Cluster Analysis with the BigML Dashboard

The BigML Team

Version 1.0
This document provides a comprehensive description of how to solve cluster analysis using the BigML Dashboard. BigML Clusters are covered in detail. Learn how to use the BigML Dashboard to configure, visualize, and interpret these unsupervised predictive models and use them to find centroids for single instances and whole datasets as well.

This document assumes that you are familiar with:

• Sources with the BigML Dashboard. The BigML Team. June 2016. [6]
• Datasets with the BigML Dashboard. The BigML Team. June 2016. [5]

To learn how to use the BigML Dashboard to build supervised predictive models read:

• Classification and Regression with the BigML Dashboard. The BigML Team. June 2016. [4]
• Time Series with the BigML Dashboard. The BigML Team. July 2017. [7]

To learn how to use the BigML Dashboard to build other unsupervised models read:

• Anomaly Detection with the BigML Dashboard. The BigML Team. June 2016. [2]
• Association Discovery with the BigML Dashboard. The BigML Team. June 2016. [3]
• Topic Modeling with the BigML Dashboard. The BigML Team. November 2016. [8]
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Introduction

There are problems that require separating datasets into subsets of instances bearing some similarities. Cluster analysis is a Machine Learning task that partitions a dataset and groups together those instances that are similar. It separates a set of instances into a number of groups so that instances in the same group, called cluster, are more similar to each other than to those in other groups. Cluster analysis does not require using previously labeled data. For this reason, it falls under the category of unsupervised learning.

BigML clusters use proprietary learning algorithms to group together the instances according to a distance measure, computed using the values of the fields as input. Each cluster group is represented by its center (or centroid). All BigML field types are valid inputs for clustering, i.e. categorical, numeric, text and items fields, although there are a few caveats. First, numeric fields are automatically scaled to ensure that their different magnitudes do not bias the distance calculation. Second, clustering does not tolerate missing values for numeric fields, so BigML provides several strategies for dealing with them (see Section 4.4), otherwise those instances are excluded to compute the clusters.

BigML clusters can be built using two different unsupervised learning algorithms:

- **K-means**: the user needs to specify the number of clusters in advance. Learn more about k-means in Section 2.1.
- **G-means**: the algorithm automatically learns the number of different clusters by iteratively taking existing cluster groups and testing whether the cluster’s neighborhood appears Gaussian in its distribution. Learn more about g-means in Section 2.2.

This chapter provides a comprehensive description of BigML clusters including how they can be created (Chapter 3) and configured (Chapter 4). Powerful visualizations are provided of the results of clustering data instances, which give insight into their internal structure (see Chapter 5). Besides their visual representations, clusters also provide a textual summary view of the most essential information about them (see Chapter 6). Clusters are actionable, since they allow you to identify the cluster that is closest to any given new data point (Chapter 7). You can even download and calculate the nearest cluster locally (see Section 8.1). It is also worth noting that you can create, update, list, and delete clusters using the BigML API (see Section 8.3).

In BigML, the fourth tab of the main menu of your Dashboard allows you to list all your available clusters. In the cluster list view (Figure 1.2), you can see, for each cluster, the dataset it was created from, as well as the cluster’s Name, Algorithm (either k-means or g-means), the number of cluster groups $K$, Age (time elapsed since it was created), Size, and number of centroids or batch centroids that have been created using that cluster. The SEARCH menu option in the top right corner of the cluster list view allows you to search your clusters by name.
When you first create an account at BigML, or every time you start a new project, your list view of clusters will be empty. (See Figure 1.2.)

Finally, in Figure 1.3 you can see the icon used to represent a cluster in BigML.
Understanding Clusters

This section describes internal details about BigML clusters. Besides being useful to better understand how BigML implements them, it will also provide the foundations for you to decide why and when to use the two available clustering algorithms. You can safely skip this section on first read.

2.1 K-Means

K-means is one of two algorithms that BigML provides for cluster analysis. K-means clustering aims to partition the data instances contained in your dataset in \( K \) clusters, such that each data instance belongs to the cluster with the nearest center.

BigML proprietary implementation of K-means is optimized for scalability, thus mitigating one of the major limitations of standard K-means. BigML adopted the mini-batch\(^1\) approach, which is known to reduce computation cost by orders of magnitude compared to the classic K-means algorithm.

One key factor when using K-means clustering is how the algorithm is initialized, which can greatly affect the quality of the identified clusters. In standard K-means, initial clusters are chosen at random. This means that the quality of the clusters identified by the algorithm usually varies a lot from run to run, so it is fair to say that standard K-means provides no guarantee of accuracy\(^2\). Therefore, alternative approaches for the selection of the initial clusters have been described in literature, such as K-means++, which is a little too slow for BigML purposes. Instead, BigML preferred approach is K-means ||\(^3\), which is similar to K-means++ but much faster.

Another dimension where BigML clusters improve on standard K-means is the way they handle categorical data. Instead of “binarizing” each category, meaning a field with 40 categories becomes 40 binary fields, BigML chose a technique called k-prototypes\(^4\) which modifies the distance function to be more category-friendly so each cluster chooses the most common category from its neighborhood. So, BigML Clusters use mode instead of mean for categorical fields.

2.2 G-Means

Sometimes, it is hard to know in advance how many clusters can be identified in a given dataset (the \( K \) in K-means). To solve this issue, an alternative algorithm has been proposed, G-means\(^5\), which uses a special technique for running K-means multiple times while adding centroids in a hierarchical fashion.

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\(^1\)http://www.eecs.tufts.edu/~dsculley/papers/fastkmeans.pdf


\(^3\)http://theory.stanford.edu/~sergei/papers/vldb12-kmpar.pdf

\(^4\)http://www.iipl.fudan.edu.cn/%7Ezhangjp/literatures/cluster%20analysis/apkdd.pdf

G-means has the advantage of being relatively resilient to covariance in clusters and has no need to compute a global covariance (as is the case with using the Mahalanobis\textsuperscript{6} distance, a popular variant on classic K-means to deal with covariance).

BigML implementation differs from the original paper. First, we reuse our sample-based K-means rather than running full K-means, with the already described performance and scalability advantage. Additionally, BigML clusters choose new candidate clusters with kmeans|| rather than the PCA calculation from the paper. While this gives us better scalability, it means BigML version of G-means is no longer deterministic as in the paper. Given the same data, we may find a different number of clusters from one run to the next (if no seed is given).

Finally, BigML G-means have different stopping criteria than the original paper. We currently enforce a maximum limit of 128 clusters. Also, if BigML algorithm does not make sufficient progress in finding Gaussian clusters after multiple iterations of G-means, it stops early. Both techniques ensure that BigML algorithm returns fewer clusters.

G-means is almost parameter-free, except for one, the \texttt{critical_value} parameter. G-means iteratively takes existing clusters and tests whether the cluster’s neighborhood appears Gaussian. If it does not, the cluster is split into two. The \texttt{critical_value} sets how strict the test is when deciding whether data looks Gaussian. The current default is 5, but ranges between 1 and 20 can be reasonable depending on the dataset. A critical value of 1 means data must look very Gaussian to pass the test and can lead to more clusters being detected. Higher \texttt{critical_values} will tend to find fewer clusters.

2.3 On the Repeatability of Clusters

As mentioned, standard K-means provides results that vary strongly from run to run due to the random selection of initial clusters. However, BigML clusters strive to ensure that obtained results are repeatable, to some extent. In particular, when applying K-means||, BigML will ensure that the same initial cluster selection is done for each given dataset.

As an end effect, if you choose the K-means algorithm, BigML Clusters are repeatable when you use the same dataset to create them. Alternatively, if you create different datasets from the same datasource, no guarantee can be provided as to the repeatability of the results.

The same considerations apply to BigML G-means repeatability.

\textsuperscript{6}https://en.wikipedia.org/wiki/Mahalanobis_distance
Creating Clusters with 1-Click

To create a cluster in BigML you have two options: you can use the BigML unique 1-click feature which provides a convenient way to create a cluster from a dataset, or you can configure a number of options that give you fine control on how the cluster is created. This section will guide you through the process of creating a cluster with just 1-click.

By far, the easiest and quickest way to create a cluster is using the 1-CLICK CLUSTER option that is available in the 1-click action menu. (See Figure 3.1.)

![Figure 3.1: 1-click cluster](image)

Alternatively, you can select the 1-CLICK CLUSTER option in the 1-click action menu from the dataset list view. (See Figure 3.2.)

![Figure 3.2: Pop up menu option to create a 1-click cluster from list view](image)

Either option builds a new cluster using default values for all available configuration options (see Chapter 4). This can give you a quick starting point to understand how your clustering behaves and how to improve it.

Creating a cluster may take a variable time, depending on how big your dataset is, your subscription plan, etc. Once your cluster is ready, it will be automatically displayed on your BigML Dashboard and
you will be able to explore it through BigML sophisticated visualizations (see Chapter 5,) and using it for predictions (see Chapter 7.)
Cluster Configuration Options

While 1-click creation (see Chapter 3) provides a convenient and easy way to create a cluster from a dataset, there are cases when you want more control. This section will focus on the options that BigML offers to configure its internal algorithms for clustering.

You can set a number of parameters that affect the way BigML creates models from a dataset. Such parameters can be grouped in two categories:

- Parameters that are permanently associated to the dataset, such as its objective field and preferred fields. Once you provide a value for a dataset’s permanent parameters, they will be used as a default value for the creation of models from that dataset.

- Parameters that only affect the model that is currently being created and that you are expected to set each time. Those include the objective field, included/excluded fields, and a number of configuration options that are described below.

Set a dataset's permanent parameters by clicking on the edit button that is displayed when you hover on the dataset's fields. This opens a modal dialog where you can set some of the field properties (See Figure 4.1).
Click on the preferred field button to make that field non-preferred.

To access the configuration panel, select the CONFIGURE CLUSTERZ menu option located in the configuration menu of your dataset's detail view. (See Figure 4.2.)

When the configuration panel is displayed, you can:

- Select or deselect individual fields for them to be included in or excluded from the cluster computation.
- Set a number of configuration options.
Chapter 4. Cluster Configuration Options

Note: when the configuration panel is displayed, the edit is not visible, so you cannot set the dataset’s permanent properties.

You can find a detailed explanation of the configuration options in the following sections.

4.1 Clustering Algorithms

BigML provides two distinct algorithms for clustering. Choose between K-means\(^1\) and G-means\(^2\) to create your cluster. (See Figure 4.3.)

![Figure 4.3: Cluster options: clustering algorithm](image)

4.1.1 K-Means Algorithm

Using the k-means algorithm requires that you already know the number of cluster groups (the \(k\) in K-means) that are present in your dataset. If you do not know it, an inappropriate choice of \(k\) may yield poor results.

The maximum number of clusters that you can specify is 300.

4.1.2 G-Means Algorithm

If you do not know which is the optimal number of cluster groups present in your dataset, you can have BigML discover it by using G-means. G-means solves the problem of trying to find the number of clusters by iteratively taking existing clusters and testing whether the cluster’s neighborhood appears Gaussian in its distribution (based on Anderson-Darling tests\(^3\)). See this blogpost\(^4\) for more information.

G-means will yield a maximum of 128 clusters.

4.2 Number of Clusters

When you select the k-means algorithm, you are required to configure the number of clusters that you know are to be found. (See Figure 4.4.)

\(^1\)https://en.wikipedia.org/wiki/K-means_clustering
\(^2\)http://papers.nips.cc/paper/2526-learning-the-k-in-k-means.pdf
\(^3\)https://en.wikipedia.org/wiki/Anderson\textendashDarling_test
\(^4\)http://blog.bigml.com/2015/02/24/divining-the-k-in-k-means-clustering/
Note: choosing an inappropriate $K$ can yield poor results. If you do not have any initial idea of how many clusters your data may contain, it is better to use G-means.

### 4.3 Critical Value

When you select the G-means algorithm, you can choose a **critical value**. (See Figure 4.5.)

The critical value determines how “strict” the G-means algorithm is when identifying clusters. When you select G-means, BigML iteratively tests new clusters looking for Gaussian distributions in the clusters’ neighborhoods. If a new cluster does not pass the test, it is split into two new clusters. The critical value sets how strict this statistical test should be when deciding if the underlying data looks Gaussian. A critical value of 1 means the data must look very Gaussian to pass the test, so it can lead to more clusters being detected. Alternatively, higher critical values loosens the Gaussian constraint and leads to fewer clusters.

By default, BigML uses a value of 5, which seems to work well in most cases. A range between 1 and 10 is acceptable.

### 4.4 Default Numeric Value

Figure 4.6: Cluster options: default numeric value
When training a cluster, BigML may encounter missing values, which can be either considered or ignored. Indeed, clusters compute the Euclidean distance\(^5\). Since the distance to a missing value is undefined, instances containing missing values will be ignored.

BigML, though, lets you use a default value in place of any missing value, by setting a default numeric value. You can choose to replace the missing numeric values with the field's maximum, mean, median, minimum or zero. There is one catch. If all the instances contain at least one missing value, this would invalidate the entire training set. In this situation, BigML automatically replaces the missing numeric values by the median.

Missing values for categorical fields are always considered valid categorical values, for example \([\text{red, green, blue, <missing>}]\). This means a cluster centroid may contain a missing value. (See Figure 4.7.)

![Figure 4.7: Example of a centroid with missing values for some categorical fields](https://en.wikipedia.org/wiki/Euclidean_distance)
4.5 Model Clusters

Choose this option to create a model for each of your clusters. Such models predict whether an instance is part of its respective cluster. This is very useful to see which fields and values are most relevant in deciding membership in a given cluster. For example, if your cluster has two relevant fields that differentiate its instances from the rest of the dataset, you will likely get a decision tree model with a rule set that only involves those two fields in deciding membership. (See Section 5.2.)

By default, BigML does not model clusters.

4.6 Scale Fields & Auto-Scaled Fields

Datasets often contain fields with very different magnitudes. For example, two fields such as age and salary. Since clusters compute the Euclidean distance\(^6\) between numeric values, salary will dominate the clustering.

BigML provides two options to re-scale your fields (Figure 4.9):

- **Scale fields**: set a specific scale for your fields using an integer multiplier. This will increase their influence as many times as the number you set to calculate the clusters. If the auto-scaled option is enabled, it will be applied first so you can control how much weight you assign to a particular field relative to others. For example, if you want the age to be twice as influential as salary you just need to set auto-scaled to true and assign a multiplier of 2 to the age field.

- **Auto-scaling**: when the auto-scaled option is enabled, all the numeric fields will be scaled so that their standard deviations are 1. This ensures each field will have equal influence.

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\(^6\)https://en.wikipedia.org/wiki/Euclidean_distance
4.7 Weights

This option allows you to assign individual weights to each instance by choosing a special weight field. This is useful when you have an unbalanced dataset, where data instances of a given kind, e.g., those indicating a fraudulent transaction, are scarce in comparison to other ones. In such case, you may want to assign more weight to the scarce instances so they are equivalent to the abundant ones.

The selected field must be numeric, and it must not contain any missing values. The field selected for weighting purposes will not be taken into account as an input to calculate cluster distances. You can select an existing field in your dataset, or you can create a new one to assign customized weights.

For example, below you can find a transactional dataset example for which we included a field called “Weight”. This field indicates that fraudulent instances weigh 10 more times than non-fraudulent ones. BigML Flatline editor is a powerful tool for adding new fields to your dataset, such as a weight field. Another field that could be used in this example may be the transaction “Amount” so that transactions with higher amounts will have higher weights in the cluster.
4.8 Sampling Options

Sometimes you do not need all the instances contained in your testing dataset to build your cluster. If you have a very large dataset, sampling may be a good way of getting faster results. (See Figure 4.11.) The same sampling options described in the Datasets with the BigML Dashboard document [5] to sample datasets are also available when building clusters. They are divided in two groups: sampling and advanced sampling options.

![Sampling options for clusters](image)

**Figure 4.11: Sampling options for clusters**

### 4.8.1 Rate

The sampling rate is the frequency of instances being extracted from the dataset and included in your sample. A sampling rate of 100% means that all instances are included; a rate of 10% means that only every tenth instance is included. This option may take any value between 0% and 100%. You can easily configure the rate by moving the slider in the configuration panel for sampling, or by typing the percentage in the tiny input box, both highlighted in Figure 4.11.
By default, BigML uses a 100% rate.

4.8.2 Range

The sampling range is the linear subset of the dataset instances that you want to include in the sample, e.g., from instance 5 to instance 1,000. The rate will be applied over the range configured.

By default, all instances are included, i.e., the range is (1, num. rows in dataset).

4.8.3 Sampling

The sampling option represents the type of the sampling process, which can be either random or deterministic.

When using deterministic sampling the random-number generator will always use the same seed, producing repeatable results.

By default, BigML uses random sampling.

4.8.4 Replacement

The replacement option controls whether a single instance can be selected multiple times or not. Sampling without replacement ensures that each instance cannot be selected more than once.

By default, BigML generates samples without replacement.

4.8.5 Out of Bag

The out of bag option allows you to include in your sample only those instances that were not selected in the first place, thus effectively inverting the sampling outcome. It is only selectable when a sample is deterministic and the sample rate is less than 100%. The total percentage of instances included in your sample will be one minus the rate (when replacement is not allowed). This can be useful for splitting a dataset into training and testing subsets.

By default, BigML will not use out of bag instances.
Visualizing Clusters

Being able to effectively visualize a model is of great help to understand how cluster groups relate one another. To this aim, BigML provides two powerful interactive visualizations for clusters, a general visualization and the histogram and planets visualization, which will be introduced below.

BigML offers you a general cluster visualization for all your clusters and two special ones in case your dataset contains less than 8 numeric values and no other categorical or text data.

5.1 General Visualization

BigML cluster general visualization is available for all clusters. (See Figure 5.1.)

![Clusters visualization](image)

Figure 5.1: Clusters visualization

It conveys a wealth of information through a natural representation of cluster groups:
• Each cluster is associated to a circle, a standard representation for clusters.
• Different cluster groups have different colors associated.
• If you click a cluster, all the clusters will be rearranged so the one you selected is in the middle. This is useful to show the relative distances between the selected cluster and the rest of clusters.

  Note: while the distances between clusters in the visualization is related to the actual distances, it is not strictly to scale. This ensures that all clusters fit the screen. (See Figure 5.1.)

• When you mouse over a cluster, additional information will be displayed in a tooltip and in a data panel on the right side.

  The tooltip includes the cluster name, ID, and the number of instances that it comprises.

  The data panel shows the distance histogram (see Subsection 5.1.1) for the data points comprising that cluster as well as the centroid information (Subsection 5.1.2). You can freeze the panel by pressing SHIFT; press ESCAPE to release the view.

5.1.1 Distance Histogram

The distance histogram represents the distribution of distances from the cluster’s center to each of the points that fall into the cluster’s neighborhood.

![Figure 5.2: Distance histogram for clusters](image)

5.1.2 Centroid

The cluster centroid is the center of the cluster. It is computed by using the mean for each numeric field and the mode for categorical ones.
For text and items fields, you will get a tag cloud where you can see the terms or items that minimize the average cosine distance between the centroid and the points in its neighborhood.
5.2 Creating a Model From a Cluster

Creating a model from a cluster is useful to predict whether an instance belongs to the cluster or which fields are most significant in deciding which instances belong to it. (See Section 4.5.)

To create a model from a cluster, select the cluster, then press SHIFT, and click the dataset icon at the bottom of the data panel to the right.

![Create a model from a cluster](image)

Figure 5.5: Create a model from a cluster

5.3 Creating a Dataset From a Cluster

Create a dataset from a cluster if you want to have all of the instances that belong to that cluster in a dataset for further analysis.

To create a dataset from a cluster, select the cluster by clicking it, then press SHIFT, and click the dataset icon at the bottom of your cluster’s data panel.
5.4 Histograms and Planets

If your dataset contains less than 8 numeric fields and no other categorical or text data, then you can visualize your clusters with the Histograms and Planets visualization.

**Note:** this is a Beta feature, so it may be change in the future.

The histograms visualization allows you to set values for your fields with the sliders and get a real-time calculation of the nearest cluster. You will also get the distance to the cluster centroid for the selected values. The histograms display measures for the clusters’ instances e.g. mean, median, maximum, minimum and sum squares.
The planets representation is very similar to the histograms view except it contains a two dimensional chart, in which you can see the predicted cluster in the center and its relative distance from the other clusters. See Figure 5.8.
Cluster Summary Report

From a cluster’s detail view, access the cluster summary report by clicking on the icon highlighted in Figure 6.1.

![Figure 6.1: Button to display a cluster's summary report](image)

The cluster summary report displays a summary about the cluster.

### 6.1 Cluster Summary

The cluster summary gives you a summarized view of your cluster, including the following metrics: data distribution, cluster metrics, centroids, and intercentroid distance. (See Figure 6.2.)

- **Data distribution**: data distribution within the clusters: for each cluster, the percentage of data instances that belong to that cluster is given. The “global” cluster always includes all of the data instances, i.e. it accounts for 100% of them.

- **Cluster metrics**: a summary of the distances between the data instances expressed in terms of various aggregate measures:
  - total\_ss: the total sum of squares of the distances between each data instance and the global centroid;
  - within\_ss: the total sum of squares of the distances between each data instance and the centroid it belongs to;
  - between\_ss: the total sum of squares of the distances between each centroid and the global centroid;
  - ratio\_ss: the ratio of between\_ss and total\_ss. This is a measure of how well your data instances can be grouped into clusters.

- **Centroids**: general statistics for each of the identified clusters, including the global one.

- **Intercentroid distance**: distribution of distances between centroids.
Cluster Summary Report

6-means Cluster (critical_value=5) with 2 centroids

Data distributions:
Cluster 0: 66.67% (100 instances)
Cluster 1: 33.33% (50 instances)

Cluster metrics:
within_ss (Total within-cluster sum of the sum of squares): 6.652650

Centroids:
Cluster 0: species: "Iris-virginica", petal length: 4.906, petal width: 1.676, sepal length: 6.262, sepal width: 2.872
Cluster 1: species: "Iris-setosa", petal length: 1.462, petal width: 0.246, sepal length: 5.906, sepal width: 3.428

Figure 6.2: Cluster summary report
Cluster Predictions: Centroids

7.1 Introduction

The ultimate goal in building a BigML cluster is being able to make predictions for previously unseen instances with an unknown label. Predictions for clusters are referred to as centroids, since they aim to identify the nearest centroid for new data. In BigML, you can make predictions with clusters based on single instances or multiple instances in batch. Each prediction tells you which is the nearest centroid to your input data along with the distance separating them.

The predictions tab in the main menu of your BigML Dashboard is where all of your saved centroids are listed (see Figure 7.1.)

![Figure 7.1: Empty Dashboard centroids view](image)

Cluster predictions are saved under the CLUSTER ANALYSIS option in the menu. (See Figure 7.2.)

![Figure 7.2: Menu options of the predictions list view](image)

From this view you can select to view the list for your single instances centroids or your batch centroids by clicking the corresponding icons. (See Figure 7.3 and Figure 7.4.)
In the predictions list view, you can see, for each prediction, the **Cluster** icon used for the prediction, the **Name** of the prediction, the nearest **Centroid** predicted, the **Distance** from the specified input data, and the **Age** (time since the prediction was created). You can also search your predictions by name by clicking the **SEARCH** icon on the top right menu in Figure 7.1.

By default, when you first create an account at BigML, or every time that you start a new project, your list view for predictions will be empty. (See Figure 7.5.)

![Figure 7.5: Empty Dashboard centroids view](image)

Centroids are saved under the **cluster icon** in the menu options on the top left corner of the **predictions list view**.

### 7.2 Predicting Centroids

As shown in Figure 7.6, BigML provides two options to create centroids from your cluster:

- **CENTROID**: to predict single instances.
- **BATCH CENTROID**: to predict multiple instances in batch.
7.2.1 Centroid

BigML allows you to quickly find the nearest centroid for single data instances by providing a form containing the fields used by the cluster, so you can easily set the input data and get an immediate response. This option is only available from the BigML Dashboard for clusters with less than 100 fields. If you want to make single instance predictions for clusters with a higher number of fields, you can use the BigML API\(^1\).

Follow the steps detailed below to create a single prediction:

1. Choose the CENTROID option under the cluster **1-click menu** (see Figure 7.7).

   ![Figure 7.7: Predict option from cluster 1-click menu](image)

2. You will be redirected to the **prediction form** where you will find all the fields used by the cluster.

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1\(^1\)https://bigml.com/api/centroids
3. **Set input values** for the cluster fields. Depending on the field type, you will need to input the values differently:

- Numeric fields: move the slider or input a specific value in the edition box.
- Categorical fields: select one class from the selector.
- Text fields: write one or several terms in the free text box.
- Date-time fields: select the appropriate values from the selector.
- Items fields: when you write the first three characters of an item name, several items matching those characters will appear, so you can select the right one. You can input more than one item for a field.

4. **Get the centroids** along with the distance displayed on the top of the form. BigML predictions are synchronous, i.e., when you send the input data you get an immediate response. Moreover, single centroids are calculated locally so when you configure the input data you can see how predictions change immediately. (Read more about local predictions in [Subsection 7.2.1.1](#)).
5. Optionally, save the prediction so you can get a view of the single clusters predictions (see Subsection 7.4.1) and also to find it afterwards in the prediction list view.

7.2.1.1 Local Predictions

BigML provides local predictions from the BigML Dashboard for single instance predictions. Local predictions allow you to get a real-time prediction without consuming any credits or requiring an internet connection. This is possible because your cluster is saved in the browser’s memory so when the input values change, BigML immediately calculates the nearest centroid in a matter of microseconds.
7.2.2 Batch Centroid

BigML batch centroids allow you to make predictions for multiple instances simultaneously. All you need is the cluster you want to use to make predictions and a dataset containing the instances for which you want to calculate the nearest centroids. BigML will create a prediction for each instance in the dataset. Follow the steps detailed below to create a batch centroid:

1. Select the **BATCH CENTROID** option under the cluster 1-click menu (see Figure 7.11) or the **CREATE BATCH CENTROID** option from the pop up menu of the list view (see Figure 7.11).

![Figure 7.11: Batch centroid option from cluster 1-click menu](image)

2. **Select the dataset** containing all the instances you want to predict. The instances should contain the input values for all the fields used by the cluster. Remember that BigML batch centroids can handle missing data in your prediction dataset only for categorical, text and items fields but not for numeric fields (see Section 4.4). Instances with missing data for numeric fields will be ignored.

3. **Optionally, select the cluster** you want to use for the prediction. BigML pre-selects the cluster you created the batch centroid from at step 1, but you can change it at any time in the batch centroid view by selecting another cluster from the cluster selector displayed in the right pane.

![Figure 7.12: Batch centroid option from cluster pop up menu](image)
4. Once the cluster and the dataset are selected, the batch centroid **configuration options** will appear along with a *preview of the prediction output* (a CSV file). The default format includes all your cluster fields and adds a last column with the cluster predictions.

**Note:** BigML does not include by default the calculated distance from the centroid, so you will have to configure your output file to include that information. You can find a detailed explanation of all configuration options in Section 7.3.

5. By default, BigML generates an output **dataset** with your batch centroids that you can later find in your datasets section in the BigML Dashboard. This dataset can be helpful to analyze your results afterwards. This option is active by default, but you can deactivate it by clicking in the icon shown in Figure 7.15.
6. Once you have your batch centroid configured, click in the green **Centroid** button to generate your batch prediction.
7. When the batch centroid is created, you will be able to **download the CSV file** containing all your dataset instances along with a prediction for each one of them. (See Figure 7.17).

![Figure 7.17: Download batch centroid output CSV file](image)

8. If you didn’t disable the option to create a dataset, explained in step 4, you will also be able to access the **output dataset** from the batch centroid view.

![Figure 7.18: View batch predictions output dataset](image)

### 7.3 Configuring Centroid Predictions

BigML provides several options to configure your centroids, such as defining the automatic **fields mapping** performed by BigML (Subsection 7.3.1) and the **output file settings** (Subsection 7.3.2)

#### 7.3.1 Field Mapping

By default, BigML maps fields based on their **names**. If there is a mismatch between the field names in your cluster and those in the input dataset you selected for the batch centroid, you can specify the
right correspondence between the two sets of fields by explicitly assigning to each field appearing in the “Cluster fields” column its associated input field in the “Dataset fields” column. (See Figure 7.19.) If the dataset’s and cluster’s field names do not match but their IDs do, which happens when corresponding fields appear in the same order, you can tell BigML to use the field ID instead of the field name to map the fields. To this aim, click the green switcher shown in Figure 7.19.

If you do not want some of the fields to be considered during the evaluation, you can also manually search for those fields and remove them from the “Dataset fields” column.

The field mapping from the BigML Dashboard has a limit of 200 fields. For batch centroids with higher number of fields, use the argument field_map from BigML API\(^2\) if you need to map your fields.

### 7.3.2 Output Settings

As mentioned, batch centroids can return a CSV file containing all input instances along with the predictions BigML calculated for each of them. Define the following settings to customize your output file:

- **Separator**: this option allows you to choose a separator for your output file values. The default separator is the comma. You can also select the semicolon, the tab, or the space.

- **New line**: this option allows you to set the new line character to use as the line break in the generated csv file: “LF”, “CRLF”.

- **Output fields**: this option allows you to include or exclude any of your dataset fields from the output file from the preview shown in Figure 7.20.

\(^2\)https://bigml.com/api/batchcentroids#bp_batch_centroid_arguments
Note: a maximum of 100 fields are displayed in the preview, but all your dataset fields are included in the output file by default unless you exclude them.

- **Headers**: this option includes or excludes a first row in the output file (and in the output dataset) with the names of each column. By default, BigML includes the headers.

- **Distance**: this option allows you to include an additional column in the output file with the distance between the instance and the centroid. By default, BigML does not include this column.

- **Centroid column name**: this option allows you to customize the name for the distance column. By default BigML uses “distance”.

![Output settings for batch centroids](image)

### 7.4 Visualizing Cluster Predictions

Centroid visualization changes depending on whether you are predicting one **single instance** CENTROID or multiple instances using the **BATCH CENTROID** option (see Subsection 7.4.1).

#### 7.4.1 Single Centroid

For single instance predictions, you can find the nearest centroid at the top of the form along with its distance from the input data. (See Figure 7.21.) You can change the value of the displayed input fields any time to have your prediction recalculated in real time.
7.4.2 Batch Predictions

For batch centroids, you always get a CSV file and an optional output dataset.

7.4.2.1 Output CSV File

From the batch centroid view, you can access the CSV file containing your predictions for each of your dataset instances in the last column (see Figure 7.22.)

You can configure several options to customize your CSV file including the separator for the columns, the name of your centroid and distance column, the dataset fields you want to include, and whether...
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you want to include the headers for your fields. You can find a detailed explanation of those options in Subsection 7.3.2.

Note: by default, BigML does not include the centroid distance in your output file. Click the relevant option from the output settings panel if you want to include it.

See an output CSV file example in Figure 7.23 where the two last columns contain the cluster and the distance for each instance.

```
Pregnancies,Glucose,Blood pressure,BMI,Age,cluster,distance
3,78,50,32,26,Cluster 3, 0.40608
7,100,0,0,30,32,Cluster 6, 0.35249
1,97,66,15,22,Cluster 5, 0.24655
10,122,78,31,45,Cluster 1, 0.36629
3,180,64,25,26,Cluster 3, 0.35246
```

Figure 7.23: An example of a batch centroid CSV file

7.4.2.2 Output Dataset

By default BigML automatically creates a dataset out of your batch centroid. (See Subsection 7.3.2.) You can access your output dataset from the batch centroid view as shown in Figure 7.25.

In the output dataset you can find an additional field (named by default “cluster”) containing the nearest centroid for each one of your instances. If you configured your batch centroid to include the distance you will be able to find it in the last field of your output dataset as shown in Figure 7.25.
7.4.2.3 Batch Centroid 1-Click Actions

From the batch centroid view you can perform the following actions shown in Figure 7.26:

- **BATCH CENTROID AGAIN**: this option will redirect you to the batch centroid creation view where you will have the same cluster and prediction dataset already selected. This option will rapidly create the batch centroid using a different configuration.

- **BATCH CENTROID WITH ANOTHER DATASET**: this option is an easy way to create a batch centroid using the same cluster and a different dataset.

- **BATCH CENTROID USING ANOTHER CLUSTER**: this option will easily create a batch centroid using the same dataset and a different cluster.

- **NEW BATCH CENTROID**: this option will redirect you to the batch centroid creation view where you can select a prediction dataset and a cluster to create your batch centroid.
Chapter 7. Cluster Predictions: Centroids

7.5 Consuming BigML Centroids Programmatically

BigML provides plenty of means for developers to integrate BigML centroids within their apps. In the following sections, we will describe how you can use BigML REST API and BigML Python bindings to work with centroids.

7.5.1 Using Centroids Via the BigML API

Centroids have full citizenship in the BigML API. This means you can programmatically create, update, list, and delete them. For example, this is how you can create a single centroid using the command line from a given cluster and defining the input data. This will require properly setting the `BIGML_AUTH` environment variable to contain your authentication credentials:

```bash
curl "https://bigml.io/centroid?$BIGML_AUTH" \\n-X POST \\n-H 'content-type: application/json' \\n-d '{"cluster": "cluster/50650bdf3c19201b64000020", "input_data": {"000001": 3, "000002": 4.5, "000003": 2.2}}'
```

For more information on using centroids through the BigML API, please refer to centroid REST API documentation.

7.5.2 Using Centroids Via BigML Bindings

BigML bindings provide a convenient way to access BigML REST API from your language of choice. They offer a higher-level view of BigML Machine Learning resources and algorithms in a number of languages, including Python, Node.js, Java, Swift, and Objective-C. For example, this is how you can create a centroid in Python using BigML bindings:

```python
from bigml.api import BigML
api = BigML()
centroid = api.create_centroid("cluster/573d997058a27e0f620038df", 
{"first field": 5,
```
BigML bindings also provide the means to calculate the nearest centroid locally, without ever hitting the network, which can greatly improve the latency of predicting from your apps. This is made possible by BigML clusters being white-box, meaning you can download and use them independently from BigML. For example, the following code snippet shows how you can download a cluster and use it for making a local prediction using BigML bindings for Python:

```python
from bigml.cluster import Model
from bigml.api import BigML
api = BigML()
cluster = api.get_cluster("cluster/502fdbff15526876610002615",
query_string="only_model=true;limit=-1")

local_cluster = Cluster(cluster)
centroid = local_cluster.centroid({"first field": 3, "second field": 1})
```

For more information on using centroids through the BigML API, please refer to BigML bindings documentation.

### 7.6 Descriptive Information

Descriptive information is what allows you to describe a centroid so you can find it later and easily recognize it among other centroids.

Each centroid has an associated **name**, **description**, **category**, and **tags**. You can find a brief description for each concept in the following subsections. In Figure 7.27, you can see the options that the More info panel gives to edit them.

![Figure 7.27: Edit centroids](image)

#### 7.6.1 Name

If you do not specify a **name** for your predictions, BigML assigns a default name depending on the type of predictions:

- **Single centroid**: the name always follows the structure “Centroid for `<objective field name>`”.
- **Batch centroid**: BigML combines your prediction dataset name and the cluster name: “Batch centroid for `<cluster name>` with `<dataset name>`”.

Centroid names are displayed in the list view and also on the top bar of a prediction view. Centroid names are indexed to be used in searches. You can rename your centroids at any time from the More info panel.
The name of a centroid cannot be longer than 256 characters. There is no restriction on the characters that can be used in a name. More than one centroids can have the same name even within the same project, since they are automatically assigned unique internal identifiers.

### 7.6.2 Description

Each cluster prediction also has a **description** that it is very useful for documenting your Machine Learning projects. Centroids take the description from the clusters used to create them.

Descriptions can be written using plain text and also [markdown](https://en.wikipedia.org/wiki/Markdown). BigML provides a simple markdown editor that accepts a subset of markdown syntax. (See Figure 7.28.)

![Markdown editor for centroids descriptions](Image)

Figure 7.28: Markdown editor for centroids descriptions

Descriptions cannot be longer than **8192** characters and can use almost any character.

### 7.6.3 Category

Each prediction has associated a **category** taken from cluster used to create it. Categories are useful to classify predictions according to the domain which your data comes from. This is useful when you use BigML to solve problems across industries or multiple customers.

A prediction category must be one of the categories listed on table Table 7.1.

---

3[https://en.wikipedia.org/wiki/Markdown](https://en.wikipedia.org/wiki/Markdown)
### Table 7.1: Categories used to classify predictions by BigML

<table>
<thead>
<tr>
<th>Category</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aerospace and Defense</td>
</tr>
<tr>
<td>Automotive, Engineering and Manufacturing</td>
</tr>
<tr>
<td>Banking and Finance</td>
</tr>
<tr>
<td>Chemical and Pharmaceutical</td>
</tr>
<tr>
<td>Consumer and Retail</td>
</tr>
<tr>
<td>Demographics and Surveys</td>
</tr>
<tr>
<td>Energy, Oil and Gas</td>
</tr>
<tr>
<td>Fraud and Crime</td>
</tr>
<tr>
<td>Healthcare</td>
</tr>
<tr>
<td>Higher Education and Scientific Research</td>
</tr>
<tr>
<td>Human Resources and Psychology</td>
</tr>
<tr>
<td>Insurance</td>
</tr>
<tr>
<td>Law and Order</td>
</tr>
<tr>
<td>Media, Marketing and Advertising</td>
</tr>
<tr>
<td>Miscellaneous</td>
</tr>
<tr>
<td>Physical, Earth and Life Sciences</td>
</tr>
<tr>
<td>Professional Services</td>
</tr>
<tr>
<td>Public Sector and Nonprofit</td>
</tr>
<tr>
<td>Sports and Games</td>
</tr>
<tr>
<td>Technology and Communications</td>
</tr>
<tr>
<td>Transportation and Logistics</td>
</tr>
<tr>
<td>Travel and Leisure</td>
</tr>
<tr>
<td>Uncategorized</td>
</tr>
<tr>
<td>Utilities</td>
</tr>
</tbody>
</table>

### 7.6.4 Tags

A prediction can also have a number of tags associated with it that can help to retrieve it via the BigML API or to provide predictions with some extra information. Your prediction inherits the tags from the cluster used to create it. Each tag is limited to a maximum of 128 characters. Each prediction can have up to 32 different tags.

### 7.7 Cluster Predictions Privacy

The link displayed in the privacy panel is the private URL of your centroid, so only a user logged into your account is able to see it. Neither single nor batch centroids can be shared from your BigML Dashboard by sharing a link, as you can do with other resources.
7.8 Moving Centroids

When you create a cluster prediction, it will be assigned to the same project where the original cluster is located. You cannot move predictions between projects as you do with other resources.

7.9 Stopping Centroids

**Single centroids** are synchronous resources, so you cannot cancel them during the creation since you get the result immediately.

**Batch centroids** are asynchronous resources, so you can stop the creation before the task is finished. You can use the DELETE option from the 1-click action menu (Figure 7.30) or from the pop up menu on the clusters list view. If you stop the prediction during its creation, you won’t be able to resume the same task again, so if you want to create the same prediction, you will have to start a new task.

7.10 Deleting Centroids

You can DELETE your single or batch centroids from the predictions view, using the 1-click action menu (see Figure 7.31) or using the pop up menu on the predictions list view (see Figure 7.32).
A modal window will be displayed asking you for confirmation. Once a prediction is deleted, it is perma-
nently deleted and there is no way you (or even the IT folks at BigML) can retrieve it.
Consuming Clusters

In the previous sections, we have described how you can create clusters, configure them, use them to make predictions, and more. This section will introduce a number of BigML features that enable powerful ways of taking advantages of BigML clusters: exporting them locally, and using them programmatically via the BigML REST API and BigML Python bindings.

8.1 Exporting and Downloading Clusters

You can download your cluster in several languages including Python, JSON PML or Node.js. Click on the downloading icon in the top menu, and select your preferred language.

By downloading your cluster, you will be able to compute centroids locally, free of latency and at no cost. It works the same way as local predictions for clusters and ensembles.

8.2 Updating Clusters

Change the names of your individual clusters by clicking on the edit icon next to each cluster’s name.
8.3 Using Clusters Via the BigML API

Clusters have full citizenship in the BigML API. This means you can programmatically create, update, list, delete, and use them for predictions. For example, this is how you can create a cluster from the command line with custom values for a few available arguments. This will require you have properly set the `BIGML_AUTH` environment variable to contain your authentication credentials:

```
curl "https://bigml.io/cluster?$BIGML_AUTH" \
-X POST \
-H 'content-type: application/json' \
-d '{"dataset": "dataset/4f66a50803ce8940c5000006", "name": "my model", "range": [25, 125]}'
```

For more information on using clusters through the BigML API, please refer to cluster REST API documentation.

8.4 Using Clusters Via the BigML Bindings

BigML bindings provide a convenient way to access the BigML REST API from your language of choice. They offer a higher-level view of BigML Machine Learning resources and algorithms in a number of languages, including Python, Node.js, Java, Swift, and Objective-C. For example, this is how you can create a cluster in Python using BigML bindings:

```
from bigml.api import BigML
api = BigML()
prediction = api.create_cluster("dataset/573d997058a27e0f620038df", "range": [1, 10], "name": "my cluster")
```

For more information on using clusters through the BigML API, please refer to BigML bindings documentation.
Clusters Limits

BigML imposes a few limits to the characteristics of a cluster:

- **K-means**: BigML K-means can handle up to 300 cluster groups.
- **G-means**: BigML G-means can handle up to 128 cluster groups.
- **Histogram & planets**: You can use the histogram & planets visualization for clusters if your dataset contains less than 8 numeric fields and no other categorical or text data.
Cluster Descriptive Information

Each cluster has an associated **name**, **description**, **category**, and **tags**. A brief description follows for each concept. In Figure 10.1, you can see the options the More info panel provides to edit them.

Figure 10.1: Panel to edit a cluster's name, category, description, and tags

### 10.1 Cluster Name

Each cluster has an associated **name** that is displayed on the list view and also on the top bar of a cluster view. Cluster names are indexed to be used in searches. When you create a cluster, by default, it gets the name of the dataset that you used to create it. You can edit it using the More info menu option on the right corner of the cluster view (see Figure 10.1). The name of a cluster cannot be longer than 256 characters. There is no restriction on the characters that can be used in a cluster name. More than one cluster can have the same name even within the same project, since they are automatically assigned unique internal identifiers.
10.2 Description

Each cluster inherits the description of the dataset used to create it. Descriptions can be very useful for documenting your Machine Learning projects. Descriptions can be written using plain text and also markdown\(^1\). BigML provides a simple markdown editor that accepts a subset of markdown syntax. (See Figure 10.2.)

![Figure 10.2: Markdown editor for cluster descriptions](https://en.wikipedia.org/wiki/Markdown)

Descriptions cannot be longer than 8192 characters and can use almost any character.

10.3 Category

Each cluster takes the category from the dataset used to create it. Categories are useful to classify clusters according to the domain which your data comes from. This is useful when you use BigML to solve problems across industries or multiple customers.

A cluster category must be one of the 24 categories listed in table Table 10.1.
Table 10.1: Categories used to classify clusters by BigML

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<td>Energy, Oil and Gas</td>
</tr>
<tr>
<td>Fraud and Crime</td>
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<tr>
<td>Healthcare</td>
</tr>
<tr>
<td>Higher Education and Scientific Research</td>
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<tr>
<td>Human Resources and Psychology</td>
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<tr>
<td>Insurance</td>
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<tr>
<td>Law and Order</td>
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<tr>
<td>Media, Marketing and Advertising</td>
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<tr>
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<tr>
<td>Physical, Earth and Life Sciences</td>
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<tr>
<td>Professional Services</td>
</tr>
<tr>
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<tr>
<td>Uncategorized</td>
</tr>
<tr>
<td>Utilities</td>
</tr>
</tbody>
</table>

10.4 Tags

A cluster can also have a number of tags associated with it that can help to retrieve it via the BigML API or to provide clusters with some extra information. Clusters inherit the tags of the dataset used to create them.

Each tag is limited to a maximum of 128 characters. Each cluster can have up to 32 different tags.

10.5 Counters

For each cluster, BigML also stores counters to track the number of other resources that have been created using that cluster as a starting point. In the cluster view, you can see a menu option that displays these counters. It also allows you to quickly jump to all the resources of one type that have been created with this cluster as shown in Figure 10.3.

Figure 10.3: Menu option to quickly access to resources created with a cluster
Clustering Privacy

Privacy options for a cluster can be defined in the More Info panel, displayed in Figure 11.1. There are two levels of privacy for BigML clusters:

- **Private**: only accessible by authorized users (the owner and those who have been granted access by him or her).

- **Shared**: by enabling the secret link you will get two different links to share your clusters. The first one is a sharing link that you can copy and send to others so they can visualize and interact with your clusters. The second one is a link to embed your clusters directly on your web page. This is very useful if you want to make local centroid predictions at no cost.

![Figure 11.1: Clusters privacy options](image_url)
Moving Clusters to Another Project

Clusters will be assigned to the same project as the dataset used to create them belongs to. However, you can move clusters between projects. The menu option to do this can be found in two places:

1. In the cluster detail view, among the 1-click actions for each cluster. (See Figure 12.1).

![Figure 12.1: Menu option to move clusters](image)

2. In the cluster list view, within the pop up menu (see Figure 12.2).
Figure 12.2: Menu option to move clusters from the cluster list view
You can also stop a cluster’s creation process, while BigML is not yet done with it, from the 1-click actions menu (Figure 13.1).

A modal window (Figure 13.2) will be displayed asking you for confirmation.

Figure 13.1: Menu option to stop a cluster’s creation

Figure 13.2: Menu option to stop a cluster’s creation
Deleting Clusters

You can delete your clusters in two ways:

- From the cluster view, using the 1-click action menu. (See Figure 14.1.)

![Menu option to delete a cluster](image)

- Using the pop up menu on the cluster list. (See Figure 14.2.)
A modal window (see Figure 14.3) will be displayed asking you for confirmation. Once you delete a cluster, it is deleted permanently and there is no way you (or even the IT folks at BigML) can retrieve it.
Takeaways

This document covered clusters in detail. We conclude it with a list of key points:

- BigML Clusters can learn how your data instances group together based on their similarity.
- Each cluster group is represented by its center, called centroid.
- To build a cluster you just need a dataset. (See Figure 15.1).
- A cluster can be an input to a prediction, to a batch prediction, to a dataset, or to a BigML model. (See Figure 15.1).
- Create centroids or batch centroids from a cluster to know to which instance group previously unseen data instances belong.
- You can also create clusters using BigML REST API or the BigML bindings for your language of choice.
- Create a BigML model or a dataset from a cluster to further analyze the instances that belong to any given group of instances discovered by training the cluster. For example, a BigML model may help you identify which fields are more relevant in determining whether a data instance should be considered member of a cluster group.
- Numeric fields are automatically scaled to prevent their different magnitudes from biasing the calculation.
- BigML provides two different methods to do the clustering: K-means and G-means. Use G-means when you do not know how many cluster groups can be found.
- When you create a BigML Cluster from a dataset, you can define a number of options, such as the number $k$ of clusters (K-means) or the critical value (G-means), field scaling and weighting, and sampling.
- BigML visualizes clusters through circles of different colors that represent found centroids. Each circle is sized according to the number of instances that belong to the corresponding cluster group.
- You can use BigML Clusters to calculate the nearest centroid to a given data instance or to a number of instances.
- You can download clusters in several languages, including Python, JSON PML, and Node.js, to use for local computation.
- At any time you can update a cluster’s descriptive information, move a cluster to a different project, rename it, or delete it permanently.
Figure 15.1: Cluster Workflows
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Glossary

Centroids  the center of a cluster found by a clustering algorithm. Centroids are computed by using the mean for numeric fields and the mode for categorical fields. For text and items fields, it selects the values which minimizes the average cosine distance between the centroid and the points in its neighborhood. ii, 1, 24, 56

Cluster neighborhood  the nearest points to the centroid which may finally conform a cluster. 1, 9, 17

Clustering  an unsupervised Machine Learning task in which dataset instances are grouped into geometrically related subsets. ii, 24, 56

Dashboard  The BigML web-based interface that helps you privately navigate, visualize, and interact with your modeling resources. ii, 1, 24

Dataset  the structured version of a BigML source. It is used as input to build your predictive models. For each field in your dataset a number of basic statistics (min, max, mean, etc.) are parsed and produced as output. ii, 30

Field  an attribute of each instance in your data. Also called "feature", "covariate", or "predictor". Each field is associated with a type (numeric, categorical, text, items, or date-time). 1

Gaussian distribution  a symmetric probability distribution in which the majority of the mass is clustered about a mean value and values increasingly far from the mean in either direction are increasingly unlikely. Also called the normal distribution or the bell curve. 1

G-means  a clustering algorithm that tries to learn the number of different clusters by iteratively taking existing clusters and testing whether the cluster's neighborhood follow a Gaussian distribution. 1

Instances  the data points that represent the entity you want to model, also known as observations or examples. They are usually the rows in your data with a value (potentially missing) for each field that describes the entity. ii, 1

K-means  the canonical clustering algorithm, which attempts to fit a pre-specified number ($k$) of clusters to the dataset. 1

Local predictions  the predictions made in your local environment, faster, at no cost, by downloading your model. 28, 44

Missing value  the data points that represent the entity you want to model may present missing value, i.e., not provide a value for all fields that compose the entity. 10

Non-preferred fields  fields that, for a number of possible reasons, are by default not included in the modeling process. One example of this is fields that contain the same value for every instance; in general, constant fields add no information to the modeling process. 8
Predicting the result of obtaining the objective field value for your new data using an existing model. The model returns the predicted value along with a performance measure (confidence for classification or expected error for regression). 24

Predictive Model a machine-learned model that has been created using statistical learning. It can help describe or infer some statistical properties of an entity using the instances provided by a dataset. ii

Project an abstract resource that helps you group related BigML resources together. 2, 25, 51

Sampling the process of partitioning your dataset to consider just a subset of your instances. 14

Unsupervised learning a type of Machine Learning problem in which the objective is not to learn a predictor, and thus does not require each instance to be labeled. Typically, unsupervised learning algorithms infer some summarizing structure over the dataset, such as a clustering or a set of association rules. ii, 1
References


