
```

Note: the ensemble JSON structure is not self-contained, meaning that it contains references to the models that the ensemble is build of, but not the information of the models themselves. To use an ensemble locally with no connection to the internet, you must make sure that not only a local copy of the ensemble JSON file is available in your computer, but also the JSON files corresponding to the models in it. This is automatically achieved when you use the `Ensemble('ensemble/50c0de043b5635198300033c')` constructor, that fetches all the related JSON files and stores them in an `./storage` directory. Next calls to `Ensemble('ensemble/50c0de043b5635198300033c')` will retrieve the files from this local storage, so that internet connection will only be needed the first time an `Ensemble` is built.

On the contrary, if you have no memory limitations and want to increase prediction speed, you can create the ensemble from a list of local model objects. Then, local model objects will only be instantiated once, and this could increase performance for large ensembles:

```
from bigml.model import Model
model_ids = ['model/50c0de043b563519830001c2', \
            'model/50c0de043b5635198300031b']
local_models = [Model(model_id) for model_id in model_ids]
local_ensemble = Ensemble(local_models)
```

The `Ensemble` object can also be instantiated using local models previously stored in disks or memory object caching systems. To retrieve these models provide a list of model ids as first argument and an extra argument named `cache_get` that should be a function receiving the model id to be retrieved and returning a local model object.

```
from bigml.model import Model
model_ids = ['model/50c0de043b563519830001c2', \
            'model/50c0de043b5635198300031b']
def cache_get(model_id):
    """ Retrieves a JSON model structure and builds a local model object

    """
    model_file = model_id.replace("/", "_")
    return Model(json.load(open(model_file)))
local_ensemble = Ensemble(model_ids, cache_get=cache_get)
```

Local Ensemble's Predictions

As in the local model's case, you can use the local ensemble to create new predictions for your test data, and set some arguments to configure the final output of the `predict` method.

The predictions' structure will vary depending on the kind of ensemble used. For `Decision Forests` local predictions will just contain the ensemble's final prediction if no other argument is used. You can add the confidence to it by setting the `with_confidence` argument to `True`.

```
from bigml.ensemble import Ensemble
ensemble = Ensemble('ensemble/5143a51a37203f2cf7020351')
ensemble.predict({"petal length": 3, "petal width": 1}, \
                with_confidence=True)
(u'Iris-versicolor', 0.91519)
```

And you can add more information to the predictions in a JSON format using:

- `add_confidence=True` includes the confidence of the prediction
- **`add_distribution=True` includes the distribution of predictions. This is** built by merging the distributions of each of the nodes predicted by every model the ensemble is composed of
- **`add_count=True` includes the sum of instances of the nodes predicted by** every model the ensemble is composed of
- **`add_median=True` for regression ensembles, it computes the prediction** based on the median (instead of the usual mean)
- **`add_min=True` adds the minimum value in the prediction's** distribution (for regressions only)
- **`add_max=True` adds the maximum value in the prediction's** distribution (for regressions only)

```
from bigml.ensemble import Ensemble
ensemble = Ensemble('ensemble/5143a51a37203f2cf7020351')
ensemble.predict({"petal length": 3, "petal width": 1}, \
                add_confidence=True, add_distribution=True)
{'distribution': [[u'Iris-versicolor', 84]],
 'confidence': 0.91519,
```

```
'prediction': u'Iris-versicolor',  
'distribution_unit': 'counts'}
```

However, Boosted Trees don't have an associated confidence measure, so only the prediction will be obtained when applied to regressions. In classifications, adding the `add_probability` or `with_probability` argument will also provide the probability of the prediction.

For consistency of interface with the `Model` class, as well as between boosted and non-boosted ensembles, local Ensembles again have a `predict_probability` method. This takes the same optional arguments as `Model.predict`: `by_name`, `missing_strategy` and `compact`, as well as a fourth optional argument, `method`, which describes whether or not the probabilities are a function of the raw model votes (`method=0`), the confidence-weighted votes (`method=1`) or the averaged probabilities of each individual model prediction (`method=2`).

As with local Models, if `compact` is `False` (the default), the output is a list of maps, each with the keys `prediction` and `probability` mapped to the class name and its associated probability.

So, for example:

```
ensemble.predict_probability({"petal length": 3, "petal width": 1})  
  
[{'prediction': u'Iris-setosa', 'probability': 0.006733220044732548},  
 {'prediction': u'Iris-versicolor', 'probability': 0.9824478534614787},  
 {'prediction': u'Iris-virginica', 'probability': 0.0108189264937886}]  
  
ensemble.predict_probability({"petal length": 3, "petal width": 1}, \  
                             method=0)  
  
[{'prediction': u'Iris-setosa', 'probability': 0.0},  
 {'prediction': u'Iris-versicolor', 'probability': 1.0},  
 {'prediction': u'Iris-virginica', 'probability': 0.0}]
```

If `compact` is `True`, only the probabilities themselves are returned, as a list in class name order, again, as is the case with local Models.

Once you have a resource, you can use the `Fields` class to generate a representation that will allow you to easily list fields, get fields ids, get a field id by name, column number, etc.

```
from bigml.api import BigML
from bigml.fields import Fields
api = BigML()
source = api.get_source("source/5143a51a37203f2cf7000974")

fields = Fields(source)
```

you can also instantiate the `Fields` object from the fields dict itself:

```
from bigml.api import BigML
from bigml.fields import Fields
api = BigML()
source = api.get_source("source/5143a51a37203f2cf7000974")

fields = Fields(source['object']['fields'])
```

The newly instantiated `Fields` object will give direct methods to retrieve different fields properties:

```
# Internal id of the 'sepal length' field
fields.field_id('sepal length')

# Field name of field with column number 0
fields.field_name(0)

# Column number of field name 'petal length'
fields.field_column_number('petal length')

# Statistics of values in field name 'petal length'
fields.stats('petal length')
```

Depending on the resource type, `Fields` information will vary. Sources will have only the name, label, description, type of field (`optype`) while dataset resources will have also the `preferred` (whether a field will is selectable as

predictor), `missing_count`, `errors` and a summary of the values found in each field. This is due to the fact that the `source` object is built by inspecting the contents of a sample of the uploaded file, while the `dataset` resource really reads all the uploaded information. Thus, `dataset`'s fields structure will always be more complete than `source`'s.

In both cases, you can extract the summarized information available using the `summary_csv` method:

```
from bigml.api import BigML
from bigml.fields import Fields
api = BigML()
dataset = api.get_dataset("dataset/5143a51a37203f2cf7300974")

fields = Fields(dataset)
fields.summary_csv("my_fields_summary.csv")
```

In this example, the information will be stored in the `my_fields_summary.csv` file. For the typical `iris.csv` data file, the summary will read:

field column	field ID	field name	field label	field description	field type	preferred	missing count	errors	contents summary	errors summary
0	000000	sepal length			numeric	true	0	0	[4.3, 7.9], mean: 5.84333	
1	000000	sepal width			numeric	false	0	0	[2, 4.4], mean: 3.05733	
2	000000	petal length			numeric	true	0	0	[1, 6.9], mean: 3.758	
3	000000	petal width			numeric	true	0	0	[0.1, 2.5], mean: 1.19933	
4	000000	species			categorical	true	0	0	3 categories: Iris-setosa (50), Iris-versicolor (50), Iris-virginica (50)	

Another utility in the `Fields` object will help you update the updatable attributes of your source or dataset fields. For instance, if you need to update the type associated to one field in your dataset, you can change the `field type` values in the previous file and use it to obtain the fields structure needed to update your source:

```
from bigml.api import BigML
from bigml.fields import Fields
api = BigML()
source = api.get_source("source/5143a51a37203f2cf7000974")

fields = Fields(source)
fields_update_info = fields.new_fields_structure("my_fields_summary.csv")
source = api.update_source(source, fields_update_info)
```

For both sources and datasets, the updatable attributes are name, label and description. In sources you can also update the type of the field, and in datasets you can update the preferred attribute.

In addition to that, you can also easily pair a list of values with fields ids what is very useful to make predictions.

For example, the following snippet may be useful to create local predictions using a csv file as input:

```
test_reader = csv.reader(open(dir + test_set))
local_model = Model(model)
for row in test_reader:
```

```
input_data = fields.pair([float(val) for val in row], objective_field)
prediction = local_model.predict(input_data, by_name=False)
```

If missing values are present, the `Fields` object can return a dict with the ids of the fields that contain missing values and its count. The following example:

```
from bigml.fields import Fields
from bigml.api import BigML
api = BigML()
dataset = api.get_dataset("dataset/5339d42337203f233e000015")

fields = Fields(dataset)
fields.missing_counts()
```

would output:

```
{'000003': 1, '000000': 1, '000001': 1}
```

if there was a missing value in each of the fields whose ids are 000003, 000000, 000001.

You can also obtain the counts of errors per field using the `errors_count` method of the api:

```
from bigml.api import BigML
api = BigML()
dataset = api.get_dataset("dataset/5339d42337203f233e000015")
api.error_counts(dataset)
```

The generated output is like the one in `missing_counts`, that is, the error counts per field:

```
{'000000': 1}
```


You can also use a local model to generate a IF-THEN rule set that can be very helpful to understand how the model works internally.

```
local_model.rules()
IF petal_length > 2.45 AND
  IF petal_width > 1.65 AND
    IF petal_length > 5.05 THEN
      species = Iris-virginica
    IF petal_length <= 5.05 AND
      IF sepal_width > 2.9 AND
        IF sepal_length > 5.95 AND
          IF petal_length > 4.95 THEN
            species = Iris-versicolor
          IF petal_length <= 4.95 THEN
            species = Iris-virginica
        IF sepal_length <= 5.95 THEN
          species = Iris-versicolor
      IF sepal_width <= 2.9 THEN
        species = Iris-virginica
  IF petal_width <= 1.65 AND
    IF petal_length > 4.95 AND
      IF sepal_length > 6.05 THEN
        species = Iris-virginica
      IF sepal_length <= 6.05 AND
        IF sepal_width > 2.45 THEN
          species = Iris-versicolor
        IF sepal_width <= 2.45 THEN
          species = Iris-virginica
    IF petal_length <= 4.95 THEN
      species = Iris-versicolor
IF petal_length <= 2.45 THEN
  species = Iris-setosa
```

Python, Tableau and Hadoop-ready Generation

If you prefer, you can also generate a Python function that implements the model and that can be useful to make the model actionable right away with `local_model.python()`.

```
local_model.python()
def predict_species(sepal_length=None,
                   sepal_width=None,
                   petal_length=None,
                   petal_width=None):
    """ Predictor for species from model/50a8e2d9eabcb404d2000293

        Predictive model by BigML - Machine Learning Made Easy
    """
    if (petal_length is None):
        return 'Iris-virginica'
    if (petal_length <= 2.45):
        return 'Iris-setosa'
    if (petal_length > 2.45):
        if (petal_width is None):
            return 'Iris-virginica'
        if (petal_width <= 1.65):
            if (petal_length <= 4.95):
                return 'Iris-versicolor'
            if (petal_length > 4.95):
                if (sepal_length is None):
                    return 'Iris-virginica'
                if (sepal_length <= 6.05):
                    if (petal_width <= 1.55):
                        return 'Iris-virginica'
                    if (petal_width > 1.55):
                        return 'Iris-versicolor'
                if (sepal_length > 6.05):
                    return 'Iris-virginica'
        if (petal_width > 1.65):
            if (petal_length <= 5.05):
                if (sepal_width is None):
```

```

        return 'Iris-virginica'
    if (sepal_width <= 2.9):
        return 'Iris-virginica'
    if (sepal_width > 2.9):
        if (sepal_length is None):
            return 'Iris-virginica'
        if (sepal_length <= 6.4):
            if (sepal_length <= 5.95):
                return 'Iris-versicolor'
            if (sepal_length > 5.95):
                return 'Iris-virginica'
        if (sepal_length > 6.4):
            return 'Iris-versicolor'
    if (petal_length > 5.05):
        return 'Iris-virginica'

```

The `local.python(hadoop=True)` call will generate the code that you need for the Hadoop map-reduce engine to produce batch predictions using [Hadoop streaming](#) . Saving the mapper and reducer generated functions in their corresponding files (let's say `/home/hduser/hadoop_mapper.py` and `/home/hduser/hadoop_reducer.py`) you can start a Hadoop job to generate predictions by issuing the following Hadoop command in your system console:

```

bin/hadoop jar contrib/streaming/hadoop-*streaming*.jar \
-file /home/hduser/hadoop_mapper.py -mapper hadoop_mapper.py \
-file /home/hduser/hadoop_reducer.py -reducer hadoop_reducer.py \
-input /home/hduser/hadoop/input.csv \
-output /home/hduser/hadoop/output_dir

```

assuming you are in the Hadoop home directory, your input file is in the corresponding dfs directory (`/home/hduser/hadoop/input.csv` in this example) and the output will be placed at `/home/hduser/hadoop/output_dir` (inside the dfs directory).

Tableau-ready rules are also available through `local_model.tableau()` for all the models except those that use text predictors.

```

local_model.tableau()
IF ISNULL([petal width]) THEN 'Iris-virginica'
ELSEIF [petal width]>0.8 AND [petal width]>1.75 AND ISNULL([petal length]) THEN 'Iris-
↪virginica'
ELSEIF [petal width]>0.8 AND [petal width]>1.75 AND [petal length]>4.85 THEN 'Iris-
↪virginica'
ELSEIF [petal width]>0.8 AND [petal width]>1.75 AND [petal length]<=4.85 AND
↪ISNULL([sepal width]) THEN 'Iris-virginica'
ELSEIF [petal width]>0.8 AND [petal width]>1.75 AND [petal length]<=4.85 AND [sepal
↪width]>3.1 THEN 'Iris-versicolor'
ELSEIF [petal width]>0.8 AND [petal width]>1.75 AND [petal length]<=4.85 AND [sepal
↪width]<=3.1 THEN 'Iris-virginica'
ELSEIF [petal width]>0.8 AND [petal width]<=1.75 AND ISNULL([petal length]) THEN
↪'Iris-versicolor'
ELSEIF [petal width]>0.8 AND [petal width]<=1.75 AND [petal length]>4.95 AND [petal
↪width]>1.55 AND [petal length]>5.45 THEN 'Iris-virginica'
ELSEIF [petal width]>0.8 AND [petal width]<=1.75 AND [petal length]>4.95 AND [petal
↪width]>1.55 AND [petal length]<=5.45 THEN 'Iris-versicolor'
ELSEIF [petal width]>0.8 AND [petal width]<=1.75 AND [petal length]>4.95 AND [petal
↪width]<=1.55 THEN 'Iris-virginica'
ELSEIF [petal width]>0.8 AND [petal width]<=1.75 AND [petal length]<=4.95 AND [petal
↪width]>1.65 THEN 'Iris-virginica'
ELSEIF [petal width]>0.8 AND [petal width]<=1.75 AND [petal length]<=4.95 AND [petal
↪width]<=1.65 THEN 'Iris-versicolor'

```

```
ELSEIF [petal width]<=0.8 THEN 'Iris-setosa'  
END
```

Summary generation

You can also print the model from the point of view of the classes it predicts with `local_model.summarize()`. It shows a header section with the training data initial distribution per class (instances and percentage) and the final predicted distribution per class.

Then each class distribution is detailed. First a header section shows the percentage of the total data that belongs to the class (in the training set and in the predicted results) and the rules applicable to all the instances of that class (if any). Just after that, a detail section shows each of the leaves in which the class members are distributed. They are sorted in descending order by the percentage of predictions of the class that fall into that leaf and also show the full rule chain that leads to it.

```
Data distribution:
  Iris-setosa: 33.33% (50 instances)
  Iris-versicolor: 33.33% (50 instances)
  Iris-virginica: 33.33% (50 instances)

Predicted distribution:
  Iris-setosa: 33.33% (50 instances)
  Iris-versicolor: 33.33% (50 instances)
  Iris-virginica: 33.33% (50 instances)

Field importance:
  1. petal length: 53.16%
  2. petal width: 46.33%
  3. sepal length: 0.51%
  4. sepal width: 0.00%

Iris-setosa : (data 33.33% / prediction 33.33%) petal length <= 2.45
  · 100.00%: petal length <= 2.45 [Confidence: 92.86%]

Iris-versicolor : (data 33.33% / prediction 33.33%) petal length > 2.45
  · 94.00%: petal length > 2.45 and petal width <= 1.65 and petal length <= 4.95
  ↳ [Confidence: 92.44%]
```

```

    · 2.00%: petal length > 2.45 and petal width <= 1.65 and petal length > 4.95 and
↪sepal length <= 6.05 and petal width > 1.55 [Confidence: 20.65%]
    · 2.00%: petal length > 2.45 and petal width > 1.65 and petal length <= 5.05 and
↪sepal width > 2.9 and sepal length > 6.4 [Confidence: 20.65%]
    · 2.00%: petal length > 2.45 and petal width > 1.65 and petal length <= 5.05 and
↪sepal width > 2.9 and sepal length <= 6.4 and sepal length <= 5.95 [Confidence: 20.
↪65%]

Iris-virginica : (data 33.33% / prediction 33.33%) petal length > 2.45
    · 76.00%: petal length > 2.45 and petal width > 1.65 and petal length > 5.05
↪[Confidence: 90.82%]
    · 12.00%: petal length > 2.45 and petal width > 1.65 and petal length <= 5.05 and
↪sepal width <= 2.9 [Confidence: 60.97%]
    · 6.00%: petal length > 2.45 and petal width <= 1.65 and petal length > 4.95 and
↪sepal length > 6.05 [Confidence: 43.85%]
    · 4.00%: petal length > 2.45 and petal width > 1.65 and petal length <= 5.05 and
↪sepal width > 2.9 and sepal length <= 6.4 and sepal length > 5.95 [Confidence: 34.24
↪%]
    · 2.00%: petal length > 2.45 and petal width <= 1.65 and petal length > 4.95 and
↪sepal length <= 6.05 and petal width <= 1.55 [Confidence: 20.65%]

```

You can also use `local_model.get_data_distribution()` and `local_model.get_prediction_distribution()` to obtain the training and prediction basic distribution information as a list (suitable to draw histograms or any further processing). The tree nodes' information (prediction, confidence, impurity and distribution) can also be retrieved in a CSV format using the method `local_model.tree_CSV()`. The output can be sent to a file by providing a `file_name` argument or used as a list.

Local ensembles have a `local_ensemble.summarize()` method too, the output in this case shows only the data distribution (only available in Decision Forests) and field importance sections.

For local clusters, the `local_cluster.summarize()` method prints also the data distribution, the training data statistics per cluster and the basic intercentroid distance statistics. There's also a `local_cluster.statistics_CSV(file_name)` method that store in a CSV format the values shown by the `summarize()` method. If no file name is provided, the function returns the rows that would have been stored in the file as a list.

Running the Tests

The test will be run using `nose`, that is installed on setup, and you'll need to set up your authentication via environment variables, as explained below. With that in place, you can run the test suite simply by issuing .. code-block:: bash

```
$ python setup.py nosetests
```

Some tests need the `numpy` and `scipy` libraries to be installed too. They are not automatically installed as a dependency, as they are quite heavy and very seldom used.

Additionally, `Tox` can be used to automatically run the test suite in virtual environments for all supported Python versions. To install Tox:

```
$ pip install tox
```

Then run the tests from the top-level project directory:

```
$ tox
```

Building the Documentation

Install the tools required to build the documentation:

```
$ pip install sphinx
```

To build the HTML version of the documentation:

```
$ cd docs/  
$ make html
```

Then launch `docs/_build/html/index.html` in your browser.

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Additional Information

For additional information about the API, see the [BigML developer's documentation](#).