cloudera
Ask Bigger Questions

Cloudera Search

Important Notice

Cloudera, Inc.
1001 Page Mill Road Bldg 2
Palo Alto, CA 94304
info@cloudera.com
US: 1-888-789-1488
Intl: 1-650-362-0488
www.cloudera.com

Release Information

Version: 5.3.x
Date: June 24, 2015

Table of Contents

Cloudera Search QuickStart Guide

This guide shows how to establish and use a sample deployment to query a real data set. At a high level, you set up a cluster, enable search, run a script to create an index and load data, and then execute queries.

Cloudera Search Quick Start Guide

This guide shows how to establish and use a sample deployment to query a real data set. At a high level, you set up a cluster, enable search, run a script to create an index and load data, and then execute queries.

Prerequisites

Before installing Search, install Cloudera Manager and a CDH cluster. The scenario in this guide works with CDH 5.3.x and Cloudera Manager 5.3.x. The `quickstart.sh` script and supporting files are included with CDH. Install Cloudera Manager, CDH, and Solr using the Cloudera Manager and CDH QuickStart Guide.

The primary services that the Search Quick Start depends on are:

- HDFS: Stores data. Deploy on all hosts.
- ZooKeeper: Coordinates Solr hosts. Deploy on one host. Use default port 2181. The examples refer to a machine named `search-zk`. You may want to give your Zookeeper machine this name to simplify reusing content exactly as it appears in this document. If you choose a different name, you must adjust some commands accordingly.
- Solr with SolrCloud: Provides search services such as document indexing and querying. Deploy on two hosts.
- Hue: Includes the Search application, which you can use to complete search queries. Deploy Hue on one host.

After you have completed the installation processes outlined in the Cloudera Manager Quick Start Guide, you can Load and Index Data in Search on page 7.

Load and Index Data in Search

Execute the script found in a subdirectory of the following locations. The path for the script often includes the product version, such as Cloudera Manager 5.3.x, so path details vary:

- Packages: `/usr/share/doc`. If Search for CDH 5.3.5 is installed to the default location using packages, the Quick Start script is found in `/usr/share/doc/search-1.0.0+cdh5.3.5+0/quickstart`.
- Parcels: `/opt/cloudera/parcels/CDH/share/doc`. If Search for CDH 5.3.5 is installed to the default location using parcels, the Quick Start script is found in `/opt/cloudera/parcels/CDH/share/doc/search-1.0.0+cdh5.3.5+0/quickstart`.

The script uses several defaults that you might want to modify:

Table 1: Script Parameters and Defaults

Parameter	Default	Notes
NAMENODE_CONNECT	`` `hostname`:8020 ``	For use on an HDFS HA cluster. If you use NAMENODE_CONNECT, do not use NAMENODE_HOST or NAMENODE_PORT.
NAMENODE_HOST	`` `hostname` ``	If you use NAMENODE_HOST and NAMENODE_PORT, do not use NAMENODE_CONNECT.

Parameter	Default	Notes
NAMENODE_PORT	8020	If you use NAMENODE_HOST and NAMENODE_PORT, do not use NAMENODE_CONNECT.
ZOOKEEPER_HOST	`hostname`	
ZOOKEEPER_PORT	2181	
ZOOKEEPER_ROOT	/solr	
HDFS_USER	${HDFS_USER:="${USER}"}	
SOLR_HOME	/opt/cloudera/parcels/SOLR/lib/solr	

By default, the script is configured to run on the NameNode host, which is also running ZooKeeper. Override these defaults with custom values when you start `quickstart.sh`. For example, to use an alternate NameNode and HDFS user ID, you could start the script as follows:

```
$ NAMENODE_HOST=nnhost HDFS_USER=jsmith ./quickstart.sh
```

The first time the script runs, it downloads required files such as the Enron data and configuration files. If you run the script again, it uses the Enron information already downloaded, as opposed to downloading this information again. On such subsequent runs, the existing data is used to re-create the `enron-email-collection` SolrCloud collection.

> **Note:** Downloading the data from its server, expanding the data, and uploading the data can be time consuming. Although your connection and CPU speed determine the time these processes require, fifteen minutes is typical and longer is not uncommon.

The script also generates a Solr configuration and creates a collection in SolrCloud. The following sections describes what the script does and how you can complete these steps manually, if desired. The script completes the following tasks:

1. Set variables such as hostnames and directories.
2. Create a directory to which to copy the Enron data and then copy that data to this location. This data is about 422 MB and in some tests took about five minutes to download and two minutes to untar.
3. Create directories for the current user in HDFS, change ownership of that directory to the current user, create a directory for the Enron data, and load the Enron data to that directory. In some tests, it took about a minute to copy approximately 3 GB of untarred data.
4. Use `solrctl` to create a template of the instance directory.
5. Use `solrctl` to create a new Solr collection for the Enron mail collection.
6. Create a directory to which the MapReduceBatchIndexer can write results. Ensure that the directory is empty.
7. Use the MapReduceIndexerTool to index the Enron data and push the result live to `enron-mail-collection`. In some tests, it took about seven minutes to complete this task.

Using Search to Query Loaded Data

After loading data into Search as described in Load and Index Data in Search on page 7, you can use Hue to query data.

Hue must have admin privileges to query loaded data. This is because querying requires Hue import collections or indexes, and these processes can only be completed with admin permissions on the Solr service.

1. Connect to Cloudera Manager and click the **Hue** service, which is often named something like HUE-1. Click **Hue Web UI**.
2. Click on the **Search** menu.
3. Select the Enron collection for import.

4. (Optional) Click the Enroncollection to configure how the search results display. For more information, see Hue Configuration.
5. Type a search string in the **Search...** text box and press **Enter**.
6. Review the results of your Search.

For more information, see:

- Cloudera Search Frequently Asked Questions
- Cloudera Search Release Notes on page 118
- Hue Project

Search Installation

This documentation describes how to install Cloudera Search powered by Solr. It also explains how to install and start supporting tools and services such as the ZooKeeper Server, MapReduce tools for use with Cloudera Search, and Flume Solr Sink.

After installing Cloudera Search as described in this document, you can configure and use Cloudera Search as described in the Cloudera Search User Guide on page 31. The user guide includes the Cloudera Search Tutorial on page 37, as well as topics that describe extracting, transforming, and loading data, establishing high availability, and troubleshooting.

Cloudera Search documentation includes:

- Cloudera Search Release Notes on page 118
- Cloudera Search Version and Download Information on page 28
- Cloudera Search User Guide on page 31
- Cloudera Search Frequently Asked Questions

About this Guide

This documentation describes how to install Cloudera Search powered by Solr. It also explains how to install and start supporting tools and services such as the ZooKeeper Server, MapReduce tools for use with Cloudera Search, and Flume Solr Sink.

After installing Cloudera Search as described in this document, you can configure and use Cloudera Search as described in the Cloudera Search User Guide on page 31. The user guide includes the Cloudera Search Tutorial on page 37, as well as topics that describe extracting, transforming, and loading data, establishing high availability, and troubleshooting.

Cloudera Search documentation includes:

- Cloudera Search Release Notes on page 118
- Cloudera Search Version and Download Information on page 28
- Cloudera Search User Guide on page 31
- Cloudera Search Frequently Asked Questions

Preparing to Install Cloudera Search

Cloudera Search provides interactive search and scalable indexing. Before you begin installing Cloudera Search:

- Ensure that your environment meets Cloudera Search requirements.
- Decide whether to install Cloudera Search using Cloudera Manager or using package management tools.
- Decide on which machines to install Cloudera Search and with which other services to collocate Search.
- Consider the sorts of tasks, workloads, and types of data you will be searching. This information can help guide your deployment process.

Cloudera Search Requirements

This topic describes Cloudera Search requirements, organized into categories.

Cloudera Product Compatibility Matrix

For the latest information on compatibility of all Cloudera products, see the Product Compatibility Matrix.

CDH and Cloudera Manager Requirements

- Cloudera Search 1.3.0 requires CDH 4.7 and supports Cloudera Manager 4.8. For more information on CDH 4, see CDH 4 Documentation. If you do not want to upgrade to CDH 4.7 or Cloudera Manager 4.8, do not use Search 1.3.0.

Operating Systems

Cloudera Search provides packages for RHEL, SLES, Ubuntu, and Debian systems as described below. All packages are 64-bit.

Operating System	Version
Red Hat compatible	
Red Hat Enterprise Linux (RHEL)	5.7
	6.2
	6.4
CentOS	5.7
	6.2
	6.4
Oracle Linux with Unbreakable Enterprise Kernel	5.6
	6.4
SLES	
SLES Linux Enterprise Server (SLES)	11 with Service Pack 1 or later
Ubuntu/Debian	
Ubuntu	Lucid (10.04) - Long-Term Support (LTS)
	Precise (12.04) - Long-Term Support (LTS)
Debian	Squeeze (6.03)

- **Note:**
  - Cloudera has received reports that our RPMs work well on Fedora, but we have not tested this.
  - If you are using an operating system that is not supported by Cloudera's packages, you can also download source tarballs from Downloads.

JDK

- Cloudera Search 1.3 works with Oracle JDK 1.6 and Oracle JDK 1.7:
  - Cloudera Search works with JDK 1.6. Search is certified with 1.6.0_31, but any later maintenance (_xx) release should be acceptable for production, following Oracle's release notes and restrictions. The minimum supported version is 1.6.0_8.
  - Cloudera Search works with JDK 1.7. Search is certified with 1.7.0_25 or 1.7.0_45, but any later maintenance (_xx) release should be acceptable for production, following Oracle's release notes and restrictions.

> **Note:**
>
> Cloudera Search supports running applications compiled with Oracle JDK 7 (JDK 1.7) with the following restrictions:
>
> - All CDH components must be running the same major version (that is, *all* deployed on JDK 6 or *all* deployed on JDK 7). For example, you cannot run Hadoop on JDK 6 while running Sqoop on JDK 7.
> - All hosts in the cluster must be running the same major JDK version: Cloudera does not support mixed environments (some hosts on JDK6 and others on JDK7).
>
> To make sure everything works correctly, symbolically link the directory where you install the JDK to `/usr/java/default` on Red Hat and similar systems, or to `/usr/lib/jvm/default-java` on Ubuntu and Debian systems.

Ports Used by Cloudera Search

Cloudera Search uses the ports listed in table below. Before you deploy Cloudera Search, make sure these ports are open on each system. The table reflects the current default settings, which are defined in the Solr defaults file located in `/etc/defaults/solr`.

Component	Service	Port	Protocol	Access Requirement	Comment
Cloudera Search	Solr search/update	8983	http	External	All Solr-specific actions, update/query.
Cloudera Search	Solr (admin)	8984	http	Internal	Solr administrative use.

Choosing Where to Deploy the Cloudera Search Processes

You can collocate a Cloudera Search server (`solr-server` package) with a Hadoop TaskTracker (MRv1) and a DataNode. When collocating with TaskTrackers, be sure that the machine resources are not oversubscribed. Start with a small number of MapReduce slots and increase them gradually.

For instructions describing how and where to install `solr-mapreduce`, see Installing MapReduce Tools for use with Cloudera Search. For information about the Search package, see the Using Cloudera Search section in the Cloudera Search Tutorial.

Guidelines for Deploying Cloudera Search

Memory

CDH initially deploys Solr with a Java virtual machine (JVM) size of 1 GB. In the context of Search, 1 GB is a small value. Starting with this small value simplifies JVM deployment, but the value is insufficient for most actual use cases. Consider the following when determining an optimal JVM size for production usage:

- The more searchable material you have, the more memory you need. All things being equal, 10 TB of searchable data requires more memory than 1 TB of searchable data.
- What is indexed in the searchable material. Indexing all fields in a collection of logs, email messages, or Wikipedia entries requires more memory than indexing only the `Date Created` field.
- The level of performance required. If the system must be stable and respond quickly, more memory may help. If slow responses are acceptable, you may be able to use less memory.

To ensure an appropriate amount of memory, consider your requirements and experiment in your environment. In general:

- 4 GB is sufficient for some smaller loads or for evaluation.
- 12 GB is sufficient for some production environments.
- 48 GB is sufficient for most situations.

Deployment Requirements

The information in this topic should be considered as guidance instead of absolute requirements. Using a sample application to benchmark different use cases and data types and sizes can help you identify the most important performance factors.

To determine how best to deploy search in your environment, define use cases. The same Solr index can have very different hardware requirements, depending on queries performed. The most common variation in hardware requirement is memory. For example, the memory requirements for faceting vary depending on the number of unique terms in the faceted field. Suppose you want to use faceting on a field that has ten unique values. In this case, only ten logical containers are required for counting. No matter how many documents are in the index, memory overhead is almost nonexistent.

Conversely, the same index could have unique timestamps for every entry, and you want to facet on that field with a `:*` query. In this case, each index requires its own logical container. With this organization, if you had a large number of documents—500 million, for example—then faceting across 10 fields would increase the RAM requirements significantly.

For this reason, use cases and some characterizations of the data is required before you can estimate hardware requirements. Important parameters to consider are:

- Number of documents. For Cloudera Search, sharding is almost always required.
- Approximate word count for each potential field.
- What information is stored in the Solr index and what information is only for searching. Information stored in the index is returned with the search results.
- Foreign language support:
  - How many different languages appear in your data?
  - What percentage of documents are in each language?
  - Is language-specific search supported? This determines whether accent folding and storing the text in a single field is sufficient.
  - What language families will be searched? For example, you could combine all Western European languages into a single field, but combining English and Chinese into a single field is not practical. Even with more similar sets of languages, using a single field for different languages can be problematic. For example, sometimes accents alter the meaning of a word, and in such a case, accent folding loses important distinctions.
- Faceting requirements:
  - Be wary of faceting on fields that have many unique terms. For example, faceting on timestamps or free-text fields typically has a high cost. Faceting on a field with more than 10,000 unique values is typically not useful. Ensure that any such faceting requirement is necessary.
  - What types of facets are needed? You can facet on queries as well as field values. Faceting on queries is often useful for dates. For example, "in the last day" or "in the last week" can be valuable. Using Solr Date Math to facet on a bare "NOW" is almost always inefficient. Facet-by-query is not memory-intensive because the number of logical containers is limited by the number of queries specified, no matter how many unique values are in the underlying field. This can enable faceting on fields that contain information such as dates or times, while avoiding the problem described for faceting on fields with unique terms.
- Sorting requirements:
  - Sorting requires one integer for each document (maxDoc), which can take up significant memory. Additionally, sorting on strings requires storing each unique string value.

- Is an "advanced" search capability planned? If so, how will it be implemented? Significant design decisions depend on user motivation levels:
  - Can users be expected to learn about the system? "Advanced" screens could intimidate e-commerce users, but these screens may be most effective if users can be expected to learn them.
  - How long will your users wait for results? Data mining results in longer user wait times. You want to limit user wait times, but other design requirements can affect response times.
- How many simultaneous users must your system accommodate?
- Update requirements. An update in Solr refers both to adding new documents and changing existing documents:
  - Loading new documents:
    - Bulk. Will the index be rebuilt from scratch in some cases, or will there only be an initial load?
    - Incremental. At what rate will new documents enter the system?
  - Updating documents. Can you characterize the expected number of modifications to existing documents?
  - How much latency is acceptable between when a document is added to Solr and when it is available in Search results?
- Security requirements. Solr has no built-in security options, although Cloudera Search supports authentication using Kerberos and authorization using Sentry. In Solr, document-level security is usually best accomplished by indexing authorization tokens with the document. The number of authorization tokens applied to a document is largely irrelevant; for example, thousands are reasonable but can be difficult to administer. The number of authorization tokens associated with a particular user should be no more than 100 in most cases. Security at this level is often enforced by appending an "fq" clause to the query, and adding thousands of tokens in an "fq" clause is expensive.
  - A *post filter*, also know as a *no-cache filter*, can help with access schemes that cannot use an "fq" clause. These are not cached and are applied only after all less-expensive filters are applied.
  - If grouping, faceting is not required to accurately reflect true document counts, so you can use some shortcuts. For example, ACL filtering is expensive in some systems, sometimes requiring database access. If completely accurate faceting is required, you must completely process the list to reflect accurate facets.
- Required query rate, usually measured in queries-per-second (QPS):
  - At a minimum, deploy machines with sufficient hardware resources to provide an acceptable response rate for a single user. You can create queries that burden the system so much that performance for even a small number of users is unacceptable. In this case, resharding is necessary.
  - If QPS is only somewhat slower than required and you do not want to reshard, you can improve performance by adding replicas to each shard.
  - As the number of shards in your deployment increases, so too does the likelihood that one of the shards will be unusually slow. In this case, the general QPS rate falls, although very slowly. This typically occurs as the number of shards reaches the hundreds.

Installing Cloudera Search

Before you get started, review Cloudera Search Requirements to ensure you have the necessary prerequisites.

You can install Cloudera Search in one of two ways:

- Using the Cloudera Manager installer, as described in Installing Cloudera Search with Cloudera Manager on page 15. This technique is recommended for reliable and verifiable Search installation.
- Using the manual process described in Installing Cloudera Search without Cloudera Manager on page 15. This process requires you to configure access to the Cloudera Search repository and then install Search packages.

> **Note:** Depending on which installation approach you use, Search is installed to different locations.
>
> - Installing Search with Cloudera Manager using parcels results in changes under `/opt/cloudera/parcels`.
> - Installing using packages, either manually or using Cloudera Manager, results in changes to various locations throughout the file system. Common locations for changes include `/usr/lib/`, `/etc/default/`, and `/usr/share/doc/`.

Installing Cloudera Search with Cloudera Manager

To install Cloudera Search using Cloudera Manager, see Installing Search. This topic includes information on how to complete an automated install using Cloudera Manager.

Once you have completed an automated install, you can deploy the Search service in your cluster.

- To deploy Search in a Cloudera Manager 4 managed cluster, see The Solr Service.
- To deploy Search in a Cloudera Manager 5 managedcluster, see The Solr Service.

Installing Cloudera Search without Cloudera Manager

- To install Cloudera Search 1.3 or earlier, which requires CDH 4, see Ways To Install CDH 4 for details on installing CDH 4 using packages.

> **Note:** This page describe how to install CDH using packages as well as how to install CDH using Cloudera Manager.

You can also elect to install Cloudera Search manually. For example, you might choose to install Cloudera Search manually if you have an existing installation to which you want to add Search.

To use Cloudera Search 1.3 with CDH 4:

- For general information about using repositories to install or upgrade Cloudera software, see Understanding Custom Installation Solutions in Understanding Custom Installation Solutions.
- For instructions on installing or upgrading CDH, see CDH 4 Installation and the instructions for Upgrading from CDH3 to CDH 4 or to see information on upgrading from an earlier CDH 4 release, see Upgrading to the Latest Version of CDH 4.
- For Cloudera Search repository locations and client `.repo` files, see Cloudera Search Version and Download Information.

Cloudera Search provides the following packages:

Package Name	Description
solr	Solr
solr-server	Platform specific service script for starting, stopping, or restart Solr.
solr-doc	Cloudera Search documentation.
solr-mapreduce	Tools to index documents using MapReduce.
solr-crunch	Tools to index documents using Crunch.
search	Examples, Contrib, and Utility code and data.

Before You Begin Installing Cloudera Search Without Cloudera Manager

The installation instructions assume that the sudo command is configured on the hosts where you are installing Cloudera Search. If sudo is not configured, use the root user (superuser) to configure Cloudera Search.

- **Important: Running services:** When starting, stopping, and restarting CDH components, always use the `service (8)` command rather than running `/etc/init.d` scripts directly. This is important because `service` sets the current working directory to the root directory (/) and removes environment variables except `LANG` and `TERM`. This creates a predictable environment in which to administer the service. If you use `/etc/init.d` scripts directly, any environment variables continue to be applied, potentially producing unexpected results. If you install CDH from packages, `service` is installed as part of the Linux Standard Base (LSB).

Install Cloudera's repository: before using the instructions in this guide to install or upgrade Cloudera Search from packages, install Cloudera's `yum`, `zypper/YaST` or `apt` repository, and install or upgrade CDH and make sure it is functioning correctly.

Installing Solr Packages

This topic describes how to complete a new installation of Solr packages. To upgrade an existing installation, see Upgrading Cloudera Search on page 22.

To install Cloudera Search on RHEL systems:

```
sudo yum install solr-server
```

To install Cloudera Search on Ubuntu and Debian systems:

```
$ sudo apt-get install solr-server
```

To install Cloudera Search on SLES systems:

```
$ sudo zypper install solr-server
```

- **Note:** See also Deploying Cloudera Search on page 16.

To list the installed files on RHEL and SLES systems:

```
$ rpm -ql solr-server solr
```

To list the installed files on Ubuntu and Debian systems:

```
$ dpkg -L solr-server solr
```

You can see that the Cloudera Search packages are configured according to the Linux Filesystem Hierarchy Standard.

Next, enable the server daemons you want to use with Hadoop. You can also enable Java-based client access by adding the JAR files in `/usr/lib/solr/` and `/usr/lib/solr/lib/` to your Java class path.

Deploying Cloudera Search

When you deploy Cloudera Search, SolrCloud partitions your data set into multiple indexes and processes, using ZooKeeper to simplify management, resulting in a cluster of coordinating Solr servers.

Note: Before you start

This section assumes that you have already installed Search. Installing Search can be accomplished:

- Using Cloudera Manager as described in Installing Search.
- Without Cloudera Manager as described in Installing Cloudera Search without Cloudera Manager on page 15.

Now you are distributing the processes across multiple hosts. Before completing this process, you may want to review Choosing where to Deploy the Cloudera Search Processes.

Installing and Starting ZooKeeper Server

SolrCloud mode uses a ZooKeeper Service as a highly available, central location for cluster management. For a small cluster, running a ZooKeeper host collocated with the NameNode is recommended. For larger clusters, you may want to run multiple ZooKeeper servers. For more information, see Installing the ZooKeeper Packages.

Initializing Solr

Once the ZooKeeper Service is running, configure each Solr host with the ZooKeeper Quorum address or addresses. Provide the ZooKeeper Quorum address for each ZooKeeper server. This could be a single address in smaller deployments, or multiple addresses if you deploy additional servers.

Configure the ZooKeeper Quorum address in `solr-env.sh`. The file location varies by installation type. If you accepted default file locations, the solr-env.sh file can be found in:

- Parcels: `/opt/cloudera/parcels/1.0.0+cdh5.3.5+0/etc/default/solr`
- Packages: `/etc/default/solr`

Edit the property to configure the hosts with the address of the ZooKeeper service. You must make this configuration change for every Solr Server host. The following example shows a configuration with three ZooKeeper hosts:

```
SOLR_ZK_ENSEMBLE=<zkhost1>:2181,<zkhost2>:2181,<zkhost3>:2181/solr
```

Configuring Solr for Use with HDFS

To use Solr with your established HDFS service, perform the following configurations:

1. Configure the HDFS URI for Solr to use as a backing store in `/etc/default/solr` or `/opt/cloudera/parcels/1.0.0+cdh5.3.5+0/etc/default/solr`. On every Solr Server host, edit the following property to configure the location of Solr index data in HDFS:

   ```
   SOLR_HDFS_HOME=hdfs://namenodehost:8020/solr
   ```

   Replace `namenodehost` with the hostname of your HDFS NameNode (as specified by `fs.default.name` or `fs.defaultFS` in your `conf/core-site.xml` file). You may also need to change the port number from the default (8020). On an HA-enabled cluster, ensure that the HDFS URI you use reflects the designated name service utilized by your cluster. This value should be reflected in `fs.default.name`; instead of a hostname, you would see `hdfs://nameservice1` or something similar.

2. In some cases, such as for configuring Solr to work with HDFS High Availability (HA), you may want to configure the Solr HDFS client by setting the HDFS configuration directory in `/etc/default/solr` or `/opt/cloudera/parcels/1.0.0+cdh5.3.5+0/etc/default/solr`. On every Solr Server host, locate the appropriate HDFS configuration directory and edit the following property with the absolute path to this directory :

   ```
   SOLR_HDFS_CONFIG=/etc/hadoop/conf
   ```

Replace the path with the correct directory containing the proper HDFS configuration files, `core-site.xml` and `hdfs-site.xml`.

Configuring Solr to Use Secure HDFS

- For information on setting up a secure CDH cluster for CDH 4, see the CDH 4 Security Guide.
- For information on setting up a secure CDH cluster for CDH 5, see the CDH 5 Security Guide.

In addition to the previous steps for Configuring Solr for use with HDFS, perform the following steps if security is enabled:

1. Create the Kerberos principals and Keytab files for every host in your cluster:
   a. Create the Solr principal using either `kadmin` or `kadmin.local`.

```
kadmin:  addprinc -randkey solr/fully.qualified.domain.name@YOUR-REALM.COM
```

```
kadmin:  xst -norandkey -k solr.keytab solr/fully.qualified.domain.name
```

   For more information, see Create and Deploy the Kerberos Principals and Keytab Files

   See Create and Deploy the Kerberos Principals and Keytab Files for information on using `kadmin` or `kadmin.local`).

2. Deploy the Kerberos Keytab files on every host in your cluster:
   a. Copy or move the keytab files to a directory that Solr can access, such as `/etc/solr/conf`.

```
$ sudo mv solr.keytab /etc/solr/conf/
```

```
$ sudo chown solr:hadoop /etc/solr/conf/solr.keytab
$ sudo chmod 400 /etc/solr/conf/solr.keytab
```

3. Add Kerberos-related settings to `/etc/default/solr` or `/opt/cloudera/parcels/1.0.0+cdh5.3.5+0/etc/default/solr` on every host in your cluster, substituting appropriate values. For a package based installation, use something similar to the following:

```
SOLR_KERBEROS_ENABLED=true
SOLR_KERBEROS_KEYTAB=/etc/solr/conf/solr.keytab
SOLR_KERBEROS_PRINCIPAL=solr/fully.qualified.domain.name@YOUR-REALM.COM
```

Creating the /solr Directory in HDFS

Before starting the Cloudera Search server, you need to create the `/solr` directory in HDFS. The Cloudera Search master runs as `solr:solr`, so it does not have the required permissions to create a top-level directory.

To create the `/solr` directory in HDFS:

```
$ sudo -u hdfs hadoop fs -mkdir /solr
$ sudo -u hdfs hadoop fs -chown solr /solr
```

Initializing the ZooKeeper Namespace

Before starting the Cloudera Search server, you need to create the `solr` namespace in ZooKeeper:

```
$ solrctl init
```

- **Warning:** `solrctl init` takes a `--force` option as well. `solrctl init --force` clears the Solr data in ZooKeeper and interferes with any running hosts. If you clear Solr data from ZooKeeper to start over, be sure to stop the cluster first.

Starting Solr

To start the cluster, start Solr Server on each host:

```
$ sudo service solr-server restart
```

After you have started the Cloudera Search Server, the Solr server should be running. To verify that all daemons are running, use the `jps` tool from the Oracle JDK, which you can obtain from the Java SE Downloads page. If you are running a pseudo-distributed HDFS installation and a Solr search installation on one machine, `jps` shows the following output:

```
$ sudo jps -lm
31407 sun.tools.jps.Jps -lm
31236 org.apache.catalina.startup.Bootstrap start
```

Runtime Solr Configuration

To start using Solr for indexing the data, you must configure a collection holding the index. A configuration for a collection requires a `solrconfig.xml` file, a `schema.xml` and any helper files referenced from the `xml` files. The `solrconfig.xml` file contains all of the Solr settings for a given collection, and the `schema.xml` file specifies the schema that Solr uses when indexing documents. For more details on how to configure a collection for your data set, see http://wiki.apache.org/solr/SchemaXml.

Configuration files for a collection are managed as part of the instance directory. To generate a skeleton of the instance directory, run the following command:

```
$ solrctl instancedir --generate $HOME/solr_configs
```

You can customize it by directly editing the `solrconfig.xml` and `schema.xml` files created in `$HOME/solr_configs/conf`.

These configuration files are compatible with the standard Solr tutorial example documents.

After configuration is complete, you can make it available to Solr by issuing the following command, which uploads the content of the entire instance directory to ZooKeeper:

```
$ solrctl instancedir --create collection1 $HOME/solr_configs
```

Use the `solrctl` tool to verify that your instance directory uploaded successfully and is available to ZooKeeper. List the contents of an instance directory as follows:

```
$ solrctl instancedir --list
```

If you used the earlier `--create` command to create `collection1`, the `--list` command should return `collection1`.

- **Important:**

  If you are familiar with Apache Solr, you might configure a collection directly in solr home: `/var/lib/solr`. Although this is possible, Cloudera recommends using `solrctl` instead.

Creating Your First Solr Collection

By default, the Solr server comes up with no collections. Make sure that you create your first collection using the `instancedir` that you provided to Solr in previous steps by using the same collection name. `numOfShards` is the number of SolrCloud shards you want to partition the collection across. The number of shards cannot exceed the total number of Solr servers in your SolrCloud cluster:

```
$ solrctl collection --create collection1 -s {{numOfShards}}
```

You should be able to check that the collection is active. For example, for the server `myhost.example.com`, you should be able to navigate to `http://myhost.example.com:8983/solr/collection1/select?q=*%3A*&wt=json&indent=true` and verify that the collection is active. Similarly, you should be able to view the topology of your SolrCloud using a URL similar to `http://myhost.example.com:8983/solr/#/~cloud`.

Adding Another Collection with Replication

To support scaling for the query load, create a second collection with replication. Having multiple servers with replicated collections distributes the request load for each shard. Create one shard cluster with a replication factor of two. Your cluster must have at least two running servers to support this configuration, so ensure Cloudera Search is installed on at least two servers. A replication factor of two causes two copies of the index files to be stored in two different locations.

1. Generate the config files for the collection:

   ```
   $ solrctl instancedir --generate $HOME/solr_configs2
   ```

2. Upload the instance directory to ZooKeeper:

   ```
   $ solrctl instancedir --create collection2 $HOME/solr_configs2
   ```

3. Create the second collection:

   ```
   $ solrctl collection --create collection2 -s 1 -r 2
   ```

4. Verify that the collection is live and that the one shard is served by two hosts. For example, for the server `myhost.example.com`, you should receive content from: `http://myhost.example.com:8983/solr/#/~cloud`.

Creating Replicas of Existing Shards

You can create additional replicas of existing shards using a command of the following form:

```
solrctl --zk <zkensemble> --solr <target solr server> core \
--create <new core name> -p collection=<collection> -p shard=<shard to replicate>
```

For example to create a new replica of collection named `collection1` that is comprised of `shard1`, use the following command:

```
solrctl --zk myZKEnsemble:2181/solr --solr mySolrServer:8983/solr core \
--create collection1_shard1_replica2 -p collection=collection1 -p shard=shard1
```

Adding a New Shard to a Solr Server

You can use `solrctl` to add a new shard to a specified solr server.

```
solrctl --solr http://<target_solr_server>:8983/solr core --create <core_name> \
-p dataDir=hdfs://<nameservice>/<index_hdfs_path> -p collection.configName=<config_name>
 \
-p collection=<collection_name> -p numShards=<int> -p shard=<shard_id>
```

Where:

- `target_solr_server`: The server to host the new shard
- `core_name`: `<collection_name><shard_id><replica_id>`
- `shard_id`: New shard identifier

For example, to add a new second shard named `shard2` to a solr server named `mySolrServer`, where the collection is named `myCollection`, you would use the following command:

```
solrctl --solr http://mySolrServer:8983/solr core --create myCore \
-p dataDir=hdfs://namenode/solr/myCollection/index -p collection.configName=myConfig
\
-p collection=myCollection -p numShards=2 -p shard=shard2
```

Installing the Spark Indexer

The Spark indexer uses a Spark or MapReduce ETL batch job to move data from HDFS files into Apache Solr. As part of this process, the indexer uses Morphlines to extract and transform data.

To use the Spark indexer, you must install the `solr-crunch` package on hosts where you want to submit a batch indexing job.

To install solr-crunch On RHEL systems:

```
$ sudo yum install solr-crunch
```

To install solr-crunch on Ubuntu and Debian systems:

```
$ sudo apt-get install solr-crunch
```

To install solr-crunch on SLES systems:

```
$ sudo zypper install solr-crunch
```

For information on using Spark to batch index documents, see the Spark Indexing Reference (CDH 5.2 or later only) on page 52.

Installing MapReduce Tools for use with Cloudera Search

Cloudera Search provides the ability to batch index documents using MapReduce jobs. Install the `solr-mapreduce` package on hosts where you want to submit a batch indexing job.

To install solr-mapreduce On RHEL systems:

```
$ sudo yum install solr-mapreduce
```

To install solr-mapreduce on Ubuntu and Debian systems:

```
$ sudo apt-get install solr-mapreduce
```

To install solr-mapreduce on SLES systems:

```
$ sudo zypper install solr-mapreduce
```

For information on using MapReduce to batch index documents, see the MapReduce Batch Indexing Reference on page 56.

Installing the Lily HBase Indexer Service

To query data stored in HBase, you must install the Lily HBase Indexer service. This service indexes the stream of records being added to HBase tables. This process is scalable, fault tolerant, transactional, and operates at near real-time (NRT). The typical delay is a few seconds between the time data arrives and the time the same data appears in search results.

Choosing where to Deploy the Lily HBase Indexer Service Processes

To accommodate the HBase ingest load, you can run as many Lily HBase Indexer services on different hosts as required. See the HBase replication documentation for details on how to plan the capacity. You can co-locate Lily HBase Indexer service processes with SolrCloud on the same set of hosts.

To install the Lily HBase Indexer service on RHEL systems:

```
$ sudo yum install hbase-solr-indexer hbase-solr-doc
```

To install the Lily HBase Indexer service on Ubuntu and Debian systems:

```
$ sudo apt-get install hbase-solr-indexer hbase-solr-doc
```

To install the Lily HBase Indexer service on SUSE-based systems:

```
$ sudo zypper install hbase-solr-indexer hbase-solr-doc
```

- **Important:** For the Lily HBase Indexer to work with CDH 5, you may need to run the following command before issuing Lily HBase MapReduce jobs:

  ```
  export HADOOP_CLASSPATH=<Path to hbase-protocol-**.jar>
  ```

Upgrading Cloudera Search

You can upgrade an existing Cloudera Search installation in several ways. Generally, you stop Cloudera Search services, update Search to the latest version, and then restart Cloudera Search services. You can update Search to the latest version by using the package management tool for your operating system and then restarting Cloudera Search services.

Upgrading with Cloudera Manager

If you are running Cloudera Manager, you can upgrade from within the Cloudera Manager Admin Console using parcels. For Search 1.x, which works with CDH 4, there is a separate parcel for Search. For Search for CDH 5, search in included in the CDH 5 parcel.

- To upgrade from CDH 4, follow the instructions for upgrading an individual parcel at Using parcels. If you need to upgrade CDH 4, you can upgrade the Search parcel at the same time; follow the instructions at Upgrading to the Latest Version of CDH 4 in a Cloudera Manager Deployment.

Upgrading Manually without Cloudera Manager

The update process is different for Search 1.x and Search for CDH 5. With Search 1.x, Search is a separate package from CDH. Therefore, to upgrade from Search 1.x, you must upgrade to CDH 5, which includes Search as part of the CDH 5 repository.

- **Important:** Before upgrading, make backup copies of the following configuration files:
  - `/etc/default/solr`
  - All collection configurations

  Make sure you copy every host that is part of the SolrCloud.

- To upgrade Search 1.x, see Upgrading to the Latest Search 1.x on page 23.
- If you are running CDH 4 and want to upgrade to Search for CDH 5, see Upgrading Search 1.x to Search for CDH 5 on page 26.

Upgrading to the Latest Search 1.x

Upgrading Cloudera Search involves stopping the Search service, using your operating system's package management tool to upgrade Search to the latest version, and then restarting the Search service.

- **Note:** To see which version of Cloudera Manager is recommended with the latest version of Search, refer to Cloudera Search Requirements on page 10.

Upgrading Search through Cloudera Manager - Parcels

To upgrade Search in a Cloudera Manager managed environment, using parcels:

1. If you originally installed using packages and now are switching to parcels, you must remove the Solr packages first.

   The list of packages you may need to remove are:

   - `solr`
   - `solr-doc`
   - `solr-mapreduce`
   - `hbase-solr`
   - `hbase-solr-doc`
   - `search`

   You can check which packages are installed using one of the following commands, depending on your operating system:

   ```
   rpm -qa              # RHEL, Oracle Linux, CentOS, Debian
   ```

   ```
   dpkg --get-selections # Debian
   ```

   Remove the packages using the appropriate `remove` command for your OS. For example:

   ```
   yum remove solr solr-doc solr-mapreduce hbase-solr hbase-solr-doc search    # RHEL,
    Oracle Linux, CentOS
   ```

2. Connect to the Cloudera Manager Admin Console.
3. Go to the **Hosts < Parcels** tab. You should see a parcel with a newer version of Search that you can upgrade to.
4. Click **Download**, then **Distribute**. (The button changes as each step completes.)
5. Click **Activate**.
6. When prompted, click **Restart** to restart the Search service.

Upgrading Search through Cloudera Manager - Packages

To upgrade Search in a Cloudera Manager managed environment, using packages:

1. Connect to the Cloudera Manager Admin Console.
2. In the **Services** tab, click the **Search** service.
3. Click **Actions** and click **Stop**.
4. Update the .repo files to point to the latest repo URLs. Depending on your version of CDH 4, you may need to upgrade your CDH 4 deployment in addition to your Search version.
   - Download the latest search `.repo` file, `cloudera-search.repo`, from `http://archive.cloudera.com/search/`. You can find links to the latest `.repo` or `.list` files at Cloudera Search Version and Download Information.

     The contents of Search `.repo` file should look similar to the following:

     ```
     [cloudera-search]
     # Packages for Cloudera Search version 1.x, on RedHat or CentOS 6 x86_64
     name=Cloudera Search version 1.x
     baseurl=http://archive.cloudera.com/search/redhat/6/x86_64/search/1/
     gpgkey =
     http://archive.cloudera.com/search/redhat/6/x86_64/search/RPM-GPG-KEY-cloudera
     gpgcheck = 1
     ```

     The contents of a `.list` file should look similar to the following:

     ```
     # Packages for Cloudera Search, version 1.x, on Debian 6.0 amd64
     deb http://archive.cloudera.com/search/debian/squeeze/amd64/search squeeze-search1
      contrib
     deb-src http://archive.cloudera.com/search/debian/squeeze/amd64/search
     squeeze-search1 contrib
     ```

   - You may also need to update your CDH 4 `.repo` or `.list` file. This can be found at `http://archive.cloudera.com/cdh4/`. Links to the CDH 4 repositories can be found at CDH 4 Version and Packaging Information.

     > **Note:** Make sure you have only one `.repo` file for a specific component. If you have a `.repo` file for a previous version, you should remove it before you download a new version.

   - To verify that you have the `.repo` files you expect:
     - `ls -l /etc/yum.repos.d/` for YUM
     - `ls -l /etc/apt/sources.list.d/` for Debian/Ubuntu
     - `ls -l /etc/zypp/repos.d/` for SLES

5. Use **one** of the following sets of commands to update Solr on each host in your cluster where Solr-server is installed:

   > **Note:** The `solr-doc` and `hbase-solr-doc` packages provide documentation and installing/updating them (as in the following commands) is optional.

   For RHEL, Oracle Linux, or CentOS systems:

   ```
   $ sudo yum clean all
   $ sudo yum update hbase-solr search solr solr-mapreduce solr-doc hbase-solr-doc
   ```

   For SUSE systems:

   ```
   $ sudo zypper clean --all
   $ sudo zypper install hbase-solr search solr solr-mapreduce solr-doc \
   hbase-solr-doc
   ```

For Debian or Ubuntu systems:

```
$ sudo apt-get install hbase-solr search solr solr-mapreduce solr-doc \
hbase-solr-doc
```

6. Connect to the Cloudera Manager Admin Console.
7. In the **Services** tab, click the Search service.
8. Click **Actions** and click **Start**.

Upgrading Search without Cloudera Manager

To upgrade Search without Cloudera Manager:

1. Stop the `solr-server` on each Search host in your cluster:

```
$ sudo service solr-server stop
```

2. Update the .repo files to point to the latest .repo URLs. Depending on your version of CDH 4, you may need to upgrade your CDH 4 deployment in addition to your Search version.
   - Download the latest search .repo file, `cloudera-search.repo`, from `http://archive.cloudera.com/search/`. You can find links to the latest .repo or .list files at Cloudera Search Version and Download Information. See the examples above for what the contents of the .repo files should look like.
   - You may also need to update your CDH 4 .repo or .list file. This can be found at `http://archive.cloudera.com/cdh4/`. Links to the CDH 4 repos can be found at CDH 4 Version and Packaging Information.

     > **Note:** Make sure you have only one .repo file for a specific component. If you have a .repo file for a previous version, you should remove it before you download a new version.

   - To verify that you have the `.repo` files you expect:
     - `ls -l /etc/yum.repos.d/` for YUM
     - `ls -l /etc/apt/sources.list.d/` for Debian/Ubuntu
     - `ls -l /etc/zypp/repos.d/` for SLES

3. Use **one** of the following sets of commands to update Search on each host in your cluster:

   > **Note:** The `solr-doc` and `hbase-solr-doc` packages provide documentation and installing/updating them (as in the following commands) is optional.

   For RHEL, Oracle Linux, or CentOS systems:

```
$ sudo yum update hbase-solr search solr solr-mapreduce solr-doc hbase-solr-doc
```

   For SUSE systems:

```
$ sudo zypper update hbase-solr search solr solr-mapreduce solr-doc \
hbase-solr-doc
```

   For Debian or Ubuntu systems:

```
$ sudo apt-get install hbase-solr search solr solr-mapreduce solr-server \
hbase-solr-indexer solr-doc hbase-solr-doc
```

4. Restart the Search service. Expect to see a process named `solrd` if the service started successfully.

```
$ sudo service solr-server start
$ ps ax | grep [s]olrd
 30574 ?        S      0:02 /bin/bash /usr/lib/solr/bin/solrd run
```

> **Note:**
>
> If the services did not start successfully (even though the `sudo service` command might display `[OK]`), check for errors in the Search log file, typically in `/var/log/solr`.

Upgrading Search 1.x to Search for CDH 5

If you are running Cloudera Manager, you must upgrade to Cloudera Manager 5 to run CDH 5. Because Search 1.x is in a separate repository from CDH 4, you must remove the Search 1.x packages and the Search `.repo` or `.list` file before upgrading CDH. This is true whether or not you are upgrading through Cloudera Manager.

1. Remove the Search packages.

   The list of packages you may need to remove are:

   - `solr`
   - `solr-doc`
   - `solr-mapreduce`
   - `hbase-solr`
   - `hbase-solr-doc`
   - `search`

   1. Check which packages are installed using one of the following commands, depending on your operating system:

```
rpm -qa              # RHEL, Oracle Linux, CentOS, Debian
```

```
dpkg --get-selections # Debian
```

   2. Remove the packages using the appropriate `remove` command for your OS. For example:

```
sudo yum remove solr solr-doc solr-mapreduce hbase-solr \
   hbase-solr-doc search      # RHEL, Oracle Linux, CentOS
```

2. Remove the Cloudera Search .repo or .list file:

Operating System	File to remove:
RHEL	`/etc/yum.repos.d/cloudera-search.repo`
SLES	`/etc/zypp/repos.d/cloudera-search.repo`
Ubuntu or Debian	`/etc/apt/sources.list.d/cloudera.list`

3. Upgrade from CDH 4 to CDH 5:

   - To upgrade using Cloudera Manager, see Upgrading to CDH 5 in a Cloudera Manager Deployment. This assumes you have upgraded to Cloudera Manager 5.
   - To upgrade without using Cloudera Manager, see Upgrading from CDH 4 to CDH 5.

4. If you upgraded to CDH 5 without using Cloudera Manager, you need to install the new version of Search:

Operating System	Command
RHEL	`sudo yum install solr-server`
SLES	`sudo zypper install solr-server`
Ubuntu or Debian	`sudo apt-get install solr-server`

Installing Hue Search

You must install and configure Hue before you can use Search with Hue.

1. Follow the instructions for Installing Hue.
2. Use **one** of the following commands to install Search applications on the Hue machine:

   For package installation on RHEL systems:

   ```
   sudo yum install hue-search
   ```

   For package installation on SLES systems:

   ```
   sudo zypper install hue-search
   ```

   For package installation on Ubuntu or Debian systems:

   ```
   sudo apt-get install hue-search
   ```

   For installation using tarballs:

   ```
   $ cd /usr/share/hue
   $ sudo tar -xzvf hue-search-####.tar.gz
   $ sudo /usr/share/hue/tools/app_reg/app_reg.py \
   --install /usr/share/hue/apps/search
   ```

3. Update the configuration information for the Solr Server:

Cloudera Manager Environment	Environment without Cloudera Manager

1. Connect to Cloudera Manager.
2. Select the **Hue** service.
3. Click **Configuration** > **View and Edit**.
4. Search for the word "safety".
5. Add information about your Solr host to **Hue Server (Base) / Advanced**. For example, if your hostname is `SOLR_HOST`, you might add the following:
`[search]`
`# URL of the Solr Server`
`solr_url=http://SOLR_HOST:8983/solr`
6. (Optional) To enable Hue in environments where Kerberos authentication is required, update the `security_enabled` property as follows:
`# Requires FQDN in solr_url if enabled`
`security_enabled=true`
	Update configuration information in `/etc/hue/hue.ini`.
	1. Specify the Solr URL. For example, to use `localhost` as your Solr host, you would add the following:
	`[search]`
	`# URL of the Solr Server, replace 'localhost' if Solr is running on another host`
	`solr_url=http://localhost:8983/solr/`
	2. (Optional) To enable Hue in environments where Kerberos authentication is required, update the `security_enabled` property as follows:
	`# Requires FQDN in solr_url if enabled`
	`security_enabled=true`

4. Configure secure impersonation for Hue.
   - If you are using Search in an environment that uses Cloudera Manager 4.8 or later, secure impersonation for Hue is automatically configured. To review secure impersonation settings in the Cloudera Manager home page:
     1. Go to the HDFS service.
     2. Click the **Configuration** tab.
     3. Select **Scope** > **All**.
     4. Select **Category** > **All**.
     5. Type hue `proxy` in the Search box.
     6. Note the Service-Wide wild card setting for **Hue Proxy Hosts** and **Hue Proxy User Groups**.
   - If you are not using Cloudera Manager or are using a version earlier than Cloudera Manager 4.8, configure Hue to impersonate any user that makes requests by modifying `/etc/default/solr`. The changes you make may vary according to the users for which you want to configure secure impersonation. For example, you might make the following changes:

     ```
     SOLR_SECURITY_ALLOWED_PROXYUSERS=hue
     SOLR_SECURITY_PROXYUSER_hue_HOSTS=*
     SOLR_SECURITY_PROXYUSER_hue_GROUPS=*
     ```

     For more information about Secure Impersonation or to set up additional users for Secure Impersonation, see Enabling Secure Impersonation on page 96.

5. (Optional) To view files in HDFS, ensure that the correct `webhdfs_url` is included in `hue.ini` and WebHDFS is properly configured as described in Configuring CDH Components for Hue.
6. Restart Hue:

   ```
   $ sudo /etc/init.d/hue restart
   ```

7. Open `http://hue-host.com:8888/search/` in your browser.

Updating Hue Search

To update Hue search, install updates and restart the Hue service.

1. On the Hue machine, update Hue search:

   ```
   $ cd /usr/share/hue
   $ sudo tar -xzvf hue-search-####.tar.gz
   $ sudo /usr/share/hue/tools/app_reg/app_reg.py \
   --install /usr/share/hue/apps/search
   ```

2. Restart Hue:

   ```
   $ sudo /etc/init.d/hue restart
   ```

Cloudera Search Version and Download Information

For installation instructions, see Search Installation on page 10.

For information about new features in the latest release and issues that are fixed or still outstanding, see the Cloudera Search Release Notes on page 118.

Search Download Information

> **Note:** All packages are 64-bit.

Search 1.3.0

Release Date: May 2014

Cloudera Search 1.3 is supported with CDH 4.7.

Repository Type	Location	Repo or List file
Yum RHEL 6/CentOS 6 (64-bit)	RHEL 6/CentOS 6 Repo Location	RHEL 6/CentOS 6 Repo File
Yum RHEL 5/CentOS 5 (64-bit)	RHEL 5/CentOS 5 Repo Location	RHEL 5/CentOS 5 Repo File
Zypper SLES 11 (64-bit)	SLES 11 Repo Location	SLES 11 Repo File
Apt-Get Ubuntu 10.04 (Lucid) (64-bit)	Ubuntu 10.04 List File Location	Ubuntu 10.04 List File
Apt-Get Ubuntu 12.04 (Precise) (64-bit)	Ubuntu 12.04 List File Location	Ubuntu 12.04 List File
Apt-Get Debian (Squeeze) (64-bit)	Debian (Squeeze) List File Location	Debian (Squeeze) List File

Search 1.2.0

Release Date: February 2014

Cloudera Search 1.2 is supported with CDH 4.6.

Repository Type	Location	Repo or List file
Yum RHEL 6/CentOS 6 (64-bit)	RHEL 6/CentOS 6 Repo Location	RHEL 6/CentOS 6 Repo File
Yum RHEL 5/CentOS 5 (64-bit)	RHEL 5/CentOS 5 Repo Location	RHEL 5/CentOS 5 Repo File
Zypper SLES 11 (64-bit)	SLES 11 Repo Location	SLES 11 Repo File
Apt-Get Ubuntu 10.04 (Lucid) (64-bit)	Ubuntu 10.04 List File Location	Ubuntu 10.04 List File
Apt-Get Ubuntu 12.04 (Precise) (64-bit)	Ubuntu 12.04 List File Location	Ubuntu 12.04 List File
Apt-Get Debian (Squeeze) (64-bit)	Debian (Squeeze) List File Location	Debian (Squeeze) List File

Search 1.1.0

Release Date: November 2013

Cloudera Search 1.1 is supported with CDH 4.5.

Repository Type	Location	Repo or List file
Yum RHEL 6/CentOS 6 (64-bit)	RHEL 6/CentOS 6 Repo Location	RHEL 6/CentOS 6 Repo File

Repository Type	Location	Repo or List file
Yum RHEL 5/CentOS 5 (64-bit)	RHEL 5/CentOS 5 Repo Location	RHEL 5/CentOS 5 Repo File
Zypper SLES 11 (64-bit)	SLES 11 Repo Location	SLES 11 Repo Location
Apt-Get Ubuntu 10.04 (Lucid) (64-bit)	Ubuntu 10.04 List File Location	Ubuntu 10.04 List File
Apt-Get Ubuntu 12.04 (Precise) (64-bit)	Ubuntu 12.04 List File Location	Ubuntu 12.04 List File
Apt-Get Debian (Squeeze) (64-bit)	Debian (Squeeze) List File Location	Debian (Squeeze) List File

Search 1.0.0

Release Date: September 2013

Cloudera Search 1.0.0 is supported with CDH 4.3 and CDH 4.4.

Repository Type	Location	Repo or List file
Yum RHEL 6/CentOS 6 (64-bit)	RHEL 6/CentOS 6 Repo Location	RHEL 6/CentOS 6 Repo File
Yum RHEL 5/CentOS 5 (64-bit)	RHEL 5/CentOS 5 Repo Location	RHEL 5/CentOS 5 Repo File
Zypper SLES 11 (64-bit)	SLES 11 Repo Location	SLES 11 Repo Location
Apt-Get Ubuntu 10.04 (Lucid) (64-bit)	Ubuntu 10.04 List File Location	Ubuntu 10.04 List File
Apt-Get Ubuntu 12.04 (Precise) (64-bit)	Ubuntu 12.04 List File Location	Ubuntu 12.04 List File
Apt-Get Debian (Squeeze) (64-bit)	Debian (Squeeze) List File Location	Debian (Squeeze) List File

Cloudera Search User Guide

This guide explains how to configure and use Cloudera Search. This includes topics such as extracting, transforming, and loading data, establishing high availability, and troubleshooting.

Cloudera Search documentation includes:

- Cloudera Search Release Notes on page 118
- Cloudera Search Version and Download Information on page 28
- Search Installation on page 10
- Cloudera Search Frequently Asked Questions on page 114

About this Guide

This guide explains how to configure and use Cloudera Search. This includes topics such as extracting, transforming, and loading data, establishing high availability, and troubleshooting.

Cloudera Search documentation includes:

- Cloudera Search Release Notes on page 118
- Cloudera Search Version and Download Information on page 28
- Search Installation on page 10
- Cloudera Search Frequently Asked Questions on page 114

Cloudera Search Overview

Cloudera Search provides near real-time (NRT) access to data stored in or ingested into Hadoop and HBase. Search provides near real-time indexing, batch indexing, full-text exploration and navigated drill-down, as well as a simple, full-text interface that requires no SQL or programming skills.

Search is fully integrated in the data-processing platform and uses the flexible, scalable, and robust storage system included with CDH. This eliminates the need to move large data sets across infrastructures to perform business tasks.

Cloudera Search incorporates Apache Solr, which includes Apache Lucene, SolrCloud, Apache Tika, and Solr Cell. Cloudera Search is tightly integrated with CDH 4.

Using Search with the CDH infrastructure provides:

- Simplified infrastructure
- Better production visibility
- Quicker insights across various data types
- Quicker problem resolution
- Simplified interaction and platform access for more users and use cases
- Scalability, flexibility, and reliability of search services on the same platform used to execute other types of workloads on the same data

The following table describes Cloudera Search features.

Table 2: Cloudera Search Features

Feature	Description
Unified management and monitoring with Cloudera Manager	Cloudera Manager provides unified and centralized management and monitoring for CDH and Cloudera Search. Cloudera Manager simplifies

Feature	Description
	deployment, configuration, and monitoring of your search services. Many existing search solutions lack management and monitoring capabilities and fail to provide deep insight into utilization, system health, trending, and other supportability aspects.
Index storage in HDFS	Cloudera Search is integrated with HDFS for index storage. Indexes created by Solr/Lucene can be directly written in HDFS with the data, instead of to local disk, thereby providing fault tolerance and redundancy. Cloudera Search is optimized for fast read and write of indexes in HDFS while indexes are served and queried through standard Solr mechanisms. Because data and indexes are co-located, data processing does not require transport or separately managed storage.
Batch index creation through MapReduce	To facilitate index creation for large data sets, Cloudera Search has built-in MapReduce jobs for indexing data stored in HDFS. As a result, the linear scalability of MapReduce is applied to the indexing pipeline.
Real-time and scalable indexing at data ingest	Cloudera Search provides integration with Flume to support near real-time indexing. As new events pass through a Flume hierarchy and are written to HDFS, those events can be written directly to Cloudera Search indexers. In addition, Flume supports routing events, filtering, and annotation of data passed to CDH. These features work with Cloudera Search for improved index sharding, index separation, and document-level access control.
Easy interaction and data exploration through Hue	A Cloudera Search GUI is provided as a Hue plug-in, enabling users to interactively query data, view result files, and do faceted exploration. Hue can also schedule standing queries and explore index files. This GUI uses the Cloudera Search API, which is based on the standard Solr API.
Simplified data processing for Search workloads	Cloudera Search relies on Apache Tika for parsing and preparation of many of the standard file formats for indexing. Additionally, Cloudera Search supports Avro, Hadoop Sequence, and Snappy file format mappings, as well as Log file formats, JSON, XML, and HTML. Cloudera Search also provides data preprocessing using Morphlines, which simplifies index configuration for these formats. Users can use the configuration for other applications, such as MapReduce jobs.
HBase search	Cloudera Search integrates with HBase, enabling full-text search of stored data without affecting HBase performance. A listener monitors the replication event stream and captures each write or update-replicated event, enabling extraction and mapping. The event is then sent directly to Solr indexers and written to indexes in HDFS, using the same process as for other indexing workloads of Cloudera Search. The indexes can be served immediately, enabling near real-time search of HBase data.

How Cloudera Search Works

In a near real-time indexing use case, Cloudera Search indexes events that are streamed through Apache Flume to be stored in CDH. Fields and events are mapped to standard Solr indexable schemas. Lucene indexes events, and integration with Cloudera Search allows the index to be directly written and stored in standard Lucene index files in HDFS. Flume event routing and storage of data in partitions in HDFS can also be applied. Events can be routed and streamed through multiple Flume agents and written to separate Lucene indexers that can write into separate index shards, for better scale when indexing and quicker responses when searching.

The indexes are loaded from HDFS to Solr cores, exactly like Solr would have read from local disk. The difference in the design of Cloudera Search is the robust, distributed, and scalable storage layer of HDFS, which helps eliminate costly downtime and allows for flexibility across workloads without having to move data. Search queries can then be submitted to Solr through either the standard Solr API, or through a simple search GUI application, included in Cloudera Search, which can be deployed in Hue.

Cloudera Search batch-oriented indexing capabilities can address needs for searching across batch uploaded files or large data sets that are less frequently updated and less in need of near-real-time indexing. For such cases, Cloudera Search includes a highly scalable indexing workflow based on MapReduce. A MapReduce workflow is launched onto specified files or folders in HDFS, and the field extraction and Solr schema mapping is executed during the mapping phase. Reducers use Solr to write the data as a single index or as index shards, depending on your configuration and preferences. Once the indexes are stored in HDFS, they can be queried using standard Solr mechanisms, as previously described above for the near-real-time indexing use case.

The Lily HBase Indexer Service is a flexible, scalable, fault tolerant, transactional, near real-time oriented system for processing a continuous stream of HBase cell updates into live search indexes. Typically, the time between data ingestion using the Flume sink to that content potentially appearing in search results is measured in seconds, although this duration is tunable. The Lily HBase Indexer uses Solr to index data stored in HBase. As HBase applies inserts, updates, and deletes to HBase table cells, the indexer keeps Solr consistent with the HBase table contents, using standard HBase replication features. The indexer supports flexible custom application-specific rules to extract, transform, and load HBase data into Solr. Solr search results can contain `columnFamily:qualifier` links back to the data stored in HBase. This way applications can use the Search result set to directly access matching raw HBase cells. Indexing and searching do not affect operational stability or write throughput of HBase because the indexing and searching processes are separate and asynchronous to HBase.

Understanding Cloudera Search

Cloudera Search fits into the broader set of solutions available for analyzing information in large data sets. With especially large data sets, it is impossible to store all information reliably on a single machine and then query that data. CDH provides both the means and the tools to store the data and run queries. You can explore data through:

- MapReduce jobs
- Cloudera Impala queries
- Cloudera Search queries

CDH provides storage of and access to large data sets using MapReduce jobs, but creating these jobs requires technical knowledge, and each job can take minutes or more to run. The longer run times associated with MapReduce jobs can interrupt the process of exploring data.

To provide more immediate queries and responses and to eliminate the need to write MapReduce applications, Cloudera offers Impala. Impala returns results in seconds instead of minutes.

Although Impala is a fast, powerful application, it uses SQL-based querying syntax. Using Impala can be challenging for users who are not familiar with SQL. If you do not know SQL, you can use Cloudera Search. In addition, Impala, Hive, and Pig all require a structure that is applied at query time, whereas Search supports free-text search on any data or fields you have indexed.

How Search Leverages Existing Infrastructure

Any data already in a CDH deployment can be indexed and made available for query by Cloudera Search. For data that is not stored in CDH, Cloudera Search provides tools for loading data into the existing infrastructure, and for indexing data as it is moved to HDFS or written to HBase.

By leveraging existing infrastructure, Cloudera Search eliminates the need to create new, redundant structures. In addition, Cloudera Search leverages services provided by CDH and Cloudera Manager in a way that does not

interfere with other tasks running in the same environment. This way, you can reuse existing infrastructure without the cost and problems associated with running multiple services in the same set of systems.

Cloudera Search and Other Cloudera Components

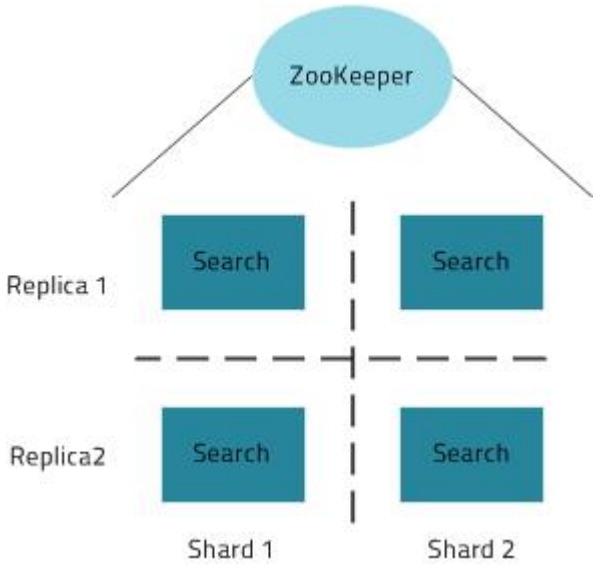
Cloudera Search interacts with other Cloudera components to solve different problems. The following table lists Cloudera components that contribute to the Search process and describes how they interact with Cloudera Search:

Component	Contribution	Applicable To
HDFS	Stores source documents. Search indexes source documents to make them searchable. Files that support Cloudera Search, such as Lucene index files and write-ahead logs, are also stored in HDFS. Using HDFS provides simpler provisioning on a larger base, redundancy, and fault tolerance. With HDFS, Cloudera Search servers are essentially stateless, so host failures have minimal consequences. HDFS also provides snapshotting, inter-cluster replication, and disaster recovery.	All cases
MapReduce	Search includes a pre-built MapReduce-based job. This job can be used for on-demand or scheduled indexing of any supported data set stored in HDFS. This job utilizes cluster resources for scalable batch indexing.	Many cases
Flume	Search includes a Flume sink that enables writing events directly to indexers deployed on the cluster, allowing data indexing during ingestion.	Many cases
Hue	Search includes a Hue front-end search application that uses standard Solr APIs. The application can interact with data indexed in HDFS. The application provides support for the Solr standard query language, visualization of faceted search functionality, and a typical full text search GUI-based.	Many cases
ZooKeeper	Coordinates distribution of data and metadata, also known as shards. It provides automatic failover to increase service resiliency.	Many cases
HBase	Supports indexing of stored data, extracting columns, column families, and key information as fields. Because HBase does not use secondary indexing, Cloudera Search can complete full-text searches of content in rows and tables in HBase.	Some cases
Cloudera Manager	Deploys, configures, manages, and monitors Cloudera Search processes and resource utilization across services on the cluster. Cloudera Manager helps simplify Cloudera Search administration, but it is not required.	Some cases
Oozie	Automates scheduling and management of indexing jobs. Oozie can check for new data and begin indexing jobs as required.	Some cases
Impala	Further analyzes search results.	Some cases
Hive	Further analyzes search results.	Some cases
Avro	Includes metadata that Cloudera Search can use for indexing.	Some cases
Sqoop	Ingests data in batch and enables data availability for batch indexing.	Some cases
Mahout	Applies machine-learning processing to search results.	Some cases

Cloudera Search Architecture

Cloudera Search runs as a distributed service on a set of servers, and each server is responsible for a portion of the entire set of content to be searched. The entire set of content is split into smaller pieces, copies are made of these pieces, and the pieces are distributed among the servers. This provides two main advantages:

- **Dividing** the content into smaller pieces distributes the task of indexing the content among the servers.
- **Duplicating** the pieces of the whole allows queries to be scaled more effectively and enables the system to provide higher levels of availability.



Each Cloudera Search server can handle requests for information. As a result, a client can send requests to index documents or perform searches to any Search server, and that server routes the request to the correct server.

Cloudera Search Tasks and Processes

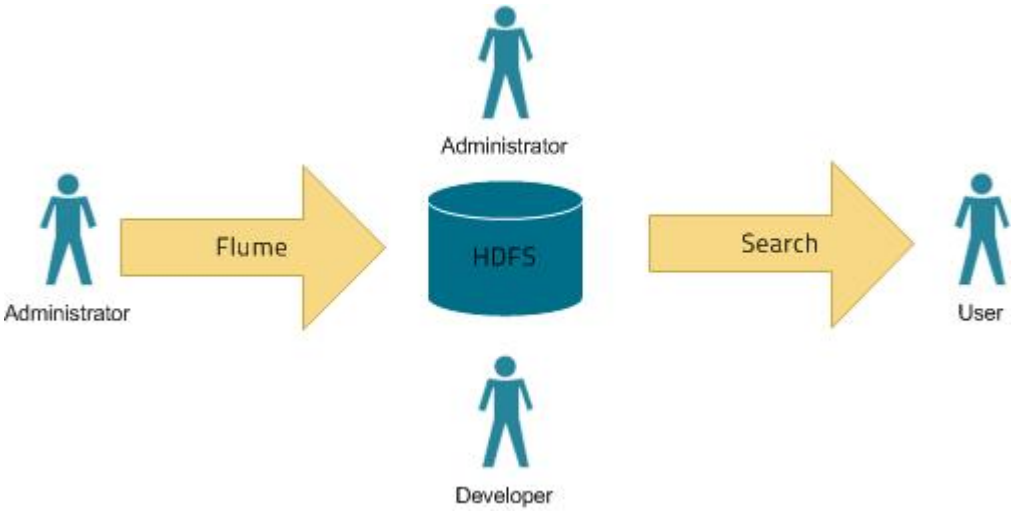
For content to be searchable, it must exist in CDH and be indexed. Content can either already exist in CDH and be indexed on demand, or it can be updated and indexed continuously. To make content searchable, first ensure that it is ingested or stored in CDH.

Ingestion

You can move content to CDH by using:

- Flume, a flexible, agent-based data ingestion framework.
- A copy utility such as `distcp` for HDFS.
- Sqoop, a structured data ingestion connector.
- `fuse-dfs`.

In a typical environment, administrators establish systems for search. For example, HDFS is established to provide storage; Flume or `distcp` are established for content ingestion. After administrators establish these services, users can use ingestion tools such as file copy utilities or Flume sinks.



Indexing

Content must be indexed before it can be searched. Indexing comprises the following steps:

1. Extraction, transformation, and loading (ETL) - Use existing engines or frameworks such as Apache Tika or Cloudera Morphlines.
   a. Content and metadata extraction
   b. Schema mapping
2. Create indexes using Lucene.
   a. Index creation
   b. Index serialization

Indexes are typically stored on a local file system. Lucene supports additional index writers and readers. One HDFS-based interface implemented as part of Apache Blur is integrated with Cloudera Search and has been optimized for CDH-stored indexes. All index data in Cloudera Search is stored in and served from HDFS.

You can index content in three ways:

Batch indexing using MapReduce

To use MapReduce to index documents, run a MapReduce job on content in HDFS to produce a Lucene index. The Lucene index is written to HDFS, and this index is subsequently used by search services to provide query results.

Batch indexing is most often used when bootstrapping a search cluster. The Map component of the MapReduce task parses input into indexable documents, and the Reduce component contains an embedded Solr server that indexes the documents produced by the Map. You can also configure a MapReduce-based indexing job to use all assigned resources on the cluster, utilizing multiple reducing steps for intermediate indexing and merging operations, and then writing the reduction to the configured set of shard sets for the service. This makes the batch indexing process as scalable as MapReduce workloads.

Near real-time (NRT) indexing using Flume

Flume events are typically collected and written to HDFS. Although any Flume event can be written, logs are most common.

Cloudera Search includes a Flume sink that enables you to write events directly to the indexer. This sink provides a flexible, scalable, fault-tolerant, near real-time (NRT) system for processing continuous streams of records to create live-searchable, free-text search indexes. Typically, data ingested using the Flume sink appears in search results in seconds, although you can tune this duration.

The Flume sink meets the needs of identified use cases that rely on NRT availability. Data can flow from multiple sources through multiple flume hosts. These hosts, which can be spread across a network, route this information to one or more Flume indexing sinks. Optionally, you can split the data flow, storing the data in HDFS while writing it to be indexed by Lucene indexers on the cluster. In that scenario, data exists both as data and as indexed data in the same storage infrastructure. The indexing sink extracts relevant data, transforms the material, and loads the results to live Solr search servers. These Solr servers are immediately ready to serve queries to end users or search applications.

This flexible, customizable system scales effectively because parsing is moved from the Solr server to the multiple Flume hosts for ingesting new content.

Search includes parsers for standard data formats including Avro, CSV, Text, HTML, XML, PDF, Word, and Excel. You can extend the system by adding additional custom parsers for other file or data formats in the form of Tika plug-ins. Any type of data can be indexed: a record is a byte array of any format, and custom ETL logic can handle any format variation.

In addition, Cloudera Search includes a simplifying ETL framework called Cloudera Morphlines that can help adapt and pre-process data for indexing. This eliminates the need for specific parser deployments, replacing them with simple commands.

Cloudera Search is designed to handle a variety of use cases:

- Search supports routing to multiple Solr collections to assign a single set of servers to support multiple user groups (multi-tenancy).
- Search supports routing to multiple shards to improve scalability and reliability.
- Index servers can be collocated with live Solr servers serving end-user queries, or they can be deployed on separate commodity hardware, for improved scalability and reliability.
- Indexing load can be spread across a large number of index servers for improved scalability and can be replicated across multiple index servers for high availability.

This flexible, scalable, highly available system provides low latency data acquisition and low latency querying. Instead of replacing existing solutions, Search complements use cases based on batch analysis of HDFS data using MapReduce. In many use cases, data flows from the producer through Flume to both Solr and HDFS. In this system, you can use NRT ingestion and batch analysis tools.

NRT indexing using some other client that uses the NRT API

Other clients can complete NRT indexing. This is done when the client first writes files directly to HDFS and then triggers indexing using the Solr REST API. Specifically, the API does the following:

1. Extract content from the document contained in HDFS, where the document is referenced by a URL.
2. Map the content to fields in the search schema.
3. Create or update a Lucene index.

This is useful if you index as part of a larger workflow. For example, you could trigger indexing from an Oozie workflow.

Querying

After data is available as an index, the query API provided by the search service allows direct queries to be executed or to be facilitated through a command-line tool or graphical interface. Cloudera Search provides a simple UI application that can be deployed with Hue, or you can create a custom application based on the standard Solr API. Any application that works with Solr is compatible and runs as a search-serving application for Cloudera Search, because Solr is the core.

Cloudera Search Tutorial

The topics in this tutorial document assume you have completed the instructions in the Cloudera Search Installation Guide.

> **Warning:** This tutorial is intended for use in an unsecured environment. In an environment that requires Kerberos authentication, this tutorial can not be completed without additional configuration.

This tutorial first describes preparatory steps:

- Validating the Deployment with the Solr REST API
- Preparing to Index Data

Following are two tutorial topics, including indexing strategies:

- Batch Indexing Using MapReduce
- Near Real Time (NRT) Indexing Using Flume and the Solr Sink

This tutorial uses a modified `schema.xml` and `solrconfig.xml` file. In the versions of these files included with the tutorial, unused fields have been removed for simplicity. Original versions of these files include many additional options. For information on all available options, see the Solr wiki:

- SchemaXml
- SolrConfigXml

Validating the Deployment with the Solr REST API

Validate the deployment by indexing and querying documents with the Solr REST API. Before beginning this process, you must have access to the Solr admin web console, as detailed in Deploying Cloudera Search on page 16.

> **Note:** Validating deployments using the Solr REST API only succeeds if Kerberos is not required. Use the following processes only if Kerberos is disabled.

Initiating the collection

1. Generate the configuration files for the collection:

```
$ solrctl instancedir --generate $HOME/solr_configs
```

2. Upload the instance directory to ZooKeeper:

```
$ solrctl instancedir --create collection1 $HOME/solr_configs
```

3. Create the new collection:

```
$ solrctl collection --create collection1 -s 2 -c collection1
```

Indexing Data

Begin by indexing data to be queried later. Sample data is provided in the installed packages. Replace `$SOLRHOST` in the example below with the name of any host running the Solr process.

- **Parcel-based Installation:**

```
$ cd /opt/cloudera/parcels/CDH/share/doc/solr-doc*/example/exampledocs
$ java -Durl=http://$SOLRHOST:8983/solr/collection1/update -jar post.jar *.xml
```

- **Package-based Installation:**

```
$ cd /usr/share/doc/solr-doc*/example/exampledocs
$ java -Durl=http://$SOLRHOST:8983/solr/collection1/update -jar post.jar *.xml
```

Running Queries

After you have indexed data, you can run a query.

To run a query:

1. Open the following link in a browser, replacing `$SOLRHOST` with the name of any host running the Solr process: `http://$SOLRHOST:8983/solr`.
2. Click the collection name in the left panel.
3. Click **Query** in the Menu and select **execute query**.

> **Note:** Choose **wt** as json and select the **indent** option in the web GUI to see more readable output.

Next Steps

Consider indexing more data using the Solr REST API, or move to batch indexing with MapReduce or NRT indexing with Flume. To learn more about Solr, see the Apache Solr Tutorial.

Preparing to Index Data

Complete the following steps to prepare for indexing example data with MapReduce or Flume:

1. Start a SolrCloud cluster containing two servers (this example uses two shards) as described in Deploying Cloudera Search on page 16. Stop and continue with the next step here after you verify the Runtime Solr Configuration.
2. Generate the configuration files for the collection, including the tweet specific `schema.xml`:
   - **Parcel-based Installation:**

     ```
     $ solrctl instancedir --generate $HOME/solr_configs2
     $ cp
     /opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/collection2/conf/schema.xml
      \
     $HOME/solr_configs2/conf
     ```

   - **Package-based Installation:**

     ```
     $ solrctl instancedir --generate $HOME/solr_configs2
     $ cp /usr/share/doc/search*/examples/solr-nrt/collection2/conf/schema.xml \
     $HOME/solr_configs2/conf
     ```

3. Upload the instance directory to ZooKeeper:

   ```
   $ solrctl instancedir --create collection2 $HOME/solr_configs2
   ```

4. Create the new collection:

   ```
   $ solrctl collection --create collection2 -s 2 -c collection2
   ```

5. Verify the collection is live. For example, for the localhost, use `http://localhost:8983/solr/#/~cloud`.
6. Prepare the configuration for use with MapReduce:

   ```
   $ cp -r $HOME/solr_configs2 $HOME/collection2
   ```

7. Locate input files suitable for indexing, and check that the directory exists. This example assumes you are running the following commands as `$USER` with access to HDFS.

- **Parcel-based Installation:**

```
$ sudo -u hdfs hadoop fs -mkdir -p /user/$USER
$ sudo -u hdfs hadoop fs -chown $USER:$USER /user/$USER
$ hadoop fs -mkdir -p /user/$USER/indir
$ hadoop fs -copyFromLocal \
/opt/cloudera/parcels/CDH/share/doc/search*/examples/test-documents/sample-statuses-*.avro
 \
/user/$USER/indir/
$ hadoop fs -ls /user/$USER/indir
```

- **Package-based Installation:**

```
$ sudo -u hdfs hadoop fs -mkdir -p /user/$USER
$ sudo -u hdfs hadoop fs -chown $USER:$USER /user/$USER
$ hadoop fs -mkdir -p /user/$USER/indir
$ hadoop fs -copyFromLocal \
/usr/share/doc/search*/examples/test-documents/sample-statuses-*.avro \
/user/$USER/indir/
$ hadoop fs -ls /user/$USER/indir
```

8. Ensure that `outdir` exists in HDFS and is empty:

```
$ hadoop fs -rm -r -skipTrash /user/$USER/outdir
$ hadoop fs -mkdir /user/$USER/outdir
$ hadoop fs -ls /user/$USER/outdir
```

9. Collect HDFS/MapReduce configuration details by downloading them from Cloudera Manager or using `/etc/hadoop`, depending on your installation mechanism for the Hadoop cluster. This example uses the configuration in `/etc/hadoop/conf.cloudera.mapreduce1`. Substitute the correct Hadoop configuration path for your cluster.

Batch Indexing Using MapReduce

The following sections include examples that illustrate using MapReduce to index tweets. These examples require that you:

- Complete the process of Preparing to Index Data on page 39.
- Install the MapReduce tools for Cloudera Search as described in Installing MapReduce Tools for use with Cloudera Search on page 21.

Batch Indexing into Online Solr Servers Using GoLive

MapReduceIndexerTool is a MapReduce batch job driver that creates a set of Solr index shards from a set of input files and writes the indexes into HDFS in a flexible, scalable, and fault-tolerant manner. Using GoLive, MapReduceIndexerTool also supports merging the output shards into a set of live customer-facing Solr servers, typically a SolrCloud. The following sample steps demonstrate these capabilities.

1. Delete all existing documents in Solr.

```
$ solrctl collection --deletedocs collection2
```

2. Run the MapReduce job using GoLive. Replace `$NNHOST` and `$ZKHOST` in the command with your NameNode and ZooKeeper host names and port numbers, as required. You do not need to specify `--solr-home-dir` because the job accesses it from ZooKeeper.

- **Parcel-based Installation:**

```
$ hadoop --config /etc/hadoop/conf.cloudera.MAPREDUCE-1 jar \
/opt/cloudera/parcels/CDH/lib/solr/contrib/mr/search-mr-*-job.jar \
org.apache.solr.hadoop.MapReduceIndexerTool -D \
'mapred.child.java.opts=-Xmx500m' --log4j \
/opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/log4j.properties
```

```
 --morphline-file \
/opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/test-morphlines/tutorialReadAvroContainer.conf
 \
--output-dir hdfs://$NNHOST:8020/user/$USER/outdir --verbose --go-live \
--zk-host $ZKHOST:2181/solr --collection collection2 \
hdfs://$NNHOST:8020/user/$USER/indir
```

- **Package-based Installation:**

```
$ hadoop --config /etc/hadoop/conf.cloudera.MAPREDUCE-1 jar \
/usr/lib/solr/contrib/mr/search-mr-*-job.jar \
org.apache.solr.hadoop.MapReduceIndexerTool -D \
'mapred.child.java.opts=-Xmx500m' --log4j \
/usr/share/doc/search*/examples/solr-nrt/log4j.properties --morphline-file \
/usr/share/doc/search*/examples/solr-nrt/test-morphlines/tutorialReadAvroContainer.conf
 \
--output-dir hdfs://$NNHOST:8020/user/$USER/outdir --verbose --go-live \
--zk-host $ZKHOST:2181/solr --collection collection2 \
hdfs://$NNHOST:8020/user/$USER/indir
```

- **Note:** This command requires a morphline file, which must include a `SOLR_LOCATOR`. Any CLI parameters for `--zkhost` and `--collection` override the parameters of the `solrLocator`. The snippet that includes the `SOLR_LOCATOR` might appear as follows:

```
SOLR_LOCATOR : {
  # Name of solr collection
  collection : collection

  # ZooKeeper ensemble
  zkHost : "$ZK_HOST"
}

morphlines : [
  {
    id : morphline1
    importCommands : ["org.kitesdk.**", "org.apache.solr.**"]
    commands : [
      { generateUUID { field : id } }

      { # Remove record fields that are unknown to Solr schema.xml.
        # Recall that Solr throws an exception on any attempt to load a
document that
        # contains a field that isn't specified in schema.xml.
        sanitizeUnknownSolrFields {
          solrLocator : ${SOLR_LOCATOR} # Location from which to fetch Solr
 schema
        }
      }

      { logDebug { format : "output record: {}", args : ["@{}"] } }

      {
        loadSolr {
          solrLocator : ${SOLR_LOCATOR}
        }
      }
    ]
  }
]
```

3. Check the job tracker status at `http://localhost:50030/jobtracker.jsp`.
4. When the job is complete, run some Solr queries. For example, for `myserver.example.com`, use: `http://myserver.example.com:8983/solr/collection2/select?q=*%3A*&wt=json&indent=true`

   For help on how to run a Hadoop MapReduce job, use the following command:

- **Parcel-based Installation:**

```
$ hadoop jar /opt/cloudera/parcels/CDH/lib/solr/contrib/mr/search-mr-*-job.jar
 \
org.apache.solr.hadoop.MapReduceIndexerTool --help
```

- **Package-based Installation:**

```
$ hadoop jar /usr/lib/solr/contrib/mr/search-mr-*-job.jar \
org.apache.solr.hadoop.MapReduceIndexerTool --help
```

- **Note:**
  - For development purposes, use the `MapReduceIndexerTool --dry-run` option to run in local mode and print documents to `stdout`, instead of loading them to Solr. Using this option causes the morphline to execute in the client process without submitting a job to MapReduce. Executing in the client process provides faster turnaround during early trial and debug sessions.
  - To print diagnostic information, such as the content of records as they pass through the morphline commands, enable TRACE log level diagnostics by adding the following entry to your `log4j.properties` file:

    ```
    log4j.logger.com.cloudera.cdk.morphline=TRACE
    ```

    The `log4j.properties` file can be passed using the `MapReduceIndexerTool --log4j` command-line option.

Batch Indexing into Offline Solr Shards

Running the MapReduce job without GoLive causes the job to create a set of Solr index shards from a set of input files and write the indexes to HDFS. You can then explicitly point each Solr server to one of the HDFS output shard directories.

Batch indexing into offline Solr shards is mainly intended for offline use-cases by experts. Cases requiring read-only indexes for searching can be handled using batch indexing without the `--go-live` option. By not using GoLive, you can avoid copying datasets between segments, thereby reducing resource demands.

1. Delete all existing documents in Solr.

```
$ solrctl collection --deletedocs collection2
$ sudo -u hdfs hadoop fs -rm -r -skipTrash /user/$USER/outdir
```

2. Run the Hadoop MapReduce job, replacing `$NNHOST` in the command with your NameNode hostname and port number, as required.

   - **Parcel-based Installation:**

```
$ hadoop --config /etc/hadoop/conf.cloudera.MAPREDUCE-1 jar \
/opt/cloudera/parcels/CDH/lib/solr/contrib/mr/search-mr-*-job.jar \
org.apache.solr.hadoop.MapReduceIndexerTool -D \
'mapred.child.java.opts=-Xmx500m' --log4j \
/opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/log4j.properties
 --morphline-file \
/opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/test-morphlines/tutorialReadAvroContainer.conf
 \
--output-dir hdfs://$NNHOST:8020/user/$USER/outdir --verbose --solr-home-dir \
$HOME/collection2 --shards 2 hdfs://$NNHOST:8020/user/$USER/indir
```

- **Package-based Installation:**

```
$ hadoop --config /etc/hadoop/conf.cloudera.MAPREDUCE-1 jar \
/usr/lib/solr/contrib/mr/search-mr-*-job.jar \
org.apache.solr.hadoop.MapReduceIndexerTool -D \
'mapred.child.java.opts=-Xmx500m' --log4j \
/usr/share/doc/search*/examples/solr-nrt/log4j.properties --morphline-file \
/usr/share/doc/search*/examples/solr-nrt/test-morphlines/tutorialReadAvroContainer.conf
 \
--output-dir hdfs://$NNHOST:8020/user/$USER/outdir --verbose --solr-home-dir \
$HOME/collection2 --shards 2 hdfs://$NNHOST:8020/user/$USER/indir
```

3. Check the job tracker status. For example, for the localhost, use `http://localhost:50030/jobtracker.jsp`.
4. After the job is completed, check the generated index files. Individual shards are written to the results directory with names of the form `part-00000`, `part-00001`, `part-00002`. There are only two shards in this example.

```
$ hadoop fs -ls /user/$USER/outdir/results
$ hadoop fs -ls /user/$USER/outdir/results/part-00000/data/index
```

5. Stop Solr on each host of the cluster.

```
$ sudo service solr-server stop
```

6. List the host name folders used as part of the path to each index in the SolrCloud cluster.

```
$ hadoop fs -ls /solr/collection2
```

7. Move index shards into place.

   a. Remove outdated files:

```
$ sudo -u solr hadoop fs -rm -r -skipTrash \
/solr/collection2/$HOSTNAME1/data/index
$ sudo -u solr hadoop fs -rm -r -skipTrash \
/solr/collection2/$HOSTNAME2/data/index
```

   b. Ensure correct ownership of required directories:

```
$ sudo -u hdfs hadoop fs -chown -R solr /user/$USER/outdir/results
```

   c. Move the two index shards into place (the two servers you set up in Preparing to Index Data on page 39):

```
$ sudo -u solr hadoop fs -mv /user/$USER/outdir/results/part-00000/data/index
\
/solr/collection2/$HOSTNAME1/data/
$ sudo -u solr hadoop fs -mv /user/$USER/outdir/results/part-00001/data/index
\
/solr/collection2/$HOSTNAME2/data/
```

8. Start Solr on each host of the cluster:

```
$ sudo service solr-server start
```

9. Run some Solr queries. For example, for `myserver.example.com`, use:
   `http://myserver.example.com:8983/solr/collection2/select?q=*%3A*&wt=json&indent=true`

Near Real Time (NRT) Indexing Using Flume and the Solr Sink

The following section describes how to use Flume to index tweets. Before beginning this process, complete the process of Preparing to Index Data.

Deploying Solr Sink into the Flume Agent

Copy the configuration files.

- **Parcel-based Installation:**

```
$ sudo cp -r $HOME/solr_configs2 /etc/flume-ng/conf/collection2
$ sudo cp
/opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/twitter-flume.conf
\
/etc/flume-ng/conf/flume.conf
$ sudo cp
/opt/cloudera/parcels/CDH/share/doc/search*/examples/solr-nrt/test-morphlines/tutorialReadAvroContainer.conf
 \
/etc/flume-ng/conf/morphline.conf
```

- **Package-based Installation:**

```
$ sudo cp -r $HOME/solr_configs2 /etc/flume-ng/conf/collection2
$ sudo cp /usr/share/doc/search*/examples/solr-nrt/twitter-flume.conf \
/etc/flume-ng/conf/flume.conf
$ sudo cp
/usr/share/doc/search*/examples/solr-nrt/test-morphlines/tutorialReadAvroContainer.conf
 \
/etc/flume-ng/conf/morphline.conf
```

Configuring the Flume Solr Sink

1. Edit `/etc/flume-ng/conf/flume.conf` to specify the Flume source details and set up the flow. You must set the relative or absolute path to the morphline configuration file:

```
agent.sinks.solrSink.morphlineFile = /etc/flume-ng/conf/morphline.conf
```

2. Edit `/etc/flume-ng/conf/morphline.conf` to specify the Solr location details using a `SOLR_LOCATOR`. The snippet that includes the `SOLR_LOCATOR` might appear as follows:

```
SOLR_LOCATOR : {
  # Name of solr collection
  collection : collection

  # ZooKeeper ensemble
  zkHost : "$ZK_HOST"
}

morphlines : [
  {
    id : morphline1
    importCommands : ["org.kitesdk.**", "org.apache.solr.**"]
    commands : [
      { generateUUID { field : id } }

      { # Remove record fields that are unknown to Solr schema.xml.
        # Recall that Solr throws an exception on any attempt to load a document
that
        # contains a field that isn't specified in schema.xml.
        sanitizeUnknownSolrFields {
          solrLocator : ${SOLR_LOCATOR} # Location from which to fetch Solr schema

        }
      }

      { logDebug { format : "output record: {}", args : ["@{}"] } }

      {
        loadSolr {
          solrLocator : ${SOLR_LOCATOR}
        }
      }
```

```
    ]
  }
]
```

3. Copy `flume-env.sh.template` to `flume-env.sh`:

```
$ sudo cp /etc/flume-ng/conf/flume-env.sh.template \
/etc/flume-ng/conf/flume-env.sh
```

4. Edit `/etc/flume-ng/conf/flume-env.sh`, inserting or replacing `JAVA_OPTS` as follows:

```
JAVA_OPTS="-Xmx500m"
```

5. (Optional) Modify Flume logging settings to facilitate monitoring and debugging:

```
$ sudo bash -c 'echo "log4j.logger.org.apache.flume.sink.solr=DEBUG" >> \
/etc/flume-ng/conf/log4j.properties'
$ sudo bash -c 'echo "log4j.logger.com.cloudera.cdk.morphline=TRACE" >> \
/etc/flume-ng/conf/log4j.properties'
```

6. (Optional) You can configure the location at which Flume finds Cloudera Search dependencies for Flume Solr Sink using `SEARCH_HOME`. For example, if you installed Flume from a tarball package, you can configure it to find required files by setting `SEARCH_HOME`. To set `SEARCH_HOME` use a command of the form:

   - **Parcel-based Installation:**

```
$ export SEARCH_HOME=/opt/cloudera/parcels/CDH/lib/search
```

   - **Package-based Installation:**

```
$ export SEARCH_HOME=/usr/lib/search
```

   - **Note:** Alternatively, you can add the same setting to `flume-env.sh`.

Configuring Flume Solr Sink to Sip from the Twitter Firehose

Edit `/etc/flume-ng/conf/flume.conf` and replace the following properties with credentials from a valid Twitter account. The Flume TwitterSource uses the Twitter 1.1 API, which requires authentication of both the consumer (application) and the user (you).

```
agent.sources.twitterSrc.consumerKey = YOUR_TWITTER_CONSUMER_KEY
agent.sources.twitterSrc.consumerSecret = YOUR_TWITTER_CONSUMER_SECRET
agent.sources.twitterSrc.accessToken = YOUR_TWITTER_ACCESS_TOKEN
agent.sources.twitterSrc.accessTokenSecret = YOUR_TWITTER_ACCESS_TOKEN_SECRET
```

Use the Twitter developer site to generate these four codes by completing the following steps:

1. Sign in to https://dev.twitter.com with a Twitter account.
2. Select **My applications** from the drop-down menu in the top-right corner, and **Create a new application**.
3. Fill in the form to represent the Search installation. This can represent multiple clusters, and does not require the callback URL. Because this is not a publicly distributed application, the values you enter for the required name, description, and website fields are not important.
4. Click **Create my access token** at the bottom of the page. You may have to refresh the page to see the access token.

Substitute the consumer key, consumer secret, access token, and access token secret into `flume.conf`. Consider this information confidential, just like your regular Twitter credentials.

To enable authentication, ensure the system clock is set correctly on all hosts where Flume connects to Twitter. You can install NTP and keep the host synchronized by running the `ntpd` service, or manually synchronize using the command `sudo ntpdate pool.ntp.org` . To confirm that the time is set correctly, make sure that the output of the command `date --utc` matches the time shown at http://www.timeanddate.com/worldclock/timezone/utc. You can also set the time manually using the `date` command.

Starting the Flume Agent

1. Delete all existing documents in Solr:

```
$ solrctl --zk collection --deletedocs collection2
```

2. Check the status of the Flume Agent to determine if it is running or not:

```
$ sudo /etc/init.d/flume-ng-agent status
```

3. Use the `start` or `restart` functions. For example, to restart a running Flume Agent:

```
$ sudo /etc/init.d/flume-ng-agent restart
```

4. Monitor progress in the Flume log file and watch for errors:

```
$ tail -f /var/log/flume-ng/flume.log
```

After restarting the Flume agent, use the Cloudera Search GUI. For example, for the localhost, use `http://localhost:8983/solr/collection2/select?q=*%3A*&sort=created_at+desc&wt=json&indent=true` to verify that new tweets have been ingested into Solr. The query sorts the result set such that the most recently ingested tweets are at the top, based on the `created_at` timestamp. If you rerun the query, new tweets show up at the top of the result set.

To print diagnostic information, such as the content of records as they pass through the morphline commands, enable TRACE log level diagnostics by adding the following to your `log4j.properties` file:

```
log4j.logger.com.cloudera.cdk.morphline=TRACE
```

In Cloudera Manager, you can use the safety valve to enable TRACE log level.

Navigate to **Menu Services** > **Flume** > **Configuration** > **View and Edit** > **Agent** > **Advanced** > **Agent Logging Safety Valve**. After setting this value, restart the service.

Indexing a File Containing Tweets with Flume HTTPSource

HTTPSource lets you ingest data into Solr by POSTing a file using HTTP. HTTPSource sends data using a channel to a sink, in this case a SolrSink. For more information, see Flume Solr BlobHandler Configuration Options on page 67.

1. Delete all existing documents in Solr:

```
$ sudo /etc/init.d/flume-ng-agent stop
$ solrctl collection --deletedocs collection2
```

2. Comment out TwitterSource in `/etc/flume-ng/conf/flume.conf` and uncomment HTTPSource:

```
# comment out “agent.sources = twitterSrc”
# uncomment “agent.sources = httpSrc”
```

3. Restart the Flume Agent:

```
$ sudo /etc/init.d/flume-ng-agent restart
```

4. Send a file containing tweets to the HTTPSource:

   - **Parcel-based Installation:**

```
$ curl --data-binary \
@/opt/cloudera/parcels/CDH/share/doc/search-1.0.0+cdh5.3.5+0/examples/test-documents/sample-statuses-20120906-141433-medium.avro
 \
'http://127.0.0.1:5140?resourceName=sample-statuses-20120906-141433-medium.avro'
 \
--header 'Content-Type:application/octet-stream' --verbose
```

   - **Package-based Installation:**

```
$ curl --data-binary \
@/usr/share/doc/search-1.0.0+cdh5.3.5+0/examples/test-documents/sample-statuses-20120906-141433-medium.avro
 \
'http://127.0.0.1:5140?resourceName=sample-statuses-20120906-141433-medium.avro'
 \
--header 'Content-Type:application/octet-stream' --verbose
```

5. Check the log for status or errors:

```
$ cat /var/log/flume-ng/flume.log
```

Use the Cloudera Search GUI at `http://localhost:8983/solr/collection2/select?q=*%3A*&wt=json&indent=true` to verify that new tweets have been ingested into Solr as expected.

Indexing a File Containing Tweets with Flume SpoolDirectorySource

`SpoolDirectorySource` specifies a directory on a local disk that Flume monitors. Flume automatically transfers data from files in this directory to Solr. `SpoolDirectorySource` sends data using a channel to a sink, in this case a SolrSink.

1. Delete all existing documents in Solr:

```
$ sudo /etc/init.d/flume-ng-agent stop
$ solrctl collection --deletedocs collection2
```

2. Comment out `TwitterSource` and `HTTPSource` in `/etc/flume-ng/conf/flume.conf` and uncomment `SpoolDirectorySource`:

```
# Comment out “agent.sources = httpSrc”
# uncomment “agent.sources = spoolSrc”
```

3. Delete any old spool directory and create a new spool directory:

```
$ rm -fr /tmp/myspooldir
$ sudo -u flume mkdir /tmp/myspooldir
```

4. Restart the Flume Agent:

```
$ sudo /etc/init.d/flume-ng-agent restart
```

5. Send a file containing tweets to the `SpoolDirectorySource`. Use the copy-then-atomic-move file system trick to ensure no partial files are ingested:

- **Parcel-based Installation:**

```
$ sudo -u flume cp \
/opt/cloudera/parcels/CDH/share/doc/search*/examples/test-documents/sample-statuses-20120906-141433-medium.avro
 \
/tmp/myspooldir/.sample-statuses-20120906-141433-medium.avro
$ sudo -u flume mv /tmp/myspooldir/.sample-statuses-20120906-141433-medium.avro
 \
/tmp/myspooldir/sample-statuses-20120906-141433-medium.avro
```

- **Package-based Installation:**

```
$ sudo -u flume cp \
/usr/share/doc/search*/examples/test-documents/sample-statuses-20120906-141433-medium.avro
 \
/tmp/myspooldir/.sample-statuses-20120906-141433-medium.avro
$ sudo -u flume mv /tmp/myspooldir/.sample-statuses-20120906-141433-medium.avro
 \
/tmp/myspooldir/sample-statuses-20120906-141433-medium.avro
```

6. Check the log for status or errors.

```
$ cat /var/log/flume-ng/flume.log
```

7. Check the completion status.

```
$ find /tmp/myspooldir
```

Use the Cloudera Search GUI. For example, for the localhost, use `http://localhost:8983/solr/collection2/select?q=*%3A*&wt=json&indent=true` to verify that new tweets have been ingested into Solr.

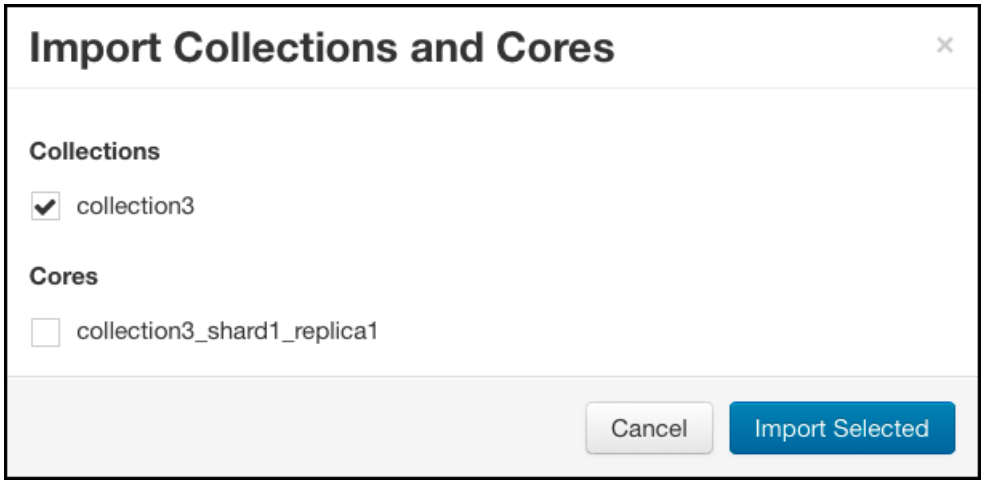
Using Hue with Cloudera Search

Hue includes a search application that provides a customizable UI. Using Hue with Cloudera Search involves importing collections. After you import collections, you can work with them through the Hue user interface.

You can watch a recording of the Hue Search Twitter Demo at Tutorial: Search Hadoop in Hue 2.4.

Importing Collections

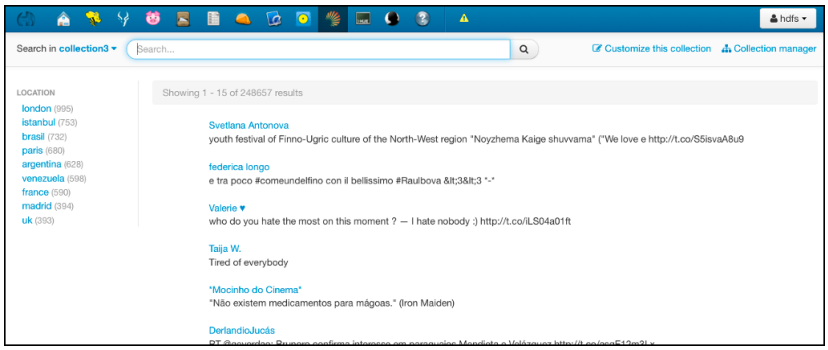
The following figure shows the collection import feature in Hue.



Generally, only collections should be imported. Importing cores is rarely useful because it enables querying a shard of the index. See A little about SolrCores and Collections for more information.

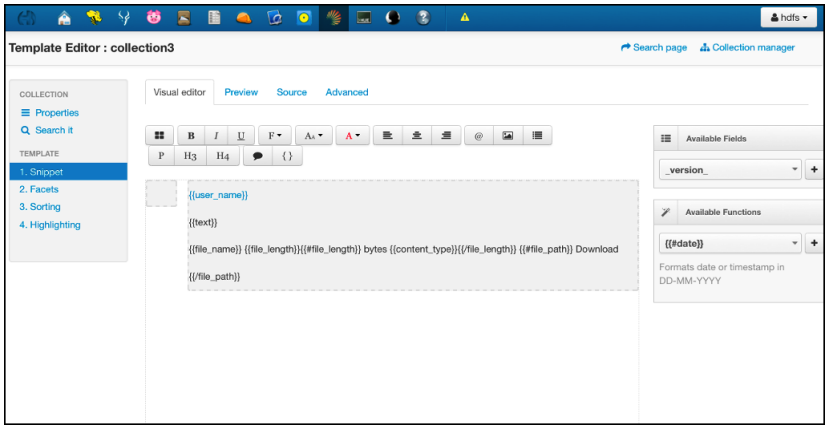
Search User Interface in Hue

The following figure shows the Search application integrated with the Hue user interface.



Customization UI

The following figure shows the Search customization interface provided in Hue.



Only superusers can access this view.

Hue Search Twitter Demo

The demo uses similar processes to those described in the Running Queries on page 39. The demo illustrates:

- That only regular Solr APIs are used.
- Faceting by fields, range, or dates, as well as sorting by time in seconds.
- The result snippet editor and preview, function for downloading, extra css/js, labels, and field picking assist.
- Showing multi-collections.
- Showing highlighting of search term.
- Showing facet ordering.
- The auto-complete handler using /suggest.

Solrctl Reference

Use the `solrctl` utility to manage a SolrCloud deployment. You can manipulate SolrCloud collections, SolrCloud collection instance directories, and individual cores.

A SolrCloud collection is the top-level object for indexing documents and providing a query interface. Each SolrCloud collection must be associated with an instance directory, though note that different collections can use the same instance directory. Each SolrCloud collection is typically replicated (sharded) among several SolrCloud instances. Each replica is called a SolrCloud core and is assigned to an individual SolrCloud host. The assignment process is managed automatically, although you can apply fine-grained control over each individual core using the `core` command. A typical deployment workflow with `solrctl` consists of deploying ZooKeeper coordination service, deploying solr-server daemons to each host, initializing the state of the ZooKeeper coordination service using `init` command, starting each solr-server daemon, generating an instance directory, uploading it to ZooKeeper, and associating a new collection with the name of the instance directory.

In general, if an operation succeeds, `solrctl` exits silently with a success exit code. If an error occurs, `solrctl` prints a diagnostics message combined with a failure exit code.

You can execute `solrctl` on any host that is configured as part of the SolrCloud. To execute any `solrctl` command on a host outside of SolrCloud deployment, ensure that SolrCloud hosts are reachable and provide `--zk` and `--solr` command line options.

The `solrctl` commands `init`, `instancedir`, `collection`, and `core`affect the entire SolrCloud deployment and are executed only once per required operation.

The `solrctl core` command affects a single SolrCloud host.

If you are using `solrctl` to manage your deployment in an environment that requires Kerberos authentication, you must have a valid Kerberos ticket, which you can get using `kinit`.

You can see examples of using `solrctl` in Deploying Cloudera Search on page 16.

Using solrctl with an HTTP proxy

Using `solrctl` to manage a deployment in an environment that uses an `http_proxy` fails because `solrctl` uses `curl`, which attempts to use the web proxy. You can disable the proxy so `solrctl` succeeds:

- Modify the settings for the current shell by exporting the `NO_PROXY`. For example:

```
$ export NO_PROXY='*'
```

- Modify the settings for single commands by prefacing `solrctl` commands with `NO_PROXY='*'`. For example:

```
$ NO_PROXY='*' solrctl collection --create yourCollectionName
```

Syntax

You can initialize the state of the entire SolrCloud deployment and each individual host within the SolrCloud deployment by using `solrctl`. The general `solrctl` command syntax is:

```
solrctl [options] command [command-arg] [command [command-arg]] ...
```

Each element and their possible values are described in the following sections.

Options

If used, the following options must precede commands:

- `--solr solr_uri`: Directs `solrctl` to a SolrCloud web API available at a given URI. This option is required for hosts running outside of SolrCloud. A sample URI might be: `http://host1.cluster.com:8983/solr`.

- `--zk zk_ensemble`: Directs `solrctl` to a particular ZooKeeper coordination service ensemble. This option is required for hosts running outside of SolrCloud. For example: `host1.cluster.com:2181,host2.cluster.com:2181/solr`.
- `--help`: Prints help.
- `--quiet`: Suppresses most `solrctl` messages.

Commands

- `init [--force]`: The `init` command, which initializes the overall state of the SolrCloud deployment, must be executed before starting solr-server daemons for the first time. Use this command cautiously because it erases all SolrCloud deployment state information. After successful initialization, you cannot recover any previous state.
- `instancedir [--generate path [-schemaless]] [--create name path] [--update name path] [--get name path] [--delete name] [--list]`: Manipulates the instance directories. The following options are supported:
  - `--generate path`: Allows users to generate the template of the instance directory. The template is stored at a designated path in a local filesystem and has configuration files under `/conf`. See Solr's README.txt for the complete layout.
    - `-schemaless` A schemaless template of the instance directory is generated. For more information on schemaless support, see Using Schemaless Mode (CDH 5.1 or later only) on page 87.
  - `--create name path`: Pushes a copy of the instance directory from the local filesystem to SolrCloud. If an instance directory is already known to SolrCloud, this command fails. See `--update` for changing name paths that already exist.
  - `--update name path`: Updates an existing SolrCloud copy of an instance directory based on the files in a local filesystem. This command is analogous to first using `--delete name` followed by `--create name path`.
  - `--get name path`: Downloads the named collection instance directory at a given path in a local filesystem. Once downloaded, files can be further edited.
  - `--delete name`: Deletes the instance directory name from SolrCloud.
  - `--list`: Prints a list of all available instance directories known to SolrCloud.
- `collection [--create name -s <numShards> [-c <collection.configName>] [-r <replicationFactor>] [-m <maxShardsPerHost>] [-n <createHostSet>]] [--delete name] [--reload name] [--stat name] [--list] [--deletedocs name]`: Manipulates collections. The following options are supported:
  - `--create name -s <numShards> [-a] [-c <collection.configName>] [-r <replicationFactor>] [-m <maxShardsPerHost>] [-n <createHostSet>]]`: Creates a new collection.

    New collections are given the specified name, and are sharded to `<numShards>`.

    The `-a` option configures auto-addition of replicas if machines hosting existing shards become unavailable.

    SolrCloud hosts are configured using the `<collection.configName>` instance directory. Replication is configured by a factor of `<replicationFactor>`. The maximum shards per host is determined by `<maxShardsPerHost>`, and the collection is allocated to the hosts specified in `<createHostSet>`.

    The only required parameters are `name` and `numShards`. If `collection.configName` is not provided, it is assumed to be the same as the name of the collection.
  - `--delete name`: Deletes a collection.
  - `--reload name`: Reloads a collection.
  - `--stat name`: Outputs SolrCloud specific run-time information for a collection.
  - `--list`: Lists all collections registered in SolrCloud.
  - `--deletedocs name`: Purges all indexed documents from a collection.

- `core [--create name [-p name=value]...] [--reload name] [--unload name] [--status name]`: Manipulates cores. This is one of two commands that you can execute on a particular SolrCloud host. Use this expert command with caution. The following options are supported:
  - `--create name [-p name=value]...]`: Creates a new core on a given SolrCloud host. The core is configured using `name=values` pairs. For more details on configuration options, see Solr documentation.
  - `--reload name`: Reloads a core.
  - `--unload name`: Unloads a core.
  - `--status name`: Prints status of a core.

Spark Indexing Reference (CDH 5.2 or later only)

Spark indexing uses the CrunchIndexerTool and requires a working MapReduce or Spark cluster, such as one installed using Cloudera Manager. Spark indexing is enabled when the CrunchIndexerTool is installed, as described in Installing the Spark Indexer on page 21.

CrunchIndexerTool is a Spark or MapReduce ETL batch job that pipes data from (splittable or non-splittable) HDFS files into Apache Solr, and runs the data through a morphline for extraction and transformation. The program is designed for flexible, scalable, fault-tolerant batch ETL pipeline jobs. It is implemented as an Apache Crunch pipeline, allowing it to run on Apache Hadoop MapReduce or the Apache Spark execution engine.

- **Note:** This command requires a morphline file, which must include a `SOLR_LOCATOR`. The snippet that includes the `SOLR_LOCATOR` might appear as follows:

```
SOLR_LOCATOR : {
  # Name of solr collection
  collection : collection

  # ZooKeeper ensemble
  zkHost : "$ZK_HOST"
}

morphlines : [
  {
    id : morphline1
    importCommands : ["org.kitesdk.**", "org.apache.solr.**"]
    commands : [
      { generateUUID { field : id } }

      { # Remove record fields that are unknown to Solr schema.xml.
       # Recall that Solr throws an exception on any attempt to load a document
 that
        # contains a field that isn't specified in schema.xml.
        sanitizeUnknownSolrFields {
          solrLocator : ${SOLR_LOCATOR} # Location from which to fetch Solr
schema
        }
      }

      { logDebug { format : "output record: {}", args : ["@{}"] } }

      {
        loadSolr {
          solrLocator : ${SOLR_LOCATOR}
        }
      }
    ]
  }
]
```

- **Note:** The Spark indexer cannot be used in an environment that requires Kerberos authentication. If your environment is configured to require Kerberos authentication, use an alternate indexer.

More details are available through command-line help:

```
MapReduceUsage: export HADOOP_CLASSPATH=$myDependencyJarPaths; hadoop jar $myDriverJar

org.apache.solr.crunch.CrunchIndexerTool --libjars $myDependencyJarFiles
[MapReduceGenericOptions]...
        [--input-file-list URI] [--input-file-format FQCN]
        [--input-file-projection-schema FILE]
        [--input-file-reader-schema FILE] --morphline-file FILE
        [--morphline-id STRING] [--pipeline-type STRING] [--xhelp]
        [--mappers INTEGER] [--dry-run] [--log4j FILE] [--chatty]
        [HDFS_URI [HDFS_URI ...]]

SparkUsage: spark-submit [SparkGenericOptions]... --master local|yarn --deploy-mode
client|cluster
--jars $myDependencyJarFiles --class org.apache.solr.crunch.CrunchIndexerTool
$myDriverJar
        [--input-file-list URI] [--input-file-format FQCN]
        [--input-file-projection-schema FILE]
        [--input-file-reader-schema FILE] --morphline-file FILE
        [--morphline-id STRING] [--pipeline-type STRING] [--xhelp]
        [--mappers INTEGER] [--dry-run] [--log4j FILE] [--chatty]
        [HDFS_URI [HDFS_URI ...]]

Spark or MapReduce ETL batch job  that  pipes data from (splittable or non-
splittable) HDFS files into Apache Solr,  and  along  the way runs the data
through a Morphline  for  extraction  and  transformation.  The  program is
designed  for  flexible,  scalable  and  fault-tolerant  batch  ETL pipeline
jobs. It is implemented as an  Apache  Crunch  pipeline and as such can run
on either the Apache Hadoop MapReduce or Apache Spark execution engine.

The program proceeds in several consecutive phases, as follows:

1) Randomization phase: This (parallel)  phase  randomizes the list of HDFS
input files in order to spread ingestion  load more evenly among the mapper
tasks of the  subsequent  phase.  This  phase  is  only  executed  for non-
splittables files, and skipped otherwise.

2) Extraction phase: This  (parallel)  phase  emits  a  series of HDFS file
input streams ( for non-splittable files) or  a series of input data records
( for splittable files).

3) Morphline  phase:  This  (parallel)  phase  receives  the  items  of the
previous phase, and  uses  a  Morphline  to  extract  the relevant content,
transform  it  and  load  zero  or  more  documents  into  Solr.  The  ETL
functionality is  flexible  and  customizable  using  chains  of  arbitrary
morphline commands that pipe  records  from  one  transformation command to
another. Commands to parse and  transform  a  set  of standard data formats
such as Avro, Parquet,  CSV,  Text,  HTML,  XML,  PDF,  MS-Office, etc. are
provided out of the box,  and  additional  custom  commands and parsers  for
additional file or data formats can  be added as custom morphline commands.
Any kind of data format can be processed  and any kind output format can be
generated by any custom Morphline ETL  logic.  Also,  this phase can be used
to send data  directly  to  a  live  SolrCloud  cluster  (via  the loadSolr
morphline command).

The program  is  implemented  as  a  Crunch  pipeline  and  as  such Crunch
optimizes the logical phases  mentioned  above  into  an efficient physical
execution plan that runs a single  mapper-only job, or as the corresponding
Spark equivalent.

Fault Tolerance: Task attempts  are  retried  on  failure  per the standard
MapReduce or Spark semantics. If the  whole  job fails you can retry simply
by rerunning the program again using the same arguments.

Comparison with MapReduceIndexerTool:

1) CrunchIndexerTool can also run on  the  Spark execution engine, not just
on MapReduce.
2)  CrunchIndexerTool  enables  interactive  low  latency  prototyping,  in
particular in Spark 'local' mode.
3) CrunchIndexerTool supports updates  (and  deletes) of existing documents
in Solr, not just inserts.
```

```
4) CrunchIndexerTool can exploit data  locality  for splittable Hadoop files
(text, avro, avroParquet).
We recommend  MapReduceIndexerTool  for  large  scale  batch  ingestion use
cases where updates (or  deletes)  of  existing  documents  in Solr are not
required, and we recommend CrunchIndexerTool  for all other use cases.

CrunchIndexerOptions:
  HDFS_URI               HDFS URI of  file  or  directory  tree  to ingest.
                         ( default: [])
  --input-file-list URI, --input-list URI
                         Local URI or  HDFS  URI  of  a  UTF-8 encoded file
                         containing a list of HDFS  URIs to ingest, one URI
                         per line in the  file.  If  '-' is specified, URIs
                         are read  from  the  standard  input.  Multiple --
                         input-file-list arguments can be specified.
  --input-file-format FQCN
                         The Hadoop FileInputFormat  to  use  for extracting
                         data from splittable HDFS  files.  Can  be a fully
                         qualified Java  class  name  or  one  of  ['text',
                         'avro', 'avroParquet']. If  this  option is present
                         the extraction phase will  emit  a series of input
                         data records rather  than  a  series  of HDFS file
                         input streams.
  --input-file-projection-schema FILE
                         Relative or absolute path  to  an Avro schema file
                         on the local file  system.  This  will  be used as
                         the projection schema  for Parquet input files.
  --input-file-reader-schema FILE
                         Relative or absolute path  to  an Avro schema file
                         on the local file  system.  This  will  be used as
                         the  reader  schema   for  Avro  or  Parquet  input
                         files.      Example:      src/test/resources/test-
                         documents/strings.avsc
  --morphline-file FILE  Relative or absolute path  to  a local config file
                         that contains one  or  more  morphlines.  The file
                         must be UTF-8  encoded.  It  will  be  uploaded to
                         each remote task. Example: /path/to/morphline.conf
  --morphline-id STRING  The identifier  of  the  morphline  that  shall be
                         executed  within   the   morphline   config   file
                         specified by --morphline-file. If the --morphline-
                         id option is  omitted  the  first  (i.e. top-most)
                         morphline  within  the   config   file   is  used.
                         Example: morphline1
  --pipeline-type STRING
                         The engine to use   for  executing  the job. Can be
                         'mapreduce' or 'spark'. ( default: mapreduce)
  --xhelp, --help, -help
                         Show  this help message and exit
  --mappers INTEGER      Tuning knob that indicates  the  maximum number of
                         MR mapper tasks to use.  -1  indicates use all map
                         slots available  on  the  cluster.  This parameter
                         only  applies   to   non-splittable   input  files
                         ( default: -1)
  --dry-run              Run the pipeline  but  print  documents  to stdout
                         instead of loading  them  into  Solr.  This can be
                         used  for quicker turnaround  during  early trial &
                         debug sessions. ( default:  false)
  --log4j FILE           Relative or absolute  path  to  a log4j.properties
                         config file on the  local  file  system. This file
                         will be uploaded  to  each  remote  task. Example:
                         /path/to/log4j.properties
  --chatty               Turn on verbose output. ( default:  false)

SparkGenericOptions:     To print all options run 'spark-submit --help'

MapReduceGenericOptions: Generic options supported are
  --conf <configuration file>
                         specify an application configuration file
  -D <property=value>    use value  for given property
  --fs <local|namenode:port>
                         specify a namenode
  --jt <local|jobtracker:port>
                         specify a job tracker
```

```
  --files <comma separated list of files>
                        specify comma separated files to  be copied to the
                        map reduce cluster
  --libjars <comma separated list of jars>
                        specify comma separated  jar  files  to include in
                        the classpath.
  --archives <comma separated list of archives>
                        specify comma separated archives  to be unarchived
                        on the compute machines.

The general command line syntax is
bin/hadoop command [genericOptions] [commandOptions]


Examples:

# Prepare - Copy input files into HDFS:
export myResourcesDir=src/test/resources #  for build from git
export myResourcesDir=/opt/cloudera/parcels/CDH/share/doc/search-*/search-crunch #
for CDH with parcels
export myResourcesDir=/usr/share/doc/search-*/search-crunch #  for CDH with packages
hadoop fs -copyFromLocal $myResourcesDir/test-documents/hello1.txt
hdfs:/user/systest/input/

# Prepare variables  for convenient reuse:
export myDriverJarDir=target #  for build from git
export myDriverJarDir=/opt/cloudera/parcels/CDH/lib/solr/contrib/crunch #  for CDH with
 parcels
export myDriverJarDir=/usr/lib/solr/contrib/crunch #  for CDH with packages
export myDependencyJarDir=target/lib #  for build from git
export myDependencyJarDir=/opt/cloudera/parcels/CDH/lib/search/lib/search-crunch #
for CDH with parcels
export myDependencyJarDir=/usr/lib/search/lib/search-crunch #  for CDH with packages
export myDriverJar=$(find $myDriverJarDir -maxdepth 1 -name 'search-crunch-*.jar' !
-name '*-job.jar' ! -name '*-sources.jar')
export myDependencyJarFiles=$(find $myDependencyJarDir -name '*.jar' | sort | tr '\n'
 ',' | head -c -1)
export myDependencyJarPaths=$(find $myDependencyJarDir -name '*.jar' | sort | tr '\n'
 ':' | head -c -1)

# MapReduce on Yarn - Ingest text file line by line into Solr:
export HADOOP_CLASSPATH=$myDependencyJarPaths; hadoop \
  --config /etc/hadoop/conf.cloudera.YARN-1 \
  jar $myDriverJar org.apache.solr.crunch.CrunchIndexerTool \
  --libjars $myDependencyJarFiles \
  -D 'mapred.child.java.opts=-Xmx500m' \
  -D morphlineVariable.ZK_HOST=$(hostname):2181/solr \
  --files $myResourcesDir/test-documents/string.avsc \
  --morphline-file $myResourcesDir/test-morphlines/loadSolrLine.conf \
  --pipeline-type mapreduce \
  --chatty \
  --log4j $myResourcesDir/log4j.properties \
  /user/systest/input/hello1.txt

# Spark in Local Mode ( for rapid prototyping) - Ingest into Solr:
spark-submit \
  --master local \
  --deploy-mode client \
  --jars $myDependencyJarFiles \
  --executor-memory 500M \
  # --driver-library-path /opt/cloudera/parcels/CDH/lib/hadoop/lib/ native #  for Snappy
 on CDH with parcels\
  # --driver-library-path /usr/lib/hadoop/lib/ native #  for Snappy on CDH with packages
 \
  --class org.apache.solr.crunch.CrunchIndexerTool \
  $myDriverJar \
  -D morphlineVariable.ZK_HOST=$(hostname):2181/solr \
  --morphline-file $myResourcesDir/test-morphlines/loadSolrLine.conf \
  --pipeline-type spark \
  --chatty \
  --log4j $myResourcesDir/log4j.properties \
  /user/systest/input/hello1.txt
```

```
# Spark on Yarn in Client Mode ( for testing) - Ingest into Solr:
Same as above, except replace '--master local' with '--master yarn'

# View the yarn executor log files (there is no GUI yet):
yarn logs --applicationId $application_XYZ

# Spark on Yarn in Cluster Mode ( for production) - Ingest into Solr:
spark-submit \
  --master yarn \
  --deploy-mode cluster \
  --jars $myDependencyJarFiles \
  --executor-memory 500M \
  --class org.apache.solr.crunch.CrunchIndexerTool \
  --files $(ls $myResourcesDir/log4j.properties),$(ls
$myResourcesDir/test-morphlines/loadSolrLine.conf) \
  $myDriverJar \
  -D hadoop.tmp.dir=/tmp \
  -D morphlineVariable.ZK_HOST=$(hostname):2181/solr \
  --morphline-file loadSolrLine.conf \
  --pipeline-type spark \
  --chatty \
  --log4j log4j.properties \
  /user/systest/input/hello1.txt
```

MapReduce Batch Indexing Reference

Cloudera Search provides the ability to batch index documents using MapReduce jobs.

If you did not install MapReduce tools required for Cloudera Search, do so on hosts where you want to submit a batch indexing job as described in Installing MapReduce Tools for use with Cloudera Search .

For information on tools related to batch indexing, see:

- MapReduceIndexerTool
- HDFSFindTool

Running an Example Indexing Job

See Cloudera Search Tutorial for examples of running a MapReduce job to index documents.

MapReduceIndexerTool

MapReduceIndexerTool is a MapReduce batch job driver that takes a morphline and creates a set of Solr index shards from a set of input files and writes the indexes into HDFS in a flexible, scalable, and fault-tolerant manner. It also supports merging the output shards into a set of live customer-facing Solr servers, typically a SolrCloud.

More details are available through the command line help:

```
$ hadoop jar target/search-mr-*-job.jar \
  org.apache.solr.hadoop.MapReduceIndexerTool --help

usage: hadoop [GenericOptions]... jar search-mr-*-job.jar \
  org.apache.solr.hadoop.MapReduceIndexerTool
       [--help] --output-dir HDFS_URI [--input-list URI]
       --morphline-file FILE [--morphline-id STRING]
       [--update-conflict-resolver FQCN] [--mappers INTEGER]
       [--reducers INTEGER] [--max-segments INTEGER]
       [--fair-scheduler-pool STRING] [--dry-run] [--log4j FILE]
       [--verbose] [--show-non-solr-cloud] [--zk-host STRING] [--go-live]
       [--collection STRING] [--go-live-threads INTEGER]
       [HDFS_URI [HDFS_URI ...]]

The MapReduce batch job is a driver that takes a  morphline  and creates a
set of Solr index shards from a set of input  files and writes the indexes
into HDFS,  in a flexible,  scalable and  fault-tolerant manner.  It  also
supports merging the output shards into a set of live customer facing Solr
```

```
servers, typically a SolrCloud. The program proceeds in several
consecutive MapReduce based phases, as follows:

1) Randomization phase: This (parallel) phase randomizes the list of
input files in order to spread indexing load more evenly among the
mappers of the subsequent phase.

2) Mapper phase: This (parallel) phase takes the input files, extracts
the relevant content, transforms it and hands SolrInputDocuments to a set
of reducers. The ETL functionality is flexible and customizable using
chains of arbitrary morphline commands that pipe records from one
transformation command to another. Commands to parse and transform a set
of standard data formats such as Avro, CSV, Text, HTML, XML, PDF, Word,
or Excel are provided out of the box, and additional custom commands
and parsers for additional file or data formats can be added as morphline
plug-ins. This is done by implementing a simple Java interface that
consumes a record (for example a file in the form of an InputStream plus
some headers plus contextual metadata) and generates as output zero or
more records. Any kind of data format can be indexed and any Solr
documents for any kind of Solr schema can be generated, and any custom
ETL logic can be registered and executed.
Record fields, including MIME types, can also explicitly be passed by
force from the CLI to the morphline, for example: hadoop ... -D
morphlineField._attachment_mimetype=text/csv

3) Reducer phase: This (parallel) phase loads the mapper's
SolrInputDocuments into one EmbeddedSolrServer per reducer. Each such
reducer and Solr server can be seen as a (micro) shard. The Solr servers
store their data in HDFS.

4) Mapper-only merge phase: This (parallel) phase merges the set of
reducer shards into the number of Solr shards expected by the user, using
a mapper-only job. This phase is omitted if the number of shards is
already equal to the number of shards expected by the user.

5) Go-live phase: This optional (parallel) phase merges the output shards
of the previous phase into a set of live customer facing Solr servers,
typically a SolrCloud. If this phase is omitted you can explicitly point
each Solr server to one of the HDFS output shard directories.

Fault Tolerance: Mapper and reducer task attempts are retried on failure
per the standard MapReduce semantics. On program startup all data in the
--output-dir is deleted if that output directory already exists. If the
whole job fails you can retry simply by rerunning the program again using
the same arguments.

positional arguments:
  HDFS_URI              HDFS URI of file or directory tree to index.
                        (default: [])

optional arguments:
  --help, -help, -h     Show this help message and exit
  --input-list URI      Local URI or HDFS URI of a UTF-8 encoded file
                        containing a list of HDFS URIs to index, one URI
                        per line in the file. If '-' is specified, URIs
                        are read from the standard input. Multiple --
                        input-list arguments can be specified.
  --morphline-id STRING The identifier of the morphline that shall be
                        executed within the morphline config file
                        specified by --morphline-file. If the --
                        morphline-id option is omitted the first (meaning
                        the top-most) morphline within the config file is
                        used. Example: morphline1
  --update-conflict-resolver FQCN
                        Fully qualified class name of a Java class that
                        implements the UpdateConflictResolver interface.
                        This enables deduplication and ordering of a
                        series of document updates for the same unique
                        document key. For example, a MapReduce batch job
                        might index multiple files in the same job where
                        some of the files contain old and new versions
                        of the very same document, using the same unique
                        document key.
```

```
                        Typically, implementations of this interface
                        forbid collisions by throwing an exception, or
                        ignore all but the most recent document version,
                        or, in the general case, order colliding updates
                        ascending from least recent to most recent
                        (partial) update. The caller of this interface
                        (i.e. the Hadoop Reducer) will then apply the
                        updates to Solr in the order returned by the
                        orderUpdates() method.
                        The                                    default
                        RetainMostRecentUpdateConflictResolver
                        implementation ignores all but the most recent
                        document version, based on a configurable
                        numeric Solr field, which defaults to the
                        file_last_modified timestamp (default: org.
                        apache.solr.hadoop.dedup.
                        RetainMostRecentUpdateConflictResolver)
  --mappers INTEGER     Tuning knob that indicates the maximum number of
                        MR mapper tasks to use. -1 indicates use all map
                        slots available on the cluster. (default: -1)
  --reducers INTEGER    Tuning knob that indicates the number of reducers
                        into which to index. To use one reducer per
                        output shard, use 0 for Search 1.x and use -2 for
                        Search for CDH 5. Using one reducer per output
                        shard disables the mtree merge MR algorithm. The
                        mtree merge MR algorithm improves scalability by
                        distributing CPU load among a set of parallel
                        reducers that can be more numerous than the
                        number of Solr shards expected by the user. It
                        can be seen as an extension of concurrent lucene
                        merges and tiered lucene merges to the clustered
                        case. -1 indicates use all reduce slots available
                        on the cluster. The subsequent mapper-only phase
                        merges the reducer output to the number of shards
                        expected by the user, again by utilizing a
                        cluster's parallelism. (default: -1)
  --max-segments INTEGER
                        Tuning knob that indicates the maximum number of
                        segments to be contained on output in the index
                        of each reducer shard. After a reducer has built
                        its output index it applies a merge policy to
                        merge segments until there are <= maxSegments
                        lucene segments left in this index. Merging
                        segments involves reading and rewriting all data
                        in all these segment files, potentially multiple
                        times, which is very I/O intensive and time
                        consuming. However, an index with fewer segments
                        can later be merged faster, and it can later be
                        queried faster once deployed to a live Solr
                        serving shard. Set maxSegments to 1 to optimize
                        the index for low query latency. In a nutshell,
                        a small maxSegments value trades indexing
                        latency for subsequently improved query latency.
                        This can be a reasonable trade-off for batch
                        indexing systems. (default: 1)
  --fair-scheduler-pool STRING
                        Optional tuning knob that indicates the name of
                        the fair scheduler pool to submit jobs to. The
                        Fair Scheduler is a pluggable MapReduce
                        scheduler that provides a way to share large
                        clusters. Fair scheduling is a method of
                        assigning resources to jobs such that all jobs
                        get, on average, an equal share of resources
                        over time. When there is a single job running,
                        that job uses the entire cluster. When other
                        jobs are submitted, tasks slots that free up are
                        assigned to the new jobs, so that each job gets
                        roughly the same amount of CPU time. Unlike the
                        default Hadoop scheduler, which forms a queue of
                        jobs, this lets short jobs finish in reasonable
                        time while not starving long jobs. It is also an
                        easy way to share a cluster between multiple of
                        users. Fair sharing can also work with job
```

```
                           priorities - the priorities are used as weights
                           to determine the fraction of total compute time
                           that each job gets.
  --dry-run                Run in local mode and print documents to stdout
                           instead of loading them into Solr. This executes
                           the morphline in the client process (without
                           submitting a job to MR) for quicker turnaround
                           during early trial and debug sessions. (default:
                           false)
  --log4j FILE             Relative or absolute path to a log4j.properties
                           config file on the local file system. This file
                           will be uploaded to each MR task. Example:
                           /path/to/log4j.properties
  --verbose, -v            Turn on verbose output. (default: false)
  --show-non-solr-cloud    Also show options for Non-SolrCloud mode as part
                           of --help. (default: false)

Required arguments:
  --output-dir HDFS_URI    HDFS directory to write Solr indexes to. Inside
                           there one output directory per shard will be
                           generated. Example: hdfs://c2202.mycompany.
                           com/user/$USER/test
  --morphline-file FILE    Relative or absolute path to a local config file
                           that contains one or more morphlines. The file
                           must be UTF-8 encoded. Example:
                           /path/to/morphline.conf

Cluster arguments:
  Arguments that provide information about your Solr cluster.

  --zk-host STRING         The address of a ZooKeeper ensemble being used
                           by a SolrCloud cluster. This ZooKeeper ensemble
                           will be examined to determine the number of
                           output shards to create as well as the Solr URLs
                           to merge the output shards into when using the --
                           go-live option. Requires that you also pass the
                           --collection to merge the shards into.

                           The --zk-host option implements the same
                           partitioning semantics as the standard SolrCloud
                           Near-Real-Time (NRT) API. This enables to mix
                           batch updates from MapReduce ingestion with
                           updates from standard Solr NRT ingestion on the
                           same SolrCloud cluster, using identical unique
                           document keys.

                           Format is: a list of comma separated host:port
                           pairs, each corresponding to a zk server.
                           Example: '127.0.0.1:2181,127.0.0.1:
                           2182,127.0.0.1:2183' If the optional chroot
                           suffix is used the example would look like:
                           '127.0.0.1:2181/solr,127.0.0.1:2182/solr,
                           127.0.0.1:2183/solr' where the client would be
                           rooted at '/solr' and all paths would be
                           relative to this root - i.e.
                           getting/setting/etc... '/foo/bar' would result
                           in operations being run on '/solr/foo/bar' (from
                           the server perspective).


Go live arguments:
  Arguments for merging the shards that are built into a live Solr
  cluster. Also see the Cluster arguments.

  --go-live                Allows you to optionally merge the final index
                           shards into a live Solr cluster after they are
                           built. You can pass the ZooKeeper address with --
                           zk-host and the relevant cluster information
                           will be auto detected. (default: false)
  --collection STRING      The SolrCloud collection to merge shards into
                           when using --go-live and --zk-host. Example:
                           collection1
  --go-live-threads INTEGER
```

```
                          Tuning knob that indicates  the maximum number of
                          live merges  to  run  in  parallel  at  one time.
                          (default: 1000)

Generic options supported are
  --conf <configuration FILE>
                          specify an application configuration file
  -D <property=value>     use value for given property
  --fs <local|namenode:port>
                          specify a namenode
  --jt <local|jobtracker:port>
                          specify a job tracker
  --files <comma separated list of files>
                          specify comma separated  files  to  be  copied to
                          the map reduce cluster
  --libjars <comma separated list of jars>
                          specify comma separated jar  files  to include in
                          the classpath.
  --archives <comma separated list of archives>
                          specify   comma   separated    archives   to   be
                          unarchived on the compute machines.

The general command line syntax is
bin/hadoop command [genericOptions] [commandOptions]

Examples:

# Index an Avro based Twitter tweet file into a live SolrCloud cluster:
sudo -u hdfs hadoop \
  --config /etc/hadoop/conf.cloudera.mapreduce1 \
  jar target/search-mr-*-job.jar org.apache.solr.hadoop.MapReduceIndexerTool \
  -D 'mapred.child.java.opts=-Xmx500m' \
  --log4j src/test/resources/log4j.properties \
  --morphline-file
../search-core/src/test/resources/test-morphlines/tutorialReadAvroContainer.conf \
  --output-dir hdfs://c2202.mycompany.com/user/$USER/test \
  --zk-host zk01.mycompany.com:2181/solr \
  --collection collection1 \
  --go-live \
  hdfs:///user/foo/indir

# Index all files that match all of the following conditions:
# 1) File is contained in dir tree hdfs:///user/$USER/solrloadtest/twitter/tweets
# 2) file name matches the glob pattern 'sample-statuses*.gz'
# 3) file was last modified less than 100000 minutes ago
# 4) file size is between 1 MB and 1 GB
# Also include extra library jar file containing JSON tweet Java parser:
hadoop jar target/search-mr-*-job.jar org.apache.solr.hadoop.HdfsFindTool \
  -find hdfs:///user/$USER/solrloadtest/twitter/tweets \
  -type f \
  -name 'sample-statuses*.gz' \
  -mmin -1000000 \
  -size -100000000c \
  -size +1000000c \
  | sudo -u hdfs hadoop \
  --config /etc/hadoop/conf.cloudera.mapreduce1 \
  jar target/search-mr-*-job.jar org.apache.solr.hadoop.MapReduceIndexerTool \
  --libjars /path/to/cdk-morphlines-twitter-0.9.2.jar \
  -D 'mapred.child.java.opts=-Xmx500m' \
  --log4j src/test/resources/log4j.properties \
  --morphline-file
../search-core/src/test/resources/test-morphlines/tutorialReadJsonTestTweets.conf \
  --output-dir hdfs://c2202.mycompany.com/user/$USER/test \
  --zk-host zk01.mycompany.com:2181/solr \
  --collection collection1 \
  --input-list -
```

MapReduceIndexerTool Metadata

The MapReduceIndexerTool generates metadata fields for each input file when indexing. These fields can be used in morphline commands. These fields can also be stored in Solr, by adding definitions like the following to

your Solr `schema.xml` file. After the MapReduce indexing process completes, the fields are searchable through Solr.

```
<!-- file metadata -->
<field name="file_download_url" type="string" indexed="false" stored="true" />
<field name="file_upload_url" type="string" indexed="false" stored="true" />
<field name="file_scheme" type="string" indexed="true" stored="true" />
<field name="file_host" type="string" indexed="true" stored="true" />
<field name="file_port" type="int" indexed="true" stored="true" />
<field name="file_path" type="string" indexed="true" stored="true" />
<field name="file_name" type="string" indexed="true" stored="true" />
<field name="file_length" type="tlong" indexed="true" stored="true" />
<field name="file_last_modified" type="tlong" indexed="true" stored="true" />
<field name="file_owner" type="string" indexed="true" stored="true" />
<field name="file_group" type="string" indexed="true" stored="true" />
<field name="file_permissions_user" type="string" indexed="true" stored="true" />
<field name="file_permissions_group" type="string" indexed="true" stored="true" />
<field name="file_permissions_other" type="string" indexed="true" stored="true" />
<field name="file_permissions_stickybit" type="boolean" indexed="true" stored="true"
/>
```

Example output:

```
"file_upload_url":"foo/test-documents/sample-statuses-20120906-141433.avro",
"file_download_url":"hdfs://host1.mycompany.com:8020/user/foo/
test-documents/sample-statuses-20120906-141433.avro",
"file_scheme":"hdfs",
"file_host":"host1.mycompany.com",
"file_port":8020,
"file_name":"sample-statuses-20120906-141433.avro",
"file_path":"/user/foo/test-documents/sample-statuses-20120906-141433.avro",
"file_last_modified":1357193447106,
"file_length":1512,
"file_owner":"foo",
"file_group":"foo",
"file_permissions_user":"rw-",
"file_permissions_group":"r--",
"file_permissions_other":"r--",
"file_permissions_stickybit":false,
```

HdfsFindTool

HdfsFindTool is essentially the HDFS version of the Linux file system `find` command. The command walks one or more HDFS directory trees, finds all HDFS files that match the specified expression, and applies selected actions to them. By default, it prints the list of matching HDFS file paths to `stdout`, one path per line. The output file list can be piped into the MapReduceIndexerTool using the MapReduceIndexerTool `--inputlist` option.

More details are available through command-line help. The command used to invoke the help varies by installation type and may vary further in custom installations.

- To invoke the command-line help in a default parcels installation, use:

```
$ hadoop jar /opt/cloudera/parcels/CDH-*/jars/search-mr-*-job.jar \
org.apache.solr.hadoop.HdfsFindTool -help
```

- To invoke the command-line help in a default packages installation, use:

```
$ hadoop jar /usr/lib/solr/contrib/mr/search-mr-job.jar \
 org.apache.solr.hadoop.HdfsFindTool -help
```

More details are available through the command line help:

```
Usage: hadoop fs [generic options]
  [-find <path> ... <expression> ...]
  [-help [cmd ...]]
  [-usage [cmd ...]]
```

```
-find <path> ... <expression> ...: Finds all files that match the specified expression
 and applies selected actions to them.

  The following primary expressions are recognised:
    -atime n
    -amin n
      Evaluates as true if the file access time subtracted from
      the start time is n days (or minutes if -amin is used).

    -blocks n
      Evaluates to true if the number of file blocks is n.

    -class classname [args ...]
      Executes the named expression class.

    -depth
      Always evaluates to true. Causes directory contents to be
      evaluated before the directory itself.

    -empty
      Evaluates as true if the file is empty or directory has no
      contents.

    -group groupname
      Evaluates as true if the file belongs to the specified
      group.

    -mtime n
    -mmin n
      Evaluates as true if the file modification time subtracted
      from the start time is n days (or minutes if -mmin is used)

    -name pattern
    -iname pattern
      Evaluates as true if the basename of the file matches the
      pattern using standard file system globbing.
      If -iname is used then the match is case insensitive.

    -newer file
      Evaluates as true if the modification time of the current
      file is more recent than the modification time of the
      specified file.

    -nogroup
      Evaluates as true if the file does not have a valid group.

    -nouser
      Evaluates as true if the file does not have a valid owner.

    -perm [-]mode
    -perm [-]onum
      Evaluates as true if the file permissions match that
      specified. If the hyphen is specified then the expression
      shall evaluate as true if at least the bits specified
      match, otherwise an exact match is required.
      The mode may be specified using either symbolic notation,
      eg 'u=rwx,g+x+w' or as an octal number.

    -print
    -print0
      Always evaluates to true. Causes the current pathname to be
      written to standard output. If the -print0 expression is
      used then an ASCII NULL character is appended.

    -prune
      Always evaluates to true. Causes the find command to not
      descend any further down this directory tree. Does not
      have any affect if the -depth expression is specified.

    -replicas n
      Evaluates to true if the number of file replicas is n.
```

```
    -size n[c]
      Evaluates to true if the file size in 512 byte blocks is n.
      If n is followed by the character 'c' then the size is in bytes.

    -type filetype
      Evaluates to true if the file type matches that specified.
      The following file type values are supported:
      'd' (directory), 'l' (symbolic link), 'f' (regular file).

    -user username
      Evaluates as true if the owner of the file matches the
      specified user.

  The following operators are recognised:
    expression -a expression
    expression -and expression
    expression expression
      Logical AND operator for joining two expressions. Returns
      true if both child expressions return true. Implied by the
      juxtaposition of two expressions and so does not need to be
      explicitly specified. The second expression will not be
      applied if the first fails.

    ! expression
    -not expression
      Evaluates as true if the expression evaluates as false and
      vice-versa.

    expression -o expression
    expression -or expression
      Logical OR operator for joining two expressions. Returns
      true if one of the child expressions returns true. The
      second expression will not be applied if the first returns
      true.

-help [cmd ...]: Displays help for given command or all commands if none
  is specified.

-usage [cmd ...]: Displays the usage for given command or all commands if none
  is specified.

Generic options supported are
-conf <configuration file>     specify an application configuration file
-D <property=value>            use value for given property
-fs <local|namenode:port>      specify a namenode
-jt <local|jobtracker:port>    specify a job tracker
-files <comma separated list of files>    specify comma separated files to be copied
to the map reduce cluster
-libjars <comma separated list of jars>    specify comma separated jar files to include
 in the classpath.
-archives <comma separated list of archives>    specify comma separated archives to be
 unarchived on the compute machines.

The general command line syntax is
bin/hadoop command [genericOptions] [commandOptions]
```

For example, to find all files that:

- Are contained in the directory tree `hdfs:///user/$USER/solrloadtest/twitter/tweets`
- Have a name matching the glob pattern `sample-statuses*.gz`
- Were modified less than 60 minutes ago
- Are between 1 MB and 1 GB

You could use the following:

```
$ hadoop jar /usr/lib/solr/contrib/mr/search-mr-*-job.jar \
org.apache.solr.hadoop.HdfsFindTool -find \
hdfs:///user/$USER/solrloadtest/twitter/tweets -type f -name \
'sample-statuses*.gz' -mmin -60 -size -1000000000c -size +1000000c
```

Flume Near Real-Time Indexing Reference

The Flume Solr Sink is a flexible, scalable, fault tolerant, transactional, near real-time (NRT) system for processing a continuous stream of records into live search indexes. Latency from the time of data arrival to the time data appears in search query results is measured in seconds and is tunable.

Data flows from sources through Flume hosts across the network to Flume Solr sinks. The sinks extract the relevant data, transform it, and load it into a set of live Solr search servers, which in turn serve queries to end users or search applications.

The ETL functionality is flexible and customizable, using chains of morphline commands that pipe records from one transformation command to another. Commands to parse and transform a set of standard data formats such as Avro, CSV, text, HTML, XML, PDF, Word, or Excel, are provided out of the box. You can add additional custom commands and parsers as morphline plug-ins for other file or data formats. Do this by implementing a simple Java interface that consumes a record such as a file in the form of an InputStream plus some headers and contextual metadata. The record consumed by the Java interface is used to generate record output. Any kind of data format can be indexed, any Solr documents for any kind of Solr schema can be generated, and any custom ETL logic can be registered and executed.

Routing to multiple Solr collections improves multi-tenancy, and routing to a SolrCloud cluster improves scalability. Flume SolrSink servers can be co-located with live Solr servers serving end user queries, or deployed on separate industry-standard hardware to improve scalability and reliability. Indexing load can be spread across a large number of Flume SolrSink servers, and Flume features such as Load balancing Sink Processor can help improve scalability and achieve high availability. .

Flume indexing provides low-latency data acquisition and querying. It complements (instead of replaces) use cases based on batch analysis of HDFS data using MapReduce. In many use cases, data flows simultaneously from the producer through Flume into both Solr and HDFS using features such as optional replicating channels to replicate an incoming flow into two output flows. You can use near real-time ingestion as well as batch analysis tools.

For a more comprehensive discussion of the Flume Architecture, see Large Scale Data Ingestion using Flume.

After configuring Flume, start it as detailed in Flume Installation.

See the Cloudera Search Tutorial for exercises that show how to configure and run a Flume SolrSink to index documents.

Flume Morphline Solr Sink Configuration Options

You can use the standard configuration file `flume.conf` to configure Flume agents, including their sources, sinks, and channels. For more information about `flume.conf`, see the Flume User Guide.

Flume Morphline SolrSink provides the following configuration options in the `flume.conf` file:

Property Name	Default	Description
`type`		The FQCN of this class: `org.apache.flume.sink.solr.morphline.MorphlineSolrSink`
`batchSize`	100	The maximum number of events to take per flume transaction.
`batchDurationMillis`	1000	The maximum duration per Flume transaction (ms). The transaction commits after this duration or when batchSize is exceeded, whichever comes first.

Property Name	Default	Description
indexerClass	org.apache.flume.sink.solr.morphline.MorphlineSolrIndexer	The FQCN of a class implementing org.apache.flume.sink.solr.morphline.SolrIndexer
morphlineFile	n/a	The location of the morphline configuration file. ▪ In a Cloudera Manager deployment, use: agent.sinks.solrSink.morphlineFile=morphlines.conf ▪ In unmanaged deployments, provide the relative or absolute path on the local file system to the morphline configuration file. For example: /etc/flume-ng/conf/tutorialReadAvroContainer.conf
morphlineId	null	Name used to identify a morphline if there are multiple morphlines in a morphline configuration file.

This example shows a `flume.conf` section for a SolrSink for the agent named `agent`:

```
agent.sinks.solrSink.type = org.apache.flume.sink.solr.morphline.MorphlineSolrSink
agent.sinks.solrSink.channel = memoryChannel
agent.sinks.solrSink.batchSize = 100
agent.sinks.solrSink.batchDurationMillis = 1000
agent.sinks.solrSink.morphlineFile = /etc/flume-ng/conf/morphline.conf
agent.sinks.solrSink.morphlineId = morphline1
```

- **Note:** The examples in this document use a Flume MemoryChannel to easily get started. For production use it is often more appropriate to configure a Flume FileChannel instead, which is a high performance transactional persistent queue.

Flume Morphline Interceptor Configuration Options

Flume can modify and drop events in-flight with the help of Interceptors, which can be attached to any Flume source. Flume MorphlineInterceptor executes the transformations of a morphline on intercepted events. For example the morphline can ignore events or alter or insert certain event headers using regular expression-based pattern matching, or it can auto-detect and set a MIME type using Apache Tika on events that are intercepted. This packet sniffing can be used for content-based routing in a Flume topology.

Flume supports multiplexing the event flow to destinations by defining a flow multiplexer that can replicate or selectively route an event to channels. This example shows a source from agent "foo" fanning out the flow to three different channels. This fan out can be replicating or multiplexing. In replicating, each event is sent to all three channels. In multiplexing, an event is delivered to a subset of available channels when that event's attribute matches a preconfigured value. For example, if an event attribute called `stream.type` is set to `application/pdf`, it goes to `channel1` and `channel3`. If the attribute is set to `avro/binary`, it goes to `channel2`, otherwise `channel3`. You can set the mapping in the `flume.conf` file.

Flume MorphlineInterceptor provides the following configuration options in the `flume.conf` file:

Property Name	Default	Description
type		The FQCN of this class: org.apache.flume.sink.solr.morphline.MorphlineInterceptor$Builder
morphlineFile	n/a	The location of the morphline configuration file. ▪ In a Cloudera Manager deployment, use: agent.sources.avroSrc.interceptors.morphlineinterceptor.morphlineFile = morphlines.conf ▪ In unmanaged deployments, provide the relative or absolute path on the local file system to the morphline configuration file. For example, /etc/flume-ng/conf/morphline.conf.
morphlineId	null	The name used to identify a morphline if a config file has multiple morphlines.

This example shows a `flume.conf` section for a MorphlineInterceptor for the agent named "agent":

```
agent.sources.avroSrc.interceptors = morphlineinterceptor
agent.sources.avroSrc.interceptors.morphlineinterceptor.type =
org.apache.flume.sink.solr.morphline.MorphlineInterceptor$Builder
agent.sources.avroSrc.interceptors.morphlineinterceptor.morphlineFile =
/etc/flume-ng/conf/morphline.conf
agent.sources.avroSrc.interceptors.morphlineinterceptor.morphlineId = morphline1
```

▪ **Note:** A morphline interceptor cannot generate more than one output record for each input event.

Flume Solr UUIDInterceptor Configuration Options

Flume can modify or drop events in-flight. This is done with the help of Interceptors, which can be attached to any Flume Source. Flume Solr UUIDInterceptor sets a universally unique identifier on all intercepted events. For example, UUID `b5755073-77a9-43c1-8fad-b7a586fc1b97` represents a 128-bit value.

You can use UUIDInterceptor to automatically assign a UUID to a document event if no application-level unique key for the event is available. Assign UUIDs to events as soon as they enter the Flume network—that is, in the first Flume source of the flow. This enables subsequent deduplication of documents in the face of replication and redelivery in a Flume network that is designed for high availability and high performance. If available, an application-level key is preferable to an auto-generated UUID because it enables subsequent updates and deletion of the document in Solr using that key.

Flume Solr UUIDInterceptor provides the following configuration options in the `flume.conf` file:

Property Name	Default	Description
type		The FQCN of this class: org.apache.flume.sink.solr.morphline.UUIDInterceptor$Builder
headerName	id	The name of the Flume header to modify.
preserveExisting	true	If the UUID header already exists, determine whether it is preserved.
prefix	""	The prefix string constant to prepend to each generated UUID.

For examples, see the BlobHandler and BlobDeserializer.

Flume Solr BlobHandler Configuration Options

Flume accepts Flume events by HTTP POST and GET with the help of HTTPSource.

By default, HTTPSource splits JSON input into Flume events. As an alternative, Flume Solr BlobHandler for HTTPSource returns an event that contains the request parameters as well as the Binary Large Object (BLOB) uploaded with this request. This approach is not suitable for very large objects because it buffers the entire BLOB.

Flume Solr BlobHandler provides the following configuration options in the `flume.conf` file:

Property Name	Default	Description
`handler`		The FQCN of this class: `org.apache.flume.sink.solr.morphline.BlobHandler`
`handler.maxBlobLength`	100000000 (100 MB)	The maximum number of bytes to read and buffer for a request.

This example shows a `flume.conf` section for a HTTPSource with a BlobHandler for the agent named `agent`:

```
agent.sources.httpSrc.type = org.apache.flume.source.http.HTTPSource
agent.sources.httpSrc.port = 5140
agent.sources.httpSrc.handler = org.apache.flume.sink.solr.morphline.BlobHandler
agent.sources.httpSrc.handler.maxBlobLength = 2000000000
agent.sources.httpSrc.interceptors = uuidinterceptor
agent.sources.httpSrc.interceptors.uuidinterceptor.type =
org.apache.flume.sink.solr.morphline.UUIDInterceptor$Builder
agent.sources.httpSrc.interceptors.uuidinterceptor.headerName = id
#agent.sources.httpSrc.interceptors.uuidinterceptor.preserveExisting = false
#agent.sources.httpSrc.interceptors.uuidinterceptor.prefix = myhostname
agent.sources.httpSrc.channels = memoryChannel
```

Flume Solr BlobDeserializer Configuration Options

Using SpoolDirectorySource, Flume can ingest data from files located in a spooling directory on disk. Unlike other asynchronous sources, `SpoolDirectorySource` does not lose data even if Flume is restarted or fails. Flume watches the directory for new files and ingests them as they are detected.

By default, `SpoolDirectorySource` splits text input on newlines into Flume events. You can change this behavior by having Flume Solr `BlobDeserializer` read Binary Large Objects (BLOBs) from `SpoolDirectorySource`. This alternative approach is not suitable for very large objects because the entire BLOB is buffered.

Flume Solr `BlobDeserializer` provides the following configuration options in the `flume.conf` file:

Property Name	Default	Description
`deserializer`		The FQCN of this class: `org.apache.flume.sink.solr.morphline.BlobDeserializer$Builder`
`deserializer.maxBlobLength`	100000000 (100 MB)	The maximum number of bytes to read and buffer for a given request.

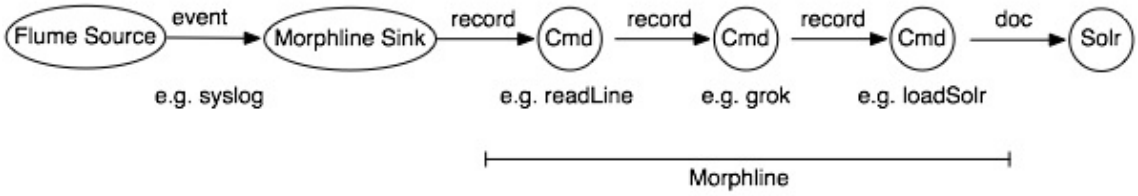
This example shows a `flume.conf` section for a `SpoolDirectorySource` with a `BlobDeserializer` for the agent named `agent`:

```
agent.sources.spoolSrc.type = spooldir
agent.sources.spoolSrc.spoolDir = /tmp/myspooldir
agent.sources.spoolSrc.ignorePattern = \.
agent.sources.spoolSrc.deserializer =
```

```
org.apache.flume.sink.solr.morphline.BlobDeserializer$Builder
agent.sources.spoolSrc.deserializer.maxBlobLength = 2000000000
agent.sources.spoolSrc.batchSize = 1
agent.sources.spoolSrc.fileHeader = true
agent.sources.spoolSrc.fileHeaderKey = resourceName
agent.sources.spoolSrc.interceptors = uuidinterceptor
agent.sources.spoolSrc.interceptors.uuidinterceptor.type =
org.apache.flume.sink.solr.morphline.UUIDInterceptor$Builder
agent.sources.spoolSrc.interceptors.uuidinterceptor.headerName = id
#agent.sources.spoolSrc.interceptors.uuidinterceptor.preserveExisting = false
#agent.sources.spoolSrc.interceptors.uuidinterceptor.prefix = myhostname
agent.sources.spoolSrc.channels = memoryChannel
```

Extracting, Transforming, and Loading Data With Cloudera Morphlines

Cloudera Morphlines is an open-source framework that reduces the time and skills required to build or change Search indexing applications. A morphline is a rich configuration file that simplifies defining an ETL transformation chain. Use these chains to consume any kind of data from any data source, process the data, and load the results into Cloudera Search. Executing in a small, embeddable Java runtime system, morphlines can be used for near real-time applications as well as batch processing applications. The following diagram shows the process flow:



Morphlines can be seen as an evolution of Unix pipelines, where the data model is generalized to work with streams of generic records, including arbitrary binary payloads. Morphlines can be embedded into Hadoop components such as Search, Flume, MapReduce, Pig, Hive, and Sqoop.

The framework ships with a set of frequently used high-level transformation and I/O commands that can be combined in application-specific ways. The plug-in system allows you to add new transformations and I/O commands and integrates existing functionality and third-party systems.

This integration enables the following:

- Rapid Hadoop ETL application prototyping
- Complex stream and event processing in real time
- Flexible log file analysis
- Integration of multiple heterogeneous input schemas and file formats
- Reuse of ETL logic building blocks across Search applications

Thehigh-performance Cloudera runtime compiles a morphline, processing all commands for a morphline in the same thread and adding no artificial overhead. For high scalability, you can deploy many morphline instances on a cluster in many Flume agents and MapReduce tasks.

The following components execute morphlines:

- MapReduceIndexerTool
- Flume Morphline Solr Sink and Flume MorphlineInterceptor

Cloudera also provides a corresponding Cloudera Search Tutorial.

Morphlines manipulate continuous or arbitrarily large streams of records. The data model can be described as follows: A record is a set of named fields where each field has an ordered list of one or more values. A value can be any Java Object. That is, a record is essentially a hash table where each hash table entry contains a String key and a list of Java Objects as values. (The implementation uses Guava's `ArrayListMultimap`, which is a `ListMultimap`). Note that a field can have multiple values and any two records need not use common field

names. This flexible data model corresponds exactly to the characteristics of the Solr/Lucene data model, meaning a record can be seen as a `SolrInputDocument`. A field with zero values is removed from the record - fields with zero values effectively do not exist.

Not only structured data, but also arbitrary binary data can be passed into and processed by a morphline. By convention, a record can contain an optional field named `_attachment_body`, which can be a Java `java.io.InputStream` or Java `byte[]`. Optionally, such binary input data can be characterized in more detail by setting the fields named `_attachment_mimetype` (such as `application/pdf`) and `_attachment_charset` (such as `UTF-8`) and `_attachment_name` (such as `cars.pdf`), which assists in detecting and parsing the data type.

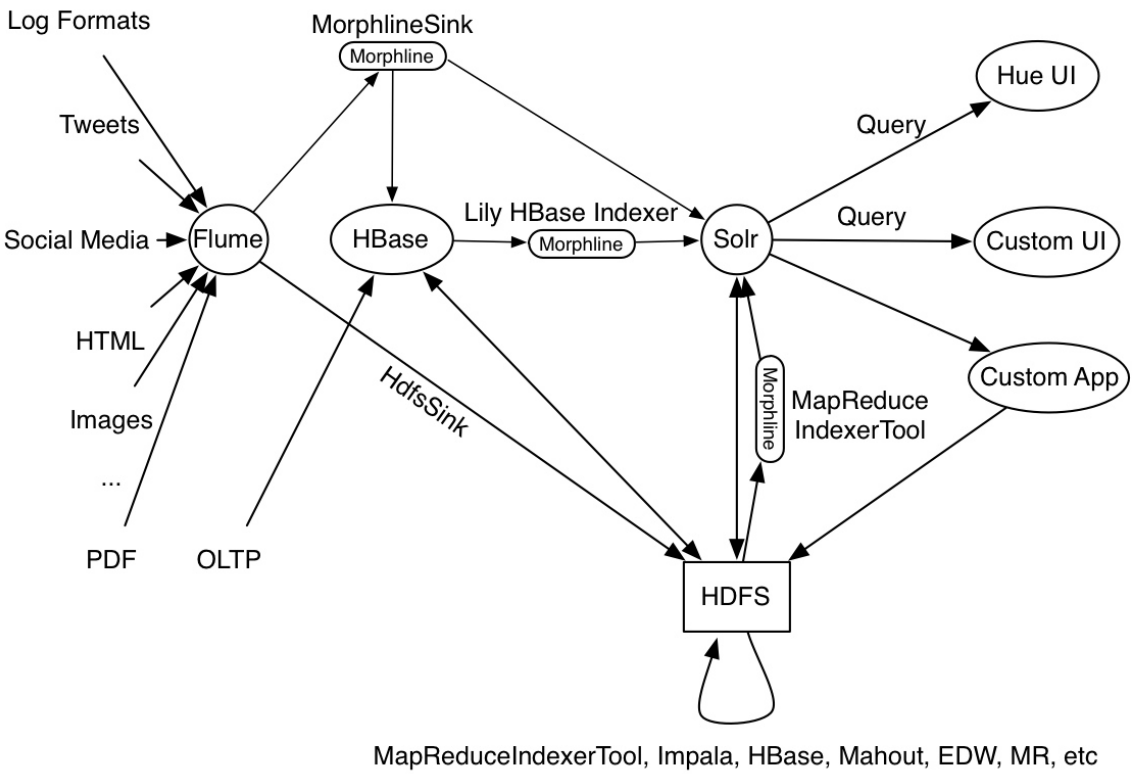
This generic data model is useful to support a wide range of applications.

A command transforms a record into zero or more records. Commands can access all record fields. For example, commands can parse fields, set fields, remove fields, rename fields, find and replace values, split a field into multiple fields, split a field into multiple values, or drop records. Often, regular expression based pattern matching is used as part of the process of acting on fields. The output records of a command are passed to the next command in the chain. A command has a Boolean return code, indicating success or failure.

For example, consider the case of a multi-line input record: A command could take this multi-line input record and divide the single record into multiple output records, one for each line. This output could then later be further divided using regular expression commands, splitting each single line record out into multiple fields in application specific ways.

A command can extract, clean, transform, join, integrate, enrich and decorate records in many other ways. For example, a command can join records with external data sources such as relational databases, key-value stores, local files or IP Geo lookup tables. It can also perform tasks such as DNS resolution, expand shortened URLs, fetch linked metadata from social networks, perform sentiment analysis and annotate the record accordingly, continuously maintain statistics for analytics over sliding windows, compute exact or approximate distinct values and quantiles.

A command can also consume records and pass them to external systems. For example, a command can load records into Solr or write them to a MapReduce Reducer or pass them into an online dashboard. The following diagram illustrates some pathways along which data might flow with the help of morphlines:



A command can contain nested commands. Thus, a morphline is a tree of commands, akin to a push-based data flow engine or operator tree in DBMS query execution engines.

A morphline has no notion of persistence, durability, distributed computing, or host failover. A morphline is basically just a chain of in-memory transformations in the current thread. There is no need for a morphline to manage multiple processes, hosts, or threads because this is already addressed by host systems such as MapReduce, Flume, or Storm. However, a morphline does support passing notifications on the control plane to command subtrees. Such notifications include BEGIN_TRANSACTION, COMMIT_TRANSACTION, ROLLBACK_TRANSACTION, SHUTDOWN.

The morphline configuration file is implemented using the HOCON format (Human-Optimized Config Object Notation). HOCON is basically JSON slightly adjusted for configuration file use cases. HOCON syntax is defined at HOCON github page and is also used by Akka and Play.

Cloudera Search includes several maven modules that contain morphline commands for integration with Apache Solr including SolrCloud, flexible log file analysis, single-line records, multi-line records, CSV files, regular expression based pattern matching and extraction, operations on record fields for assignment and comparison, operations on record fields with list and set semantics, if-then-else conditionals, string and timestamp conversions, scripting support for dynamic Java code, a small rules engine, logging, metrics and counters, integration with Avro, integration with Apache SolrCell and all Apache Tika parsers, integration with Apache Hadoop Sequence Files, auto-detection of MIME types from binary data using Apache Tika, and decompression and unpacking of arbitrarily nested container file formats, among others. These are described in the following chapters.

Example Morphline Usage

The following examples show how you can use morphlines.

Using Morphlines to Index Avro

This example illustrates using a morphline to index an Avro file with a schema.

1. View the content of the Avro file to understand the data:

```
$ wget http://archive.apache.org/dist/avro/avro-1.7.4/java/avro-tools-1.7.4.jar
$ java -jar avro-tools-1.7.4.jar tojson \
/usr/share/doc/search*/examples/test-documents/sample-statuses-20120906-141433.avro
```

2. Inspect the schema of the Avro file:

```
$ java -jar avro-tools-1.7.4.jar getschema
/usr/share/doc/search*/examples/test-documents/sample-statuses-20120906-141433.avro

{
  "type" : "record",
  "name" : "Doc",
  "doc" : "adoc",
  "fields" : [ {
    "name" : "id",
    "type" : "string"
  }, {
    "name" : "user_statuses_count",
    "type" : [ "int", "null" ]
  }, {
    "name" : "user_screen_name",
    "type" : [ "string", "null" ]
  }, {
    "name" : "created_at",
    "type" : [ "string", "null" ]
  }, {
    "name" : "text",
    "type" : [ "string", "null" ]
  }

  ...

  ]
}
```

3. Extract the `id`, `user_screen_name`, `created_at`, and `text` fields from the Avro records, and then store and index them in Solr, using the following Solr schema definition in `schema.xml`:

```
<fields>
  <field name="id" type="string" indexed="true" stored="true" required="true"
multiValued="false" />
  <field name="username" type="text_en" indexed="true" stored="true" />
  <field name="created_at" type="tdate" indexed="true" stored="true" />
  <field name="text" type="text_en" indexed="true" stored="true" />

  <field name="_version_" type="long" indexed="true" stored="true"/>
  <dynamicField name="ignored_*" type="ignored"/>
</fields>
```

The Solr output schema omits some Avro input fields, such as `user_statuses_count`.Suppose you want to rename the input field `user_screen_name` to the output field `username`. Also suppose that the time format for the `created_at` field is `yyyy-MM-dd'T'HH:mm:ss'Z'`. Finally, suppose any unknown fields present are to be removed. Recall that Solr throws an exception on any attempt to load a document that contains a field that is not specified in `schema.xml`.

4. These transformation rulescan be expressed with morphline commands called `readAvroContainer`, `extractAvroPaths`, `convertTimestamp`, `sanitizeUnknownSolrFields` and `loadSolr`, by editing a `morphline.conf` file.

> **Note:** The following example uses the Kite SDK, which applies to Search for CDH 5. In the case of `morphlines.conf` files used with Search 5.3.5 and earlier, which uses CDK, the `importCommands` are different.

For the following `morphlines.conf` file to apply to CDK, you replace `importCommands : ["org.kitesdk.morphline.**", "com.ngdata.**"]` with `importCommands : ["com.cloudera.cdk.morphline.**", "com.ngdata.**"]`.

```
# Specify server locations in a SOLR_LOCATOR variable; used later in
# variable substitutions:
SOLR_LOCATOR : {
  # Name of solr collection
  collection : collection1

  # ZooKeeper ensemble
  zkHost : "127.0.0.1:2181/solr"
}

# Specify an array of one or more morphlines, each of which defines an ETL
# transformation chain. A morphline consists of one or more potentially
# nested commands. A morphline is a way to consume records such as Flume events,
# HDFS files or blocks, turn them into a stream of records, and pipe the stream
# of records through a set of easily configurable transformations on its way to
# Solr.
morphlines : [
  {
    # Name used to identify a morphline. For example, used if there are multiple

    # morphlines in a morphline config file.
    id : morphline1

    # Import all morphline commands in these java packages and their subpackages.

    # Other commands that may be present on the classpath are not visible to this

    # morphline.
    importCommands : ["org.kitesdk.**", "org.apache.solr.**"]

    commands : [
      {
        # Parse Avro container file and emit a record for each Avro object
        readAvroContainer {
          # Optionally, require the input to match one of these MIME types:
          # supportedMimeTypes : [avro/binary]

          # Optionally, use a custom Avro schema in JSON format inline:
          # readerSchemaString : """<json can go here>"""

          # Optionally, use a custom Avro schema file in JSON format:
          # readerSchemaFile : /path/to/syslog.avsc
        }
      }

      {
        # Consume the output record of the previous command and pipe another
        # record downstream.
        #
        # extractAvroPaths is a command that uses zero or more Avro path
        # excodeblockssions to extract values from an Avro object. Each
excodeblockssion
       # consists of a record output field name, which appears to the left of the

        # colon ':' and zero or more path steps, which appear to the right.
        # Each path step is separated by a '/' slash. Avro arrays are
        # traversed with the '[]' notation.
        #
       # The result of a path excodeblockssion is a list of objects, each of which

        # is added to the given record output field.
        #
        # The path language supports all Avro concepts, including nested
        # structures, records, arrays, maps, unions, and others, as well as a
flatten
        # option that collects the primitives in a subtree into a flat list. In
the
        # paths specification, entries on the left of the colon are the target
Solr
```

```
        # field and entries on the right specify the Avro source paths. Paths are
 read
        # from the source that is named to the right of the colon and written to
the
        # field that is named on the left.
        extractAvroPaths {
          flatten : false
          paths : {
            id : /id
            username : /user_screen_name
            created_at : /created_at
            text : /text
          }
        }
      }

      # Consume the output record of the previous command and pipe another
      # record downstream.
      #
      # convert timestamp field to native Solr timestamp format
      # such as 2012-09-06T07:14:34Z to 2012-09-06T07:14:34.000Z
      {
        convertTimestamp {
          field : created_at
          inputFormats : ["yyyy-MM-dd'T'HH:mm:ss'Z'", "yyyy-MM-dd"]
          inputTimezone : America/Los_Angeles
          outputFormat : "yyyy-MM-dd'T'HH:mm:ss.SSS'Z'"

          outputTimezone : UTC
        }
      }

      # Consume the output record of the previous command and pipe another
      # record downstream.
      #
      # This command deletes record fields that are unknown to Solr
      # schema.xml.
      #
      # Recall that Solr throws an exception on any attempt to load a document
      # that contains a field that is not specified in schema.xml.
      {
        sanitizeUnknownSolrFields {
          # Location from which to fetch Solr schema
          solrLocator : ${SOLR_LOCATOR}
        }
      }

      # log the record at DEBUG level to SLF4J
      { logDebug { format : "output record: {}", args : ["@{}"] } }

      # load the record into a Solr server or MapReduce Reducer
      {
        loadSolr {
          solrLocator : ${SOLR_LOCATOR}
        }
      }
    ]
  }
]
```

Using Morphlines with Syslog

The following example illustrates using a morphline to extract information from a `syslog` file. A syslog file contains semi-structured lines of the following form:

```
<164>Feb  4 10:46:14 syslog sshd[607]: listening on 0.0.0.0 port 22.
```

The program extracts the following record from the log line and loads it into Solr:

```
syslog_pri:164
syslog_timestamp:Feb  4 10:46:14
syslog_hostname:syslog
syslog_program:sshd
syslog_pid:607
syslog_message:listening on 0.0.0.0 port 22.
```

Use the following rules to create a chain of transformation commands, which are expressed with the `readLine`, `grok`, and `logDebug` morphline commands, by editing a `morphline.conf` file.

> **Note:** The following example uses the Kite SDK, which applies to Search for CDH 5. In the case of `morphlines.conf` files used with Search 5.3.5 and earlier, which uses CDK, the `importCommands` are different.

For the following `morphlines.conf` file to apply to CDK, you replace `importCommands : ["org.kitesdk.**", "com.ngdata.**"]` with `importCommands : ["com.cloudera.cdk.morphline.**", "com.ngdata.**"]`.

```
# Specify server locations in a SOLR_LOCATOR variable; used later in
# variable substitutions:
SOLR_LOCATOR : {
  # Name of solr collection
  collection : collection1

  # ZooKeeper ensemble
  zkHost : "127.0.0.1:2181/solr"
}

# Specify an array of one or more morphlines, each of which defines an ETL
# transformation chain. A morphline consists of one or more potentially
# nested commands. A morphline is a way to consume records such as Flume events,
# HDFS files or blocks, turn them into a stream of records, and pipe the stream
# of records through a set of easily configurable transformations on the way to
# a target application such as Solr.
morphlines : [
  {
    id : morphline1
    importCommands : ["org.kitesdk.**"]

    commands : [
      {
        readLine {
          charset : UTF-8
        }
      }

      {
        grok {
          # a grok-dictionary is a config file that contains prefabricated regular
expressions
          # that can be referred to by name.
          # grok patterns specify such a regex name, plus an optional output field
name.
          # The syntax is %{REGEX_NAME:OUTPUT_FIELD_NAME}
          # The input line is expected in the "message" input field.
          dictionaryFiles : [target/test-classes/grok-dictionaries]
          expressions : {
            message : """<%{POSINT:syslog_pri}>%{SYSLOGTIMESTAMP:syslog_timestamp}
%{SYSLOGHOST:syslog_hostname} %{DATA:syslog_program}(?:\[%{POSINT:syslog_pid}\])?:
%{GREEDYDATA:syslog_message}"""
          }
        }
      }

      # Consume the output record of the previous command and pipe another
      # record downstream.
      #
```

```
      # This command deletes record fields that are unknown to Solr
      # schema.xml.
      #
      # Recall that Solr throws an exception on any attempt to load a document
      # that contains a field that is not specified in schema.xml.
      {
        sanitizeUnknownSolrFields {
          # Location from which to fetch Solr schema
          solrLocator : ${SOLR_LOCATOR}
        }
      }

      # log the record at DEBUG level to SLF4J
      { logDebug { format : "output record: {}", args : ["@{}"] } }

      # load the record into a Solr server or MapReduce Reducer
      {
        loadSolr {
          solrLocator : ${SOLR_LOCATOR}
        }
      }

    ]
  }
]
```

Next Steps

Learn more about morphlines and Kite. Cloudera Search 5.3.5 includes CDK version 0.9.1. For more information, see:

- CDK Morphlines Reference Guide.
- More example morphlines can be found in the unit tests.

Using the Lily HBase Batch Indexer for Indexing

With Cloudera Search, you can batch index HBase tables using MapReduce jobs. This batch indexing does not require:

- HBase replication
- The Lily HBase Indexer Service
- Registering a Lily HBase Indexer configuration with the Lily HBase Indexer Service

The indexer supports flexible, custom, application-specific rules to extract, transform, and load HBase data into Solr. Solr search results can contain `columnFamily:qualifier` links back to the data stored in HBase. This way, applications can use the search result set to directly access matching raw HBase cells.

Batch indexing column families of tables in an HBase cluster requires:

- Populating an HBase table
- Creating a corresponding SolrCloud collection
- Creating a Lily HBase Indexer configuration
- Creating a Morphline configuration file
- Understanding the `extractHBaseCells` morphline command
- Running HBaseMapReduceIndexerTool

Populating an HBase table

After configuring and starting your system, create an HBase table and add rows to it. For example:

```
$ hbase shell
```

```
hbase(main):002:0> create 'record', {NAME => 'data'}
hbase(main):002:0> put 'record', 'row1', 'data', 'value'
hbase(main):001:0> put 'record', 'row2', 'data', 'value2'
```

Creating a corresponding SolrCloud collection

A SolrCloud collection used for HBase indexing must have a Solr schema that accommodates the types of HBase column families and qualifiers that are being indexed. To begin, consider adding the all-inclusive `data` field to a default schema. Once you decide on a schema, create a SolrCloud collection using a command of the form:

```
$ solrctl instancedir --generate $HOME/hbase-collection1
$ edit $HOME/hbase-collection1/conf/schema.xml
$ solrctl instancedir --create hbase-collection1 $HOME/hbase-collection1
$ solrctl collection --create hbase-collection1
```

Creating a Lily HBase Indexer configuration

Configure individual Lily HBase Indexers using the `hbase-indexer` command-line utility. Typically, there is one Lily HBase Indexer configuration for each HBase table, but there can be as many Lily HBase Indexer configurations as there are tables and column families and corresponding collections in the SolrCloud. Each Lily HBase Indexer configuration is defined in an XML file, such as `morphline-hbase-mapper.xml`.

An indexer configuration XML file must refer to the `MorphlineResultToSolrMapper` implementation and point to the location of a Morphline configuration file, as shown in the following`morphline-hbase-mapper.xml`indexer configuration file:

```
$ cat $HOME/morphline-hbase-mapper.xml

<?xml version="1.0"?>
<indexer table="record"
mapper="com.ngdata.hbaseindexer.morphline.MorphlineResultToSolrMapper">

   <!-- The relative or absolute path on the local file system to the morphline
configuration file. -->
   <!-- Use relative path "morphlines.conf" for morphlines managed by Cloudera Manager
 -->
   <param name="morphlineFile" value="/etc/hbase-solr/conf/morphlines.conf"/>

  <!-- The optional morphlineId identifies a morphline if there are multiple morphlines
 in morphlines.conf -->
   <!-- <param name="morphlineId" value="morphline1"/> -->

</indexer>
```

The Lily HBase Indexer configuration file also supports the standard attributes of any HBase Lily Indexer on the top-level`<indexer>`element: `table`, `mapping-type`, `read-row`, `unique-key-formatter`, `unique-key-field`, `row-field`, and `column-family-field`. It does not support the`<field>`element and`<extract>`elements.

Creating a Morphline Configuration File

After creating an indexer configuration XML file, control its behavior by configuring morphline ETL transformation commands in a `morphlines.conf` configuration file. The `morphlines.conf` configuration file can contain any number of morphline commands. Typically, an`extractHBaseCells`command is the first command. The `readAvroContainer` or `readAvro` morphline commands are often used to extract Avro data from the HBase byte array. This configuration file can be shared among different applications that use morphlines.

> **Note:** The following example uses the Kite SDK, which applies to Search for CDH 5. In the case of `morphlines.conf` files used with Search 5.3.5 and earlier, which uses CDK, the `importCommands` are different.

For the following `morphlines.conf` file to apply to CDK, you replace `importCommands : ["org.kitesdk.morphline.**", "com.ngdata.**"]` with `importCommands : ["com.cloudera.cdk.morphline.**", "com.ngdata.**"]`.

```
$ cat /etc/hbase-solr/conf/morphlines.conf

morphlines : [
  {
    id : morphline1
    importCommands : ["org.kitesdk.morphline.**", "com.ngdata.**"]

    commands : [
      {
        extractHBaseCells {
          mappings : [
            {
              inputColumn : "data:*"
              outputField : "data"
              type : string
              source : value
            }

            #{
            #  inputColumn : "data:item"
            #  outputField : "_attachment_body"
            #  type : "byte[]"
            #  source : value
            #}
          ]
        }
      }

      #for avro use with type : "byte[]" in extractHBaseCells mapping above
      #{ readAvroContainer {} }
      #{
      #  extractAvroPaths {
      #    paths : {
      #      data : /user_name
      #    }
      #  }
      #}

      { logTrace { format : "output record: {}", args : ["@{}"] } }
    ]
  }
]
```

> **Note:** To function properly, the morphline must not contain a `loadSolr` command. The enclosing Lily HBase Indexer must load documents into Solr, instead the morphline itself.

Understanding the `extractHBaseCells` morphline command

The `extractHBaseCells` morphline command extracts cells from an HBase result and transforms the values into a `SolrInputDocument`. The command consists of an array of zero or more mapping specifications.

Each mapping has:

- The `inputColumn` parameter, which specifies the data from HBase for populating a field in Solr. It has the form of a column family name and qualifier, separated by a colon. The qualifier portion can end in an asterisk, which is interpreted as a wildcard. In this case, all matching column-family and qualifier expressions are used. The following are examples of valid `inputColumn` values:
  - `mycolumnfamily:myqualifier`
  - `mycolumnfamily:my*`
  - `mycolumnfamily:*`

- The `outputField` parameter specifies the morphline record field to which to add output values. The morphline record field is also known as the Solr document field. Example: `first_name`.
- Dynamic output fields are enabled by the `outputField` parameter ending with a * wildcard. For example:

```
inputColumn : "m:e:*"
outputField : "belongs_to_*"
```

  In this case, if you make these puts in HBase:

```
put 'table_name' , 'row1' , 'm:e:1' , 'foo'
put 'table_name' , 'row1' , 'm:e:9' , 'bar'
```

  Then the fields of the Solr document are as follows:

```
belongs_to_1 : foo
belongs_to_9 : bar
```

- The `type` parameter defines the data type of the content in HBase. All input data is stored in HBase as byte arrays, but all content in Solr is indexed as text, so a method for converting byte arrays to the actual data type is required. The type parameter can be the name of a type that is supported by `org.apache.hadoop.hbase.util.Bytes.to*` (which currently includes `byte[]`, `int`, `long`, `string`, `boolean`, `float`, `double`, `short`, and `bigdecimal`). Use type `byte[]` to pass the byte array through to the morphline without conversion.
  - `type:byte[]` copies the byte array unmodified into the record output field
  - `type:int` converts with `org.apache.hadoop.hbase.util.Bytes.toInt`
  - `type:long` converts with `org.apache.hadoop.hbase.util.Bytes.toLong`
  - `type:string` converts with `org.apache.hadoop.hbase.util.Bytes.toString`
  - `type:boolean` converts with `org.apache.hadoop.hbase.util.Bytes.toBoolean`
  - `type:float` converts with `org.apache.hadoop.hbase.util.Bytes.toFloat`
  - `type:double` converts with `org.apache.hadoop.hbase.util.Bytes.toDouble`
  - `type:short` converts with `org.apache.hadoop.hbase.util.Bytes.toShort`
  - `type:bigdecimal` converts with `org.apache.hadoop.hbase.util.Bytes.toBigDecimal`

  Alternatively, the `type` parameter can be the name of a Java class that implements the `com.ngdata.hbaseindexer.parse.ByteArrayValueMapper` interface.
- The `source` parameter determines which portion of an HBase KeyValue is used as indexing input. Valid choices are `value` or `qualifier`. When `value` is specified, the HBase cell value is used as input for indexing. When `qualifier` is specified, then the HBase column qualifier is used as input for indexing. The default is `value`.

Running HBaseMapReduceIndexerTool

Run HBaseMapReduceIndexerTool to index the HBase table using a MapReduce job, as follows:

```
hadoop --config /etc/hadoop/conf jar \
/usr/lib/hbase-solr/tools/hbase-indexer-mr-*-job.jar --conf \
/etc/hbase/conf/hbase-site.xml -D 'mapred.child.java.opts=-Xmx500m' \
--hbase-indexer-file $HOME/morphline-hbase-mapper.xml --zk-host \
127.0.0.1/solr --collection hbase-collection1 --go-live --log4j \
src/test/resources/log4j.properties
```

> **Note:** For development purposes, use the `--dry-run` option to run in local mode and print documents to `stdout`, instead of loading them to Solr. Using this option causes the morphline to execute in the client process without submitting a job to MapReduce. Executing in the client process provides quicker results during early trial and debug sessions.

- **Note:** To print diagnostic information, such as the content of records as they pass through morphline commands, enable TRACE log level diagnostics by adding the following to your `log4j.properties` file:

```
log4j.logger.com.cloudera.cdk.morphline=TRACE
log4j.logger.com.ngdata=TRACE
```

  The `log4j.properties` file can be passed using the `--log4j` command-line option.

HBaseMapReduceIndexerTool

HBaseMapReduceIndexerTool is a MapReduce batch job driver that takes input data from an HBase table, creates Solr index shards, and writes the indexes into HDFS in a flexible, scalable, and fault-tolerant manner. It also supports merging the output shards into a set of live customer-facing Solr servers in SolrCloud.

More details are available through command-line help:

```
$ hadoop jar /usr/lib/hbase-solr/tools/hbase-indexer-mr-*-job.jar --help

usage: hadoop [GenericOptions]... jar hbase-indexer-mr-*-job.jar
       [--hbase-indexer-zk STRING] [--hbase-indexer-name STRING]
       [--hbase-indexer-file FILE] [--hbase-table-name STRING]
       [--hbase-start-row BINARYSTRING] [--hbase-end-row BINARYSTRING]
       [--hbase-start-time STRING] [--hbase-end-time STRING]
       [--hbase-timestamp-format STRING] [--zk-host STRING] [--go-live]
       [--collection STRING] [--go-live-threads INTEGER] [--help]
       [--output-dir HDFS_URI] [--overwrite-output-dir]
       [--morphline-file FILE] [--morphline-id STRING]
       [--update-conflict-resolver FQCN] [--reducers INTEGER]
       [--max-segments INTEGER] [--fair-scheduler-pool STRING] [--dry-run]
       [--log4j FILE] [--verbose] [--show-non-solr-cloud]

MapReduce batch job driver that takes input data from an HBase table and
creates Solr index shards and writes the indexes into HDFS, in a flexible,
scalable, and fault-tolerant manner. It also supports merging the output
shards into a set of live customer-facing Solr servers in SolrCloud.
Optionally, documents can be sent directly from the mapper tasks to
SolrCloud, which is a much less scalable approach but enables updating
existing documents in SolrCloud. The program proceeds in one or multiple
consecutive MapReduce-based phases, as follows:

1) Mapper phase: This (parallel) phase scans over the input HBase table,
extracts the relevant content, and transforms it into SolrInputDocuments.
If run as a mapper-only job, this phase also writes the SolrInputDocuments
directly to a live SolrCloud cluster. The conversion from HBase records
into Solr documents is performed via a hbase-indexer configuration and
typically based on a morphline.

2) Reducer phase: This (parallel) phase loads the mapper's
SolrInputDocuments into one EmbeddedSolrServer per reducer. Each such
reducer and Solr server can be seen as a (micro) shard. The Solr servers
store their data in HDFS.

3) Mapper-only merge phase: This (parallel) phase merges the set of
reducer shards into the number of Solr shards expected by the user, using
a mapper-only job. This phase is omitted if the number of shards is
already equal to the number of shards expected by the user

4) Go-live phase: This optional (parallel) phase merges the output shards
of the previous phase into a set of live customer-facing Solr servers in
SolrCloud. If this phase is omitted you can explicitly point each Solr
server to one of the HDFS output shard directories

Fault Tolerance: Mapper and reducer task attempts are retried on failure
per the standard MapReduce semantics. On program startup all data in the --
output-dir is deleted if that output directory already exists and --
overwrite-output-dir is specified. This means that if the whole job fails
you can retry simply by rerunning the program again using the same
arguments.
```

```
HBase Indexer parameters:
  Parameters for specifying the  HBase  indexer  definition and/or where it
  should be loaded from.

  --hbase-indexer-zk STRING
                         The address of the  ZooKeeper  ensemble from which
                         to fetch  the  indexer  definition  named --hbase-
                         indexer-name.  Format  is:  a  list  of  comma
                         separated host:port pairs,  each  corresponding to
                         a zk  server.  Example: '127.0.0.1:2181,127.0.0.1:
                         2182,127.0.0.1:2183'
  --hbase-indexer-name STRING
                         The name of  the  indexer  configuration  to fetch
                         from the  ZooKeeper  ensemble  specified  with  --
                         hbase-indexer-zk. Example: myIndexer
  --hbase-indexer-file FILE
                         Relative  or  absolute  path  to  a  local  HBase
                         indexer XML configuration file.  If supplied, this
                         overrides --hbase-indexer-zk  and --hbase-indexer-
                         name. Example: /path/to/morphline-hbase-mapper.xml

HBase scan parameters:
  Parameters for specifying what data is included while reading from HBase.

  --hbase-table-name STRING
                         Optional name of  the  HBase  table containing the
                         records  to  be  indexed.  If  supplied,  this
                         overrides the  value  from  the  --hbase-indexer-*
                         options. Example: myTable
  --hbase-start-row BINARYSTRING
                         Binary string  representation  of  start  row from
                         which to start  indexing  (inclusive).  The format
                         of the supplied row  key  should use two-digit hex
                         values prefixed by \x for non-ASCII characters (e.
                         g. 'row\x00'). The semantics  of this argument are
                         the same as those  for  the HBase Scan#setStartRow
                         method. The default is  to  include  the first row
                         of the table. Example: AAAA
  --hbase-end-row BINARYSTRING
                         Binary string representation of  end row prefix at
                         which  to  stop  indexing  (exclusive).  See  the
                         description  of  --hbase-start-row  for  more
                         information. The default  is  to  include the last
                         row of the table. Example: CCCC
  --hbase-start-time STRING
                         Earliest timestamp (inclusive)  in  time  range of
                         HBase cells  to  be  included  for  indexing.  The
                         default is to include all cells. Example: 0
  --hbase-end-time STRING
                         Latest timestamp (exclusive) of  HBase cells to be
                         included for indexing. The  default  is to include
                         all cells. Example: 123456789
  --hbase-timestamp-format STRING
                         Timestamp format to be  used to interpret --hbase-
                         start-time and --hbase-end-time.  This  is a java.
                         text.SimpleDateFormat compliant format  (see http:
                         //docs.oracle.
                         com/javase/6/docs/api/java/text/SimpleDateFormat.
                         html). If  this  parameter  is  omitted  then  the
                         timestamps  are  interpreted  as  number  of
                         milliseconds  since  the  standard  epoch  (Unix
                         time). Example: "yyyy-MM-dd'T'HH:mm:ss.SSSZ"

Solr cluster arguments:
  Arguments that provide information about your Solr cluster.

  --zk-host STRING        The address of a ZooKeeper  ensemble being used by
                         a SolrCloud cluster. This  ZooKeeper ensemble will
                         be examined  to  determine  the  number  of output
                         shards to create  as  well  as  the  Solr  URLs to
                         merge the output shards into  when using the --go-
                         live option. Requires that  you  also  pass the --
                         collection to merge the shards into.
```

```
                        The --zk-host option implements the same
                        partitioning semantics as the standard SolrCloud
                        Near-Real-Time (NRT) API. This enables to mix
                        batch updates from MapReduce ingestion with
                        updates from standard Solr NRT ingestion on the
                        same SolrCloud cluster, using identical unique
                        document keys.

                        Format is: a list of comma separated host:port
                        pairs, each corresponding to a zk server.
                        Example: '127.0.0.1:2181,127.0.0.1:2182,127.0.0.1:
                        2183' If the optional chroot suffix is used the
                        example would look like: '127.0.0.1:2181/solr,
                        127.0.0.1:2182/solr,127.0.0.1:2183/solr' where
                        the client would be rooted at '/solr' and all
                        paths would be relative to this root - i.e.
                        getting/setting/etc... '/foo/bar' would result in
                        operations being run on '/solr/foo/bar' (from the
                        server perspective).


Go live arguments:
  Arguments for merging the shards that are built into a live Solr
  cluster. Also see the Cluster arguments.

  --go-live             Allows you to optionally merge the final index
                        shards into a live Solr cluster after they are
                        built. You can pass the ZooKeeper address with --
                        zk-host and the relevant cluster information will
                        be auto detected. (default: false)
  --collection STRING   The SolrCloud collection to merge shards into
                        when using --go-live and --zk-host. Example:
                        collection1
  --go-live-threads INTEGER
                        Tuning knob that indicates the maximum number of
                        live merges to run in parallel at one time.
                        (default: 1000)

Optional arguments:
  --help, -help, -h     Show this help message and exit
  --output-dir HDFS_URI HDFS directory to write Solr indexes to. Inside
                        there one output directory per shard will be
                        generated. Example: hdfs://c2202.mycompany.
                        com/user/$USER/test
  --overwrite-output-dir
                        Overwrite the directory specified by --output-dir
                        if it already exists. Using this parameter will
                        result in the output directory being recursively
                        deleted at job startup. (default: false)
  --morphline-file FILE Relative or absolute path to a local config file
                        that contains one or more morphlines. The file
                        must be UTF-8 encoded. The file will be uploaded
                        to each MR task. If supplied, this overrides the
                        value from the --hbase-indexer-* options.
                        Example: /path/to/morphlines.conf
  --morphline-id STRING The identifier of the morphline that shall be
                        executed within the morphline config file, e.g.
                        specified by --morphline-file. If the --morphline-
                        id option is omitted the first (i.e. top-most)
                        morphline within the config file is used. If
                        supplied, this overrides the value from the --
                        hbase-indexer-* options. Example: morphline1
  --update-conflict-resolver FQCN
                        Fully qualified class name of a Java class that
                        implements the UpdateConflictResolver interface.
                        This enables deduplication and ordering of a
                        series of document updates for the same unique
                        document key. For example, a MapReduce batch job
                        might index multiple files in the same job where
                        some of the files contain old and new versions of
                        the very same document, using the same unique
                        document key.
```

```
                        Typically, implementations of this interface
                        forbid collisions by throwing an exception, or
                        ignore all but the most recent document version,
                        or, in the general case, order colliding updates
                        ascending from least recent to most recent
                        (partial) update. The caller of this interface (i.
                        e. the Hadoop Reducer) will then apply the
                        updates to Solr in the order returned by the
                        orderUpdates() method.
                        The                                      default
                        RetainMostRecentUpdateConflictResolver
                        implementation ignores all but the most recent
                        document version, based on a configurable numeric
                        Solr field, which defaults to the
                        file_last_modified timestamp (default: org.apache.
                        solr.hadoop.dedup.
                        RetainMostRecentUpdateConflictResolver)
  --reducers INTEGER    Tuning knob that indicates the number of reducers
                        to index into. 0 indicates that no reducers
                        should be used, and documents should be sent
                        directly from the mapper tasks to live Solr
                        servers. -1 indicates use all reduce slots
                        available on the cluster. -2 indicates use one
                        reducer per output shard, which disables the
                        mtree merge MR algorithm. The mtree merge MR
                        algorithm improves scalability by spreading load
                        (in particular CPU load) among a number of
                        parallel reducers that can be much larger than
                        the number of solr shards expected by the user.
                        It can be seen as an extension of concurrent
                        lucene merges and tiered lucene merges to the
                        clustered case. The subsequent mapper-only phase
                        merges the output of said large number of
                        reducers to the number of shards expected by the
                        user, again by utilizing more available
                        parallelism on the cluster. (default: -1)
  --max-segments INTEGER
                        Tuning knob that indicates the maximum number of
                        segments to be contained on output in the index
                        of each reducer shard. After a reducer has built
                        its output index it applies a merge policy to
                        merge segments until there are <= maxSegments
                        lucene segments left in this index. Merging
                        segments involves reading and rewriting all data
                        in all these segment files, potentially multiple
                        times, which is very I/O intensive and time
                        consuming. However, an index with fewer segments
                        can later be merged faster, and it can later be
                        queried faster once deployed to a live Solr
                        serving shard. Set maxSegments to 1 to optimize
                        the index for low query latency. In a nutshell, a
                        small maxSegments value trades indexing latency
                        for subsequently improved query latency. This can
                        be a reasonable trade-off for batch indexing
                        systems. (default: 1)
  --fair-scheduler-pool STRING
                        Optional tuning knob that indicates the name of
                        the fair scheduler pool to submit jobs to. The
                        Fair Scheduler is a pluggable MapReduce scheduler
                        that provides a way to share large clusters. Fair
                        scheduling is a method of assigning resources to
                        jobs such that all jobs get, on average, an equal
                        share of resources over time. When there is a
                        single job running, that job uses the entire
                        cluster. When other jobs are submitted, tasks
                        slots that free up are assigned to the new jobs,
                        so that each job gets roughly the same amount of
                        CPU time. Unlike the default Hadoop scheduler,
                        which forms a queue of jobs, this lets short jobs
                        finish in reasonable time while not starving long
                        jobs. It is also an easy way to share a cluster
                        between multiple of users. Fair sharing can also
                        work with job priorities - the priorities are
```

```
                          used as  weights  to  determine  the  fraction  of
                          total compute time that each job gets.
  --dry-run               Run in local mode  and  print  documents to stdout
                          instead of loading them  into  Solr. This executes
                          the  morphline  in  the  client  process  (without
                          submitting a job  to  MR)  for  quicker turnaround
                          during early  trial  &  debug  sessions. (default:
                          false)
  --log4j FILE            Relative or absolute  path  to  a log4j.properties
                          config file on the  local  file  system. This file
                          will  be  uploaded  to   each  MR  task.  Example:
                          /path/to/log4j.properties
  --verbose, -v           Turn on verbose output. (default: false)

Generic options supported are
  --conf <configuration file>
                          specify an application configuration file
  -D <property=value>     use value for given property
  --fs <local|namenode:port>
                          specify a namenode
  --jt <local|jobtracker:port>
                          specify a job tracker
  --files <comma separated list of files>
                          specify comma separated files to  be copied to the
                          map reduce cluster
  --libjars <comma separated list of jars>
                          specify comma separated  jar  files  to include in
                          the classpath.
  --archives <comma separated list of archives>
                          specify comma separated archives  to be unarchived
                          on the compute machines.

The general command line syntax is
bin/hadoop command [genericOptions] [commandOptions]

Examples:

# (Re)index a table in GoLive mode based on a local indexer config file
hadoop --config /etc/hadoop/conf jar hbase-indexer-mr-*-job.jar --conf \
/etc/hbase/conf/hbase-site.xml -D 'mapred.child.java.opts=-Xmx500m' \
--hbase-indexer-file indexer.xml --zk-host 127.0.0.1/solr --collection \
collection1 --go-live --log4j src/test/resources/log4j.properties

# (Re)index a table in GoLive mode using a local morphline-based indexer config file
hadoop --config /etc/hadoop/conf jar hbase-indexer-mr-*-job.jar --conf \
/etc/hbase/conf/hbase-site.xml -D 'mapred.child.java.opts=-Xmx500m' \
--hbase-indexer-file src/test/resources/morphline_indexer_without_zk.xml \
--zk-host 127.0.0.1/solr --collection collection1 --go-live --morphline-file \
src/test/resources/morphlines.conf --output-dir \
hdfs://c2202.mycompany.com/user/$USER/test --overwrite-output-dir --log4j \
src/test/resources/log4j.properties

# (Re)index a table in GoLive mode
hadoop --config /etc/hadoop/conf jar hbase-indexer-mr-*-job.jar --conf \
/etc/hbase/conf/hbase-site.xml -D 'mapred.child.java.opts=-Xmx500m' \
--hbase-indexer-file indexer.xml --zk-host 127.0.0.1/solr --collection \
collection1 --go-live --log4j src/test/resources/log4j.properties

# (Re)index a table with direct writes to SolrCloud
hadoop --config /etc/hadoop/conf jar hbase-indexer-mr-*-job.jar --conf \
/etc/hbase/conf/hbase-site.xml -D 'mapred.child.java.opts=-Xmx500m' \
--hbase-indexer-file indexer.xml --zk-host 127.0.0.1/solr --collection \
collection1 --reducers 0 --log4j src/test/resources/log4j.properties

# (Re)index a table based on a indexer config stored in ZK
hadoop --config /etc/hadoop/conf jar hbase-indexer-mr-*-job.jar --conf \
/etc/hbase/conf/hbase-site.xml -D 'mapred.child.java.opts=-Xmx500m' \
--hbase-indexer-zk zk01 --hbase-indexer-name docindexer --go-live --log4j \
src/test/resources/log4j.properties
```

Configuring the Lily HBase NRT Indexer Service for Use with Cloudera Search

The Lily HBase NRT Indexer Service is a flexible, scalable, fault-tolerant, transactional, near real-time (NRT) system for processing a continuous stream of HBase cell updates into live search indexes. Typically it takes seconds for data ingested into HBase to appear in search results; this duration is tunable. The Lily HBase Indexer uses SolrCloud to index data stored in HBase. As HBase applies inserts, updates, and deletes to HBase table cells, the indexer keeps Solr consistent with the HBase table contents, using standard HBase replication. The indexer supports flexible custom application-specific rules to extract, transform, and load HBase data into Solr. Solr search results can contain `columnFamily:qualifier` links back to the data stored in HBase. This way, applications can use the Search result set to directly access matching raw HBase cells. Indexing and searching do not affect operational stability or write throughput of HBase because the indexing and searching processes are separate and asynchronous to HBase.

The Lily HBase NRT Indexer Service must be deployed in an environment with a running HBase cluster, a running SolrCloud cluster, and at least one ZooKeeper cluster. This can be done with or without Cloudera Manager. See The Lily HBase Indexer Service in Managing Clusters with Cloudera Manager for more information.

Enabling Cluster-wide HBase Replication

The Lily HBase Indexer is implemented using HBase replication, presenting indexers as region servers of the slave cluster. This requires HBase replication on the HBase cluster, as well as the individual tables to be indexed. An example of settings required for configuring cluster-wide HBase replication is shown in `/usr/share/doc/hbase-solr-doc*/demo/hbase-site.xml`. You must add these settings to all of the `hbase-site.xml` configuration files on the HBase cluster, except the `replication.replicationsource.implementation` property. You can use the Cloudera Manager HBase Indexer Service GUI to do this. After making these updates, restart your HBase cluster.

Pointing a Lily HBase NRT Indexer Service at an HBase Cluster that Needs to Be Indexed

Before starting Lily HBase NRT Indexer services, you must configure individual services with the location of a ZooKeeper ensemble that is used for the target HBase cluster. Add the following property to `/etc/hbase-solr/conf/hbase-indexer-site.xml`. Remember to replace `hbase-cluster-zookeeper` with the actual ensemble string found in the `hbase-site.xml` configuration file:

```
<property>
   <name>hbase.zookeeper.quorum</name>
   <value>hbase-cluster-zookeeper</value>
</property>
```

Configure all Lily HBase NRT Indexer Services to use a particular ZooKeeper ensemble to coordinate with one other. Add the following property to `/etc/hbase-solr/conf/hbase-indexer-site.xml`, and replace `hbase-cluster-zookeeper:2181` with the actual ensemble string:

```
<property>
   <name>hbaseindexer.zookeeper.connectstring</name>
   <value>hbase-cluster-zookeeper:2181</value>
</property>
```

Starting an Lily HBase NRT Indexer Service

You can use the Cloudera Manager GUI to start Lily HBase NRT Indexer Service on a set of machines. In non-managed deployments, you can start a Lily HBase Indexer Daemon manually on the local host with the following command:

```
sudo service hbase-solr-indexer restart
```

After starting the Lily HBase NRT Indexer Services, verify that all daemons are running using the jps tool from the Oracle JDK, which you can obtain from the Java SE Downloads page. If you are running a pseudo-distributed HDFS installation and a Lily HBase NRT Indexer Service installation on one machine, jps shows the following output:

```
$ sudo jps -lm
31407 sun.tools.jps.Jps -lm
26393 com.ngdata.hbaseindexer.Main
```

Using the Lily HBase NRT Indexer Service

To indexfor column families of tables in an HBase cluster:

- Enable replication on HBase column families
- Create collections and configurations
- Register a Lily HBase Indexer configuration with the Lily HBase Indexer Service
- Verify that indexing is working

Enabling Replication on HBase Column Families

Ensure that cluster-wide HBase replication is enabled. Use the HBase shell to define column-family replication settings.

For every existing table, set the `REPLICATION_SCOPE` on every column family that needs to be indexed by issuing a command of the form:

```
$ hbase shell
hbase shell> disable 'record'
hbase shell> alter 'record', {NAME => 'data', REPLICATION_SCOPE => 1}
hbase shell> enable 'record'
```

For every new table, set the `REPLICATION_SCOPE` on every column family that needs to be indexed by issuing a command of the form:

```
$ hbase shell
hbase shell> create 'record', {NAME => 'data', REPLICATION_SCOPE => 1}
```

Creating Collections and Configurations

The tasks required for the Lily HBase NRT Indexer Services are the same as those described for the Lily HBase Batch Indexer. Follow the steps described in these sections:

- Creating a corresponding SolrCloud collection on page 76
- Creating a Lily HBase Indexer configuration on page 76
- Creating a Morphline Configuration File on page 76

Registering a Lily HBase Indexer Configuration with the Lily HBase Indexer Service

When the content of the Lily HBase Indexer configuration XML file is satisfactory, register it with the Lily HBase Indexer Service.This is done with a given SolrCloud collection by uploading the Lily HBase Indexer configuration XML file to ZooKeeper. For example:

```
$ hbase-indexer add-indexer \
--name myIndexer \
--indexer-conf $HOME/morphline-hbase-mapper.xml \
--connection-param solr.zk=solr-cloude-zk1,solr-cloude-zk2/solr \
--connection-param solr.collection=hbase-collection1 \
--zookeeper hbase-cluster-zookeeper:2181
```

Verify that the indexer was successfully created as follows:

```
$ hbase-indexer list-indexers
Number of indexes: 1

myIndexer
  + Lifecycle state: ACTIVE
  + Incremental indexing state: SUBSCRIBE_AND_CONSUME
  + Batch indexing state: INACTIVE
  + SEP subscription ID: Indexer_myIndexer
  + SEP subscription timestamp: 2013-06-12T11:23:35.635-07:00
  + Connection type: solr
  + Connection params:
    + solr.collection = hbase-collection1
    + solr.zk = localhost/solr
  + Indexer config:
      110 bytes, use -dump to see content
  + Batch index config:
      (none)
  + Default batch index config:
      (none)
  + Processes
    + 1 running processes
    + 0 failed processes
```

Use the `update-indexer` and `delete-indexer` command-line options of the `hbase-indexer` utility to manipulate existing Lily HBase Indexers.

For more help, use the following commands:

```
$ hbase-indexer add-indexer --help
$ hbase-indexer list-indexers --help
$ hbase-indexer update-indexer --help
$ hbase-indexer delete-indexer --help
```

- **Note:** The `morphlines.conf` configuration file must be present on every host that runs an indexer.

- **Note:** You can use the Cloudera Manager Admin Console to update `morphlines.conf`:

  1. On the Cloudera Manager **Home** page, click the Key-Value Indexer Store, often **KS_INDEXER-1**.
  2. Click **Configuration** > **View and Edit**.
  3. Expand **Service-Wide** and click **Morphlines**.
  4. For the **Morphlines File** property, paste the new `morphlines.conf` content into the **Value** field.

  Cloudera Manager automatically copies pasted configuration files to the current working directory of all Lily HBase Indexer cluster processes on start and restart of the Lily HBase Indexer Service. In this case, the file location `/etc/hbase-solr/conf/morphlines.conf` is not applicable.

- **Note:** Morphline configuration files can be changed without re-creating the indexer itself. In such a case, you must restart the Lily HBase Indexer service.

Verifying that Indexing Works

Add rows to the indexed HBase table. For example:

```
$ hbase shell
hbase(main):001:0> put 'record', 'row1', 'data', 'value'
hbase(main):002:0> put 'record', 'row2', 'data', 'value2'
```

If the put operation succeeds, wait a few seconds, navigate to the SolrCloud UI query page, and query the data. Note the updated rows in Solr.

To print diagnostic information, such as the content of records as they pass through the morphline commands, enable the TRACE log level. For example, you might add two lines to your `log4j.properties` file:

```
log4j.logger.com.cloudera.cdk.morphline=TRACE
log4j.logger.com.ngdata=TRACE
```

In Cloudera Manager 4, navigate to **Services** > **KS_INDEXER** > **Configuration** > **View** and **Edit** > **Lily HBase Indexer** > **Advanced** > **Lily HBase Indexer Logging Safety Valve**, and then restart the Lily HBase Indexer Service.

> **Note:** Before Cloudera Manager 4.8, the service was referred to as **Keystore Indexer service**.

In Cloudera Manager 5, navigate to **Clusters** > **KS_INDEXER-1** > **Configuration** > **View** and **Edit** > **Lily HBase Indexer** > **Advanced** > **Lily HBase Indexer Logging Safety Valve**, and then restart the Lily HBase Indexer Service.

> **Note:** The name of the particular key-value store indexer can vary. The most common variation is a different number at the end of the name.

Examine the log files in `/var/log/hbase-solr/lily-hbase-indexer-*` for details.

Using Schemaless Mode (CDH 5.1 or later only)

Schemaless mode removes the need to design a schema before beginning to use Search. This can help you begin using Search more quickly, but schemaless mode is typically less efficient and effective than using a deliberately designed schema.

> **Note:** Cloudera recommends pre-defining a schema before moving to production.

With the default non-schemaless mode, you create a schema by writing a `schema.xml` file before loading data into Solr so it can be used by Cloudera Search. You typically write a different schema definition for each type of data being ingested, because the different types usually have different field names and values. This is done by examining the data to be imported so its structure can be understood, and then creating a schema that accommodates that data. For example, emails might have a field for recipients and log files might have a field for IP addresses for machines reporting errors. Conversely, emails typically do not have an IP address field and log files typically do not have recipients. Therefore, The schema you use to import emails is different from the schema you use to import log files.

Cloudera Search offers schemaless mode to help facilitate sample deployments without the need to pre-define a schema. While schemaless is not suitable for production environments, it can help demonstrate the functionality and features of Cloudera Search. Schemaless mode operates based on three principles:

1. The schema is automatically updated using an API. When not using schemaless mode, users manually modify the `schema.xml` file or use the Schema API.
2. As data is ingested, it is analyzed and a guess is made about the type of data in the field. Supported types include Boolean, Integer, Long, Float, Double, Date, and Text.
3. When a new field is encountered, the schema is automatically updated using the API. The update is based on the guess about the type of data in the field.

For example, if schemaless encounters a field that contains "6.022", this would be determined to be type Float, whereas "Mon May 04 09:51:52 CDT 2009" would be determined to be type Date.

By combining these techniques, Schemaless:

1. Starts without a populated schema.
2. Intakes and analyzes data.
3. Modifies the schema based on guesses about the data.
4. Ingests the data so it can be searched based on the schema updates.

To generate a configuration for use in Schemaless mode, use `solrctl instancedir --generate path -schemaless`. Then, create the instancedir and collection as with non-schemaless mode. For more information, see Solrctl Reference on page 50.

Best Practices

User Defined Schemas Recommended for Production Use Cases

Schemaless Solr is useful for getting started quickly and for understanding the underlying structure of the data you wish to search. However, Schemaless Solr is not recommended for production use cases. Because the schema is automatically generated, a mistake like misspelling the name of the field alters the schema, rather than producing an error. The mistake may not be caught until much later and once caught, may require re-indexing to fix. Also, an unexpected input format may cause the type guessing to pick a field type that is incompatible with data that is subsequently ingested, preventing further ingestion until the incompatibility is manually addressed. Such a case is rare, but could occur. For example, if the first instance of a field was an integer, such as '9', but subsequent entries were text such as '10 Spring Street', the schema would make it impossible to properly ingest those subsequent entries. Therefore, Schemaless Solr may be useful for deciding on a schema during the exploratory stage of development, but Cloudera recommends defining the schema in the traditional way before moving to production.

Give each Collection its own unique Instancedir

Solr supports using the same instancedir for multiple collections. In schemaless mode, automatic schema field additions actually change the underlying instancedir. Thus, if two collections are using the same instancedir, schema field additions meant for one collection will actually affect the other one as well. Therefore, it is recommended that each collection have its own instancedir.

Using Search through a Proxy for High Availability

For most clusters that have multiple users and production availability requirements, you might set up a proxy server to relay requests to and from the Solr service. This configuration has the following advantages:

- Applications connect to a single well-known host and port, rather than keeping track of the hosts where the Solr service is running.
- If any host running the Solr service becomes unavailable, application connection requests still succeed because you always connect to the proxy server.
- The "coordinator host" for each Search query potentially requires more memory and CPU cycles than the other hosts that process the query. The proxy server can issue queries using round-robin scheduling, so that each connection uses a different coordinator host. This load-balancing technique lets the hosts running the Solr service share this additional work, rather than concentrating it on a single machine.

> **Note:** Cloudera Search does not support using a proxy for high availability in an environment that requires Kerberos authentication.

The following setup steps are a general outline that apply to any load-balancing proxy software.

1. Download the load-balancing proxy software. It should only need to be installed and configured on a single host.
2. Configure the software, typically by editing a configuration file. Set up a port on which the load balancer listens to relay Search requests back and forth.
3. Specify the host and port settings for each Solr service host. These are the hosts that the load balancer chooses from when relaying each query. In most cases, use 8983, the default query and update port.
4. Run the load-balancing proxy server, pointing it at the configuration file that you set up.

Migrating Solr Replicas

Migrating replicas is valuable in cases such as when a node is to be replaced. In such a case, migrating any collections on that node to a new node can help ensure optimal performance by deliberately migrating the replica rather than depending on failure recovery.

To migrate a replica to a new node

This procedure uses the following sample names:

- Node names `origin` and `destination`.
- Collection name `email`
- Replica names `email_shard1_replica2`, which is on `origin` and `email_shard1_replica3`, which will be on `destination`.

Cloudera recommends using API calls for creating and unloading cores. Do not use the Cloudera Manager Admin Console for these tasks.

1. Use `curl` to add the new collection on the `destination` server using the CREATE API. For example:

```
curl
http://destination.example.com:8983/solr/admin/cores?action=CREATE&name=email_shard1_replica3&collection=email&shard=shard1
```

   - **Note:** For consistency, Cloudera recommends you construct a new name using the convention of `collection_shard#_replica#`. The previous example assumes two replicas exist in the current shard, so the example uses the name `replica3` to avoid conflicts.

2. In the Cloudera Manager Admin Console, verify core creation succeeds, and that the core moves from recovery state to **UP**.
3. Use `curl` to remove the `core.properties` from `/var/lib/solr` on the origin node using the UNLOAD API. For example:

```
http://origin.example.com:8983/solr/admin/cores?action=UNLOAD&core=email_shard1_replica2&deleteInstanceDir=yes
```

   - **Note:** If the origin node is down or Solr unavailable, this command fails. In such a case, manually remove `core.properties` from `/var/lib/solr/collection_shard#_replica#` so the node does not attempt to register the replica if it starts.

4. In the Cloudera Manager Admin Console, verify that the old replica has been removed.

   - **Note:** To reduce recovery time, suspend NRT ingestion until the new replica is fully replicated from the leader. Re-enable NRT-ingestion after replication is complete.

Configuring Search to Use Kerberos

Cloudera Search supports Kerberos authentication. All necessary packages are installed when you install Search. To enable Kerberos, create principals and keytabs and then modify default configurations.

The following instructions only apply to configuring Kerberos in an unmanaged environment. Kerberos configuration is automatically handled by Cloudera Manager if you are using Search in a Cloudera Manager environment.

To create principals and keytabs

Repeat this process on all Solr server hosts.

1. Create a Solr service user principal using the syntax: `solr/<fully.qualified.domain.name>@<YOUR-REALM>`. This principal is used to authenticate with the Hadoop cluster. where: `fully.qualified.domain.name` is the host where the Solr server is running `YOUR-REALM` is the name of your Kerberos realm.

   ```
   $ kadmin
   kadmin: addprinc -randkey solr/fully.qualified.domain.name@YOUR-REALM.COM
   ```

2. Create a HTTP service user principal using the syntax: `HTTP/<fully.qualified.domain.name>@<YOUR-REALM>`. This principal is used to authenticate user requests coming to the Solr web-services. where: `fully.qualified.domain.name` is the host where the Solr server is running `YOUR-REALM` is the name of your Kerberos realm.

   ```
   kadmin: addprinc -randkey HTTP/fully.qualified.domain.name@YOUR-REALM.COM
   ```

   > **Note:**
   >
   > The `HTTP/` component of the HTTP service user principal must be upper case as shown in the syntax and example above.

3. Create keytab files with both principals.

   ```
   kadmin: xst -norandkey -k solr.keytab solr/fully.qualified.domain.name \
   HTTP/fully.qualified.domain.name
   ```

4. Test that credentials in the merged keytab file work. For example:

   ```
   $ klist -e -k -t solr.keytab
   ```

5. Copy the `solr.keytab` file to the Solr configuration directory. The owner of the `solr.keytab` file should be the `solr` user and the file should have owner-only read permissions.

To modify default configurations

Repeat this process on all Solr server hosts.

1. Ensure that the following properties appear in `/etc/default/solr` and that they are uncommented. Modify these properties to match your environment. The relevant properties to be uncommented and modified are:

   ```
   SOLR_AUTHENTICATION_TYPE=kerberos
   SOLR_AUTHENTICATION_SIMPLE_ALLOW_ANON=true
   SOLR_AUTHENTICATION_KERBEROS_KEYTAB=/etc/solr/conf/solr.keytab
   SOLR_AUTHENTICATION_KERBEROS_PRINCIPAL=HTTP/localhost@LOCALHOST
   SOLR_AUTHENTICATION_KERBEROS_NAME_RULES=DEFAULT
   SOLR_AUTHENTICATION_JAAS_CONF=/etc/solr/conf/jaas.conf
   ```

   > **Note:** Modify the values for these properties to match your environment. For example, the `SOLR_AUTHENTICATION_KERBEROS_PRINCIPAL=HTTP/localhost@LOCALHOST` must include the principal instance and Kerberos realm for your environment. That is often different from `localhost@LOCALHOST`.

2. Set `hadoop.security.auth_to_local` to match the value specified by `SOLR_AUTHENTICATION_KERBEROS_NAME_RULES` in `/etc/default/solr`.

   > **Note:** For information on how to configure the rules, see Configuring the Mapping from Kerberos Principals to Short Names. For additional information on using Solr with HDFS, see Configuring Solr for Use with HDFS on page 17.

3. If using applications that use the `solrj` library, set up the Java Authentication and Authorization Service (JAAS).

   a. Create a `jaas.conf` file in the Solr configuration directory containing the following settings. This file and its location must match the `SOLR_AUTHENTICATION_JAAS_CONF` value. Make sure that you substitute a value for `principal` that matches your particular environment.

      ```
      Client {
        com.sun.security.auth.module.Krb5LoginModule required
      ```

```
  useKeyTab=true
  useTicketCache=false
  keyTab="/etc/solr/conf/solr.keytab"
  principal="solr/fully.qualified.domain.name@<YOUR-REALM>";
};
```

Using Kerberos

The process of enabling Solr clients to authenticate with a secure Solr is specific to the client. This section demonstrates:

- Using Kerberos and curl
- Using solrctl
- Configuring SolrJ Library Usage.

  This enables technologies including:

  - Command line solutions
  - Java applications
  - The MapReduceIndexerTool
- Configuring Flume Morphline Solr Sink Usage

Secure Solr requires that the CDH components that it interacts with are also secure. Secure Solr interacts with HDFS, ZooKeeper and optionally HBase, MapReduce, andFlume. See Cloudera Security or the CDH 4 Security Guide for more information.

Using Kerberos and curl

You can use Kerberos authentication with clients such as `curl`. To use `curl`, begin by acquiring valid Kerberos credentials and then execute the desired command. For example, you might use commands similar to the following:

```
$ kinit -kt username.keytab username
$ curl --negotiate -u foo:bar http://solrserver:8983/solr/
```

- **Note:** Depending on the tool used to connect, additional arguments may be required. For example, with `curl`, `--negotiate` and `-u` are required. The username and password specified with `-u` is not actually checked because Kerberos is used. As a result, any value such as foo:bar or even just : is acceptable. While any value can be provided for `-u`, note that the option is required. Omitting `-u` results in a 401 Unauthorized error, even though the `-u` value is not actually used.

Using solrctl

If you are using `solrctl` to manage your deployment in an environment that requires Kerberos authentication, you must have valid Kerberos credentials, which you can get using `kinit`. For more information on `solrctl`, see Solrctl Reference on page 50

Configuring SolrJ Library Usage

If using applications that use the solrj library, begin by establishing a Java Authentication and Authorization Service (JAAS) configuration file.

Create a JAAS file:

- If you have already used `kinit` to get credentials, you can have the client use those credentials. In such a case, modify your `jaas-client.conf` file to appear as follows:

```
Client {
 com.sun.security.auth.module.Krb5LoginModule required
 useKeyTab=false
 useTicketCache=true
 principal="user/fully.qualified.domain.name@<YOUR-REALM>";
 };
```

  where `user/fully.qualified.domain.name@<YOUR-REALM>` is replaced with your credentials.
- You want the client application to authenticate using a keytab you specify:

```
Client {
 com.sun.security.auth.module.Krb5LoginModule required
 useKeyTab=true
 keyTab="/path/to/keytab/user.keytab"
 storeKey=true
 useTicketCache=false
 principal="user/fully.qualified.domain.name@<YOUR-REALM>";
};
```

  where `/path/to/keytab/user.keytab` is the keytab file you wish to use and `user/fully.qualified.domain.name@<YOUR-REALM>` is the principal in that keytab you wish to use.

Use the JAAS file to enable solutions:

- **Command line solutions**

  Set the property when invoking the program. For example, if you were using a jar, you might use:

```
java -Djava.security.auth.login.config=/home/user/jaas-client.conf -jar app.jar
```

- **Java applications**

  Set the Java system property `java.security.auth.login.config`. For example, if the JAAS configuration file is located on the filesystem as `/home/user/jaas-client.conf`. The Java system property `java.security.auth.login.config` must be set to point to this file. Setting a Java system property can be done programmatically, for example using a call such as:

```
System.setProperty("java.security.auth.login.config",
"/home/user/jaas-client.conf");
```

- **The MapReduceIndexerTool**

  The MapReduceIndexerTool uses SolrJ to pass the JAAS configuration file. Using the MapReduceIndexerTool in a secure environment requires the use of the `HADOOP_OPTS` variable to specify the JAAS configuration file. For example, you might issue a command such as the following:

```
HADOOP_OPTS="-Djava.security.auth.login.config=/home/user/jaas.conf" \
hadoop jar MapReduceIndexerTool
```

- **Configuring the hbase-indexer CLI**

  Certain hbase-indexer CLI commands such as `replication-status` attempt to read ZooKeeper hosts owned by HBase. To successfully use these commands in Search for CDH 4 in a secure environment, edit `/etc/hbase-indexer/conf` and add the environment variable. For example, change:

```
export HBASE_INDEXER_OPTS="-XX:+UseConcMarkSweepGC"
```

To:

```
export
HBASE_INDEXER_OPTS="-Djava.security.auth.login.config=/home/user/hbase-jaas.conf
-XX:+UseConcMarkSweepGC"
```

Configuring Flume Morphline Solr Sink Usage

Repeat this process on all Flume hosts:

1. If you have not created a keytab file, do so now at `/etc/flume-ng/conf/flume.keytab`. This file should contain the service principal `flume/<fully.qualified.domain.name>@<YOUR-REALM>`. See the CDH 5 Security Guide for more information.
2. Create a JAAS configuration file for flume at `/etc/flume-ng/conf/jaas-client.conf`. The file should appear as follows:

```
Client {
 com.sun.security.auth.module.Krb5LoginModule required
 useKeyTab=true
 useTicketCache=false
 keyTab="/etc/flume-ng/conf/flume.keytab"
 principal="flume/<fully.qualified.domain.name>@<YOUR-REALM>";
};
```

3. Add the flume JAAS configuration to the `JAVA_OPTS` in `/etc/flume-ng/conf/flume-env.sh`. For example, you might change:

```
JAVA_OPTS="-Xmx500m"
```

to:

```
JAVA_OPTS="-Xmx500m
-Djava.security.auth.login.config=/etc/flume-ng/conf/jaas-client.conf"
```

Enabling Sentry Authorization for Search

Sentry enables role-based, fine-grained authorization for Cloudera Search. Sentry can apply a range of restrictions to various tasks, such accessing data or creating collections. These restrictions are consistently applied, regardless of the way users attempt to complete actions. For example, restricting access to data in a collection restricts that access whether queries come from the command line, from a browser, or through the admin console.

Follow the instructions below to configure Sentry under CDH 4.5 or later or CDH 5. Sentry is included in the Search installation.

> **Note:** Sentry for Search depends on Kerberos authentication. For additional information on using Kerberos with Search, see Configuring Search to Use Kerberos on page 89 and Using Kerberos on page 91.

Note that this document is for configuring Sentry for Cloudera Search. For information about alternate ways to configure Sentry or for information about installing Sentry for other services, see:

- Setting Up Search Authorization with Sentry for instructions for using Cloudera Manager 4 to install and configure Search Authorization with Sentry.
- Impala Security for instructions on using Impala with Sentry.
- Sentry Installation to install the version of Sentry that was provided with CDH 4.
- Sentry Installation to install the version of Sentry that was provided with CDH 5.

Roles and Collection-Level Privileges

Sentry uses a role-based privilege model. A role is a set of rules for accessing a given Solr collection. Access to each collection is governed by privileges: `Query`, `Update`, or `All (*)`.

For example, a rule for the `Query` privilege on collection `logs` would be formulated as follows:

```
collection=logs->action=Query
```

A role can contain multiple such rules, separated by commas. For example the `engineer_role` might contain the `Query` privilege for `hive_logs` and `hbase_logs` collections, and the `Update` privilege for the `current_bugs` collection. You would specify this as follows:

```
engineer_role = collection=hive_logs->action=Query, collection=hbase_logs->action=Query,
 collection=current_bugs->action=Update
```

Users and Groups

- Auseris an entity that is permitted by the Kerberos authentication system to access the Search service.
- Agroupconnects the authentication system with the authorization system. It is a set of one or more users who have been granted one or more authorization roles. Sentry allows a set of roles to be configured for a group.
- A configured group providerdetermines a user's affiliation with a group. The current release supports HDFS-backed groups and locally configured groups. For example,

```
dev_ops = dev_role, ops_role
```

Here the group dev_ops is granted the roles `dev_role` and `ops_role`. The members of this group can complete searches that are allowed by these roles.

User to Group Mapping

You can configure Sentry to use either Hadoop groups or groups defined in the policy file.

> **Important:** You can use either Hadoop groups or local groups, but not both at the same time. Use local groups if you want to do a quick proof-of-concept. For production, use Hadoop groups.

To configure Hadoop groups:

Set the `sentry.provider` property in `sentry-site.xml` to `org.apache.sentry.provider.file.HadoopGroupResourceAuthorizationProvider`.

> **Note:** Note that, by default, this uses local shell groups. See the Group Mapping section of the HDFS Permissions Guide for more information.

OR

To configure local groups:

1. Define local groups in a `[users]` section of the Sentry Configuration File on page 96, `sentry-site.xml`. For example:

```
[users]
user1 = group1, group2, group3
user2 = group2, group3
```

2. In `sentry-site.xml`, set `search.sentry.provider` as follows:

```
<property>
    <name>sentry.provider</name>

<value>org.apache.sentry.provider.file.LocalGroupResourceAuthorizationProvider</value>

  </property>
```

Setup and Configuration

This release of Sentry stores the configuration as well as privilege policies in files. The `sentry-site.xml` file contains configuration options such as privilege policy file location. The Policy File on page 95 contains the privileges and groups. It has a `.ini` file format and should be stored on HDFS.

Sentry is automatically installed when you install Cloudera Search for CDH or Cloudera Search 1.1.0 or later.

Policy File

The sections that follow contain notes on creating and maintaining the policy file.

- **Warning:** An invalid configuration disables all authorization while logging an exception.

Storing the Policy File

Considerations for storing the policy file(s) include:

1. Replication count - Because the file is read for each query, you should increase this; 10 is a reasonable value.
2. Updating the file - Updates to the file are only reflected when the Solr process is restarted.

Defining Roles

Keep in mind that role definitions are not cumulative; the newer definition replaces the older one. For example, the following results in `role1` having `privilege2`, not `privilege1` and `privilege2`.

```
role1 = privilege1
role1 = privilege2
```

Sample Configuration

This section provides a sample configuration.

- **Note:** Sentry with CDH Search does not support multiple policy files. Other implementations of Sentry such as Sentry for Hive do support different policy files for different databases, but Sentry for CDH Search has no such support for multiple policies.

Policy File

The following is an example of a CDH Search policy file. The `sentry-provider.ini` would exist in an HDFS location such as `hdfs://ha-nn-uri/user/solr/sentry/sentry-provider.ini`.

- **Note:** Use separate policy files for each Sentry-enabled service. Using one file for multiple services results in each service failing on the other services' entries. For example, with a combined Hive and Search file, Search would fail on Hive entries and Hive would fail on Search entries.

sentry-provider.ini

```
[groups]
# Assigns each Hadoop group to its set of roles
engineer = engineer_role
ops = ops_role
dev_ops = engineer_role, ops_role
hbase_admin = hbase_admin_role

[roles]
# The following grants all access to source_code.
# "collection = source_code" can also be used as syntactic
# sugar for "collection = source_code->action=*"
engineer_role = collection = source_code->action=*

# The following imply more restricted access.
ops_role = collection = hive_logs->action=Query
dev_ops_role = collection = hbase_logs->action=Query

#give hbase_admin_role the ability to create/delete/modify the hbase_logs collection
hbase_admin_role = collection=admin->action=*, collection=hbase_logs->action=*
```

Sentry Configuration File

The following is an example of a `sentry-site.xml` file.

sentry-site.xml

```
<configuration>
  <property>
    <name>hive.sentry.provider</name>

<value>org.apache.sentry.provider.file.HadoopGroupResourceAuthorizationProvider</value>

  </property>

  <property>
    <name>sentry.solr.provider.resource</name>
    <value>/path/to/authz-provider.ini</value>
    <!--
        If the HDFS configuration files (core-site.xml, hdfs-site.xml)
        pointed to by SOLR_HDFS_CONFIG in /etc/default/solr
        point to HDFS, the path will be in HDFS;
        alternatively you could specify a full path,
        e.g.:hdfs://namenode:port/path/to/authz-provider.ini
    -->
  </property>
```

Enabling Secure Impersonation

Secure Impersonation is a feature that allows a user to make requests as another user in a secure way. For example, to allow the following impersonations:

- User hue can make requests as any user from any host.
- User `foo` can make requests as any member of group `bar`, from `host1` or `host2`.

  Configure the following properties in `/etc/default/solr`:

  ```
  SOLR_SECURITY_ALLOWED_PROXYUSERS=hue,foo
  SOLR_SECURITY_PROXYUSER_hue_HOSTS=*
  SOLR_SECURITY_PROXYUSER_hue_GROUPS=*
  SOLR_SECURITY_PROXYUSER_foo_HOSTS=host1,host2
  SOLR_SECURITY_PROXYUSER_foo_GROUPS=bar
  ```

`SOLR_SECURITY_ALLOWED_PROXYUSERS` lists all of the users allowed to impersonate. For a user `x` in `SOLR_SECURITY_ALLOWED_PROXYUSERS`, `SOLR_SECURITY_PROXYUSER_x_HOSTS` list the hosts `x` is allowed to connect from in order to impersonate, and `SOLR_SECURITY_PROXYUSERS_x_GROUPS` lists the groups that the

users is allowed to impersonate members of. Both `GROUPS` and `HOSTS` support the wildcard * and both `GROUPS` and `HOSTS` must be defined for a specific user.

> **Note:** Cloudera Manager has its own management of secure impersonation for Hue. To add additional users for Secure Impersonation, use the environment variable safety value for Solr to set the environment variables as above. Be sure to include hue in `SOLR_SECURITY_ALLOWED_PROXYUSERS` if you want to use secure impersonation for hue.

Debugging Failed Sentry Authorization Requests

Sentry logs all facts that lead up to authorization decisions at the debug level. If you do not understand why Sentry is denying access, the best way to debug is to temporarily turn on debug logging:

- In Cloudera Manager, add `log4j.logger.org.apache.sentry=DEBUG` to the logging settings for your service through the corresponding **Logging Safety Valve** field for the Impala, Hive Server 2, or Solr Server services.
- On systems not managed by Cloudera Manager, add `log4j.logger.org.apache.sentry=DEBUG` to the `log4j.properties` file on each host in the cluster, in the appropriate configuration directory for each service.

Specifically, look for exceptions and messages such as:

```
FilePermission server..., RequestPermission server...., result [true|false]
```

which indicate each evaluation Sentry makes. The `FilePermission` is from the policy file, while `RequestPermission` is the privilege required for the query. A `RequestPermission` will iterate over all appropriate `FilePermission` settings until a match is found. If no matching privilege is found, Sentry returns `false` indicating "Access Denied" .

Appendix: Authorization Privilege Model for Search

The tables below refer to the request handlers defined in the generated `solrconfig.xml.secure`. If you are not using this configuration file, the below may not apply.

`admin` is a special collection in sentry used to represent administrative actions. A non-administrative request may only require privileges on the collection on which the request is being performed. This is called `collection1` in this appendix. An administrative request may require privileges on both the `admin` collection and `collection1`. This is denoted as `admincollection1` in the tables below.

Table 3: Privilege table for non-administrative request handlers

Request Handler	Required Privilege	Collections that Require Privilege
`select`	`QUERY`	`collection1`
`query`	`QUERY`	`collection1`
`get`	`QUERY`	`collection1`
`browse`	`QUERY`	`collection1`
`tvrh`	`QUERY`	`collection1`
`clustering`	`QUERY`	`collection1`
`terms`	`QUERY`	`collection1`
`elevate`	`QUERY`	`collection1`
`analysis/field`	`QUERY`	`collection1`
`analysis/document`	`QUERY`	`collection1`
`update`	`UPDATE`	`collection1`

Request Handler	Required Privilege	Collections that Require Privilege
update/json	UPDATE	collection1
update/csv	UPDATE	collection1

Table 4: Privilege table for collections admin actions

Collection Action	Required Privilege	Collections that Require Privilege
create	UPDATE	admin, collection1
delete	UPDATE	admin, collection1
reload	UPDATE	admin, collection1
createAlias	UPDATE	admin, collection1 **Note:** collection1 here refers to the name of the alias, not the underlying collection(s). For example, http://YOUR-HOST:8983/solr/admin/collections?action=CREATEALIAS&name=collection1&collections=underlyingCollection
deleteAlias	UPDATE	admin, collection1 **Note:** collection1 here refers to the name of the alias, not the underlying collection(s). For example, http://YOUR-HOST:8983/solr/admin/collections?action=DELETEALIAS&name=collection1
syncShard	UPDATE	admin, collection1
splitShard	UPDATE	admin, collection1
deleteShard	UPDATE	admin, collection1

Table 5: Privilege table for core admin actions

Collection Action	Required Privilege	Collections that Require Privilege
create	UPDATE	admin, collection1
rename	UPDATE	admin, collection1
load	UPDATE	admin, collection1
unload	UPDATE	admin, collection1
status	UPDATE	admin, collection1
persist	UPDATE	admin
reload	UPDATE	admin, collection1
swap	UPDATE	admin, collection1

Collection Action	Required Privilege	Collections that Require Privilege
mergeIndexes	UPDATE	admin, collection1
split	UPDATE	admin, collection1
prepRecover	UPDATE	admin, collection1
requestRecover	UPDATE	admin, collection1
requestSyncShard	UPDATE	admin, collection1
requestApplyUpdates	UPDATE	admin, collection1

Table 6: Privilege table for Info and AdminHandlers

Request Handler	Required Privilege	Collections that Require Privilege
LukeRequestHandler	QUERY	admin
SystemInfoHandler	QUERY	admin
SolrInfoMBeanHandler	QUERY	admin
PluginInfoHandler	QUERY	admin
ThreadDumpHandler	QUERY	admin
PropertiesRequestHandler	QUERY	admin
LogginHandler	QUERY, UPDATE (or *)	admin
ShowFileRequestHandler	QUERY	admin

Search High Availability

Mission critical, large-scale online production systems need to make progress without downtime despite some issues. Cloudera Search provides two routes to configurable, highly available, and fault-tolerant data ingestion:

- Near Real Time (NRT) ingestion using the Flume Solr Sink
- MapReduce based batch ingestion using the MapReduceIndexerTool

Production versus Test Mode

Some exceptions are generally transient, in which case the corresponding task can simply be retried. For example, network connection errors or timeouts are recoverable exceptions. Conversely, tasks associated with an unrecoverable exception cannot simply be retried. Corrupt or malformed parser input data, parser bugs, and errors related to unknown Solr schema fields produce unrecoverable exceptions.

Different modes determine how Cloudera Search responds to different types of exceptions.

- **Configuration parameter isProductionMode=false** (Non-production mode or test mode): Default configuration. Cloudera Search throws exceptions to quickly reveal failures, providing better debugging diagnostics to the user.
- **Configuration parameter isProductionMode=true** (Production mode): Cloudera Search logs and ignores unrecoverable exceptions, enabling mission-critical large-scale online production systems to make progress without downtime, despite some issues.

- **Note:** Categorizing exceptions as recoverable or unrecoverable addresses most cases, though it is possible that an unrecoverable exception could be accidentally misclassified as recoverable. Cloudera provides the `isIgnoringRecoverableExceptions` configuration parameter to address such a case. In a production environment, if an unrecoverable exception is discovered that is classified as recoverable, change `isIgnoringRecoverableExceptions` to `true`. Doing so allows systems to make progress and avoid retrying an event forever. This configuration flag should only be enabled if a misclassification bug has been identified. Please report such bugs to Cloudera.

If Cloudera Search throws an exception according the rules described above, the caller, meaning Flume Solr Sink and MapReduceIndexerTool, can catch the exception and retry the task if it meets the criteria for such retries.

Near Real Time Indexing with the Flume Solr Sink

The Flume Solr Sink uses the settings established by the `isProductionMode` and `isIgnoringRecoverableExceptions` parameters. If a SolrSink does nonetheless receive an exception, the SolrSink rolls the transaction back and pauses. This causes the Flume channel, which is essentially a queue, to redeliver the transaction's events to the SolrSink approximately five seconds later. This redelivering of the transaction event retries the ingest to Solr. This process of rolling back, backing off, and retrying continues until ingestion eventually succeeds.

Here is a corresponding example Flume configuration file `flume.conf`:

```
agent.sinks.solrSink.isProductionMode = true
agent.sinks.solrSink.isIgnoringRecoverableExceptions = true
```

In addition, Flume SolrSink automatically attempts to load balance and failover among the hosts of a SolrCloud before it considers the transaction rollback and retry. Load balancing and failover is done with the help of ZooKeeper, which itself can be configured to be highly available.

Further, Cloudera Manager can configure Flume so it automatically restarts if its process crashes.

To tolerate extended periods of Solr downtime, you can configure Flume to use a high-performance transactional persistent queue in the form of a FileChannel. A FileChannel can use any number of local disk drives to buffer significant amounts of data. For example, you might buffer many terabytes of events corresponding to a week of data. Further, using the optional replicating channels Flume feature, you can configure Flume to replicate the same data both into HDFS as well as into Solr. Doing so ensures that if the Flume SolrSink channel runs out of disk space, data delivery is still delivered to HDFS, and this data can later be ingested from HDFS into Solr using MapReduce.

Many machines with many Flume Solr Sinks and FileChannels can be used in a failover and load balancing configuration to improve high availability and scalability. Flume SolrSink servers can be either co-located with live Solr servers serving end user queries, or Flume SolrSink servers can be deployed on separate industry standard hardware for improved scalability and reliability. By spreading indexing load across a large number of Flume SolrSink servers you can improve scalability. Indexing load can be replicated across multiple Flume SolrSink servers for high availability, for example using Flume features such as Load balancing Sink Processor.

Batch Indexing with MapReduceIndexerTool

The Mappers and Reducers of the MapReduceIndexerTool follow the settings established by the `isProductionMode` and `isIgnoringRecoverableExceptions` parameters. However, if a Mapper or Reducer of the `MapReduceIndexerTool` does receive an exception, it does not retry at all. Instead it lets the MapReduce task fail and relies on the Hadoop Job Tracker to retry failed MapReduce task attempts several times according to standard Hadoop semantics. Cloudera Manager can configure the Hadoop Job Tracker to be highly available. On `MapReduceIndexerTool` startup, all data in the output directory is deleted if that output directory already exists. To retry an entire job that has failed, rerun the program using the same arguments.

For example:

```
hadoop ... MapReduceIndexerTool ... -D isProductionMode=true -D
isIgnoringRecoverableExceptions=true ...
```

Renaming Cloudera Manager Managed Hosts

Cloudera Search supports renaming hosts.

- **Note:** This will require a cluster-wide outage.

- **Note:** This procedure should not be used in environments running JobTracker high availability (HA). If you are running JobTracker HA, contact Cloudera customer support for further assistance.

Renaming hosts involves stopping services and agents, changing settings, and restarting services and agents. You must not restart services or agents before you are instructed to do so. Starting services or agents early may result in a nonfunctional system state.

This topic describes how to change some or all host names in your cluster. Begin by shutting down all services in the cluster.

Prerequisites

Before changing host names, back up the Cloudera Manager database using a tool such as `mysqldump`. For more information, see the MySQL Reference Manual. Store this backup in a safe location. If problems occur, this backup can be used to restore the original cluster state.

Stopping Cloudera Manager Services

Shut down all CDH and Cloudera Manager management services in the cluster.

1. For services that are managed as part of the cluster, click the down-arrow and choose **Stop**.
2. For any services that are still running, right-click each running service, and click **Stop**.
3. After you have stopped all services, shutdown Cloudera manager server.

   RHEL-compatible or SLES systems:

   ```
   $ sudo service cloudera-scm-server stop
   ```

   Debian/Ubuntu systems:

   ```
   $ sudo /usr/sbin/service cloudera-scm-server stop
   ```

4. Shutdown the Cloudera agents on the hosts whose names you are changing.

   RHEL-compatible or SLES systems:

   ```
   $ sudo service cloudera-scm-agent stop
   ```

   Debian/Ubuntu systems:

   ```
   $ sudo /usr/sbin/service cloudera-scm-agent stop
   ```

Editing the server_host Value

If you are renaming the host running Cloudera Manager, you must edit the `server_host` value in the `config.ini` file on all hosts that are managed by Cloudera Manager. In most cases, the `config.ini` file is found at `/etc/cloudera-scm-agent/`. The `config.ini` file may be found elsewhere if tarballs were used for installation. For example, if you were renaming the Cloudera Manager host to `newhostname.example.com`, you would modify the `server_host` value so it read as follows:

```
server_host=newhostname.example.com
```

Repeat this edit for all hosts that are managed by Cloudera Manager.

Updating Name Services

Update the names of the hosts using the name service method that applies for your operating system.

1. Edit the network or hostname file.

   For Red Hat-compatible systems, edit the `HOSTNAME` value in the `network` file to be the new hostname. For example, you might change `HOSTNAME` in `/etc/sysconfig/network` to:

   ```
   HOSTNAME=new.host.name.FQDN
   ```

   For Debian systems, edit the hostname entries in the `hostname` file to include new hostname. For example, you might delete the old hostname and add the new hostname to the `/etc/hostname` file so it reads:

   ```
   new.host.name.FQDN
   ```

   For SLES systems, edit the hostname entries in the `HOSTNAME` file to include new hostname. For example, you might delete the old hostname and add the new hostname to the `/etc/HOSTNAME` file so it reads:

   ```
   new.host.name.FQDN
   ```

2. Edit the `/etc/hosts` file. Replace all instances of the old hostname with the new hostname.

Updating the Cloudera Manager Database

Modify the Cloudera Manager database to reflect the new names. The commands vary depending on the type of database you are using. For example, for MySQL, using the following process:

1. Log into mysql as root and use the Cloudera Manager database. For example, for a database named `cm`, you might use the following command

   ```
   # mysql -h localhost -u scm -p
   use cm;

   mysql> select HOST_ID, HOST_IDENTIFIER, NAME from HOSTS;
   ```

   Note the `HOST_ID` value for each of the hosts you are modifying. This will be `$ROW_ID` in the subsequent commands.

2. For the hosts you're changing use a command of the form:

   ```
   mysql> update HOSTS set HOST_IDENTIFIER = 'new.host.name.FQDN' where HOST_ID =
   $ROW_ID;
   ```

   For example, a full transcript of user input from such a process might be:

   ```
    # mysql -u root -p
   password>

   mysql> show databases;
   ```

```
mysql> use cm;
mysql> select HOST_ID, HOST_IDENTIFIER, NAME from HOSTS;
mysql> update HOSTS set HOST_IDENTIFIER = 'new.host.name.FQDN' where HOST_ID = 2;
```

Starting Cloudera Manager Services

Restart the Cloudera Manager server and agents using commands of the form:

1. Start Cloudera agent on the hosts whose names you changed.

   RHEL-compatible or SLES systems:

   ```
   $ sudo service cloudera-scm-agent start
   ```

   Debian/Ubuntu systems:

   ```
   $ sudo /usr/sbin/service cloudera-scm-agent start
   ```

2. Start the Cloudera Manager Server.

   RHEL-compatible or SLES systems:

   ```
   $ sudo service cloudera-scm-server start
   ```

   Debian/Ubuntu systems:

   ```
   $ sudo /usr/sbin/service cloudera-scm-server start
   ```

Updating for NameNode High Availability Automatic Failover

If NameNode high availability automatic failover is enabled, you must update the ZooKeeper Failover Controller (ZKFC) to reflect the name changes. If you are not using NameNode high availability, skip to the next section.

> **Note:** As stated earlier, this procedure should not be used in environments running JobTracker High Availability (HA). If you have already completed the preceding steps in an environment with JobTracker HA enabled, the subsequent steps should not be completed in your environment. Contact support now.

To update the ZKFC host:

1. Start the ZooKeeper services using the Cloudera Manager Admin Console.

   > **Note:** Do not start any other services. It is especially important that you not start HDFS.

2. Log into one of the hosts that is hosting the ZooKeeper server role.
3. Delete the nameservice znode. For a package based installation, delete the `zkCli.sh` file using a command similar to:

   ```
   $ rm -f /usr/lib/zookeeper/bin/zkCli.sh
   ```

   For a parcel-based installation, delete the `zkCli.sh` file using a command similar to:

   ```
   $ rm -f /opt/cloudera/parcels/CDH/lib/zookeeper/bin/zkCli.sh
   ```

4. Verify that the HA znode exists by checking for the `hadoop-ha`. For example:

   ```
   zkCli$ ls /hadoop-ha
   ```

If the HA znode does not exist, use the Cloudera Manager Admin Console to select the HDFS service and then choose **Initialize High Availability State in ZooKeeper**.

5. Delete the old znode. For example use a command similar to:

```
zkCli$ rm -rf /hadoop-ha/nameservice1
```

6. Use the Cloudera Manager Admin Console to initialize HA in ZooKeeper by clicking **HDFS** > **Instances** > **Action** > **Initialize High Availability State in Zookeeper...**.

Updating Cloudera Management Service Host Information

If you have changed the names of hosts hosting management services, you must update the management service with the new host name. Management services include Host Monitor, Service Monitor, Reports Manager, Activity Monitor, and Navigator. You must do this for each service that is hosted on a host whose name has changed.

To update management service host name configuration

1. In the Cloudera Manager Admin Console, click the service and click **Configuration**.
2. Edit the **Database Hostname** value so it reflects the new hostname.

Returning the System to a Running State

Now that you have renamed hosts and updated settings to reflect these new names, redeploy client configuration files.

- For Cloudera Manager 4, see Redeploying the Client Configuration Files Manually in Deploying Client Configuration Files.
- For Cloudera Manager 5, see Manually RedeployingClient Configuration Files in Client Configuration Files.

Start any services that were previously stopped.

Tuning the Solr Server

Solr performance tuning is a complex task. The following sections provide more details.

Tuning to Complete During Setup

Some tuning is best completed during the setup of you system or may require some re-indexing.

Configuring Lucene Version Requirements

You can configure Solr to use a specific version of Lucene. This can help ensure that the Lucene version that Search uses includes the latest features and bug fixes. At the time that a version of Solr ships, Solr is typically configured to use the appropriate Lucene version, in which case there is no need to change this setting. If a subsequent Lucene update occurs, you can configure the Lucene version requirements by directly editing the `luceneMatchVersion` element in the `solrconfig.xml` file. Versions are typically of the form `x.y`, such as `4.4`. For example, to specify version 4.4, you would ensure the following setting exists in `solrconfig.xml`:

```
<luceneMatchVersion>4.4</luceneMatchVersion>
```

Designing the Schema

When constructing a schema, use data types that most accurately describe the data that the fields will contain. For example:

- Use the `tdate` type for dates. Do this instead of representing dates as strings.

- Consider using the `text` type that applies to your language, instead of using `String`. For example, you might use `text_en`. `Text` types support returning results for subsets of an entry. For example, querying on "john" would find "John Smith", whereas with the string type, only exact matches are returned.
- For IDs, use the string type.

General Tuning

The following tuning categories can be completed at any time. It is less important to implement these changes before beginning to use your system.

General Tips

- Enabling multi-threaded faceting can provide better performance for field faceting. When multi-threaded faceting is enabled, field faceting tasks are completed in a parallel with a thread working on every field faceting task simultaneously. Performance improvements do not occur in all cases, but improvements are likely when all of the following are true:
  - The system uses highly concurrent hardware.
  - Faceting operations apply to large data sets over multiple fields.
  - There is not an unusually high number of queries occurring simultaneously on the system. Systems that are lightly loaded or that are mainly engaged with ingestion and indexing may be helped by multi-threaded faceting; for example, a system ingesting articles and being queried by a researcher. Systems heavily loaded by user queries are less likely to be helped by multi-threaded faceting; for example, an e-commerce site with heavy user-traffic.

  - **Note:** Multi-threaded faceting only applies to field faceting and not to query faceting.
    - Field faceting identifies the number of unique entries for a field. For example, multi-threaded faceting could be used to simultaneously facet for the number of unique entries for the fields, "color" and "size". In such a case, there would be two threads, and each thread would work on faceting one of the two fields.
    - Query faceting identifies the number of unique entries that match a query for a field. For example, query faceting could be used to find the number of unique entries in the "size" field are between 1 and 5. Multi-threaded faceting does not apply to these operations.

  To enable multi-threaded faceting, add `facet-threads` to queries. For example, to use up to 1000 threads, you might use a query as follows:

  ```
  http://localhost:8983/solr/collection1/select?q=*:*&facet=true&fl=id&facet.field=f0_ws&facet.threads=1000
  ```

  If `facet-threads` is omitted or set to 0, faceting is single-threaded. If `facet-threads` is set to a negative value, such as -1, multi-threaded faceting will use as many threads as there are fields to facet up to the maximum number of threads possible on the system.

- If your environment does not require Near Real Time (NRT), turn off soft auto-commit in `solrconfig.xml`.
- In most cases, do not change the default batch size setting of 1000. If you are working with especially large documents, you may consider decreasing the batch size.
- To help identify any garbage collector (GC) issues, enable GC logging in production. The overhead is low and the JVM supports GC log rolling as of 1.6.0_34.
  - The minimum recommended GC logging flags are: `-XX:+PrintGCTimeStamps -XX:+PrintGCDateStamps -XX:+PrintGCDetails`.
  - To rotate the GC logs: `-Xloggc: -XX:+UseGCLogFileRotation -XX:NumberOfGCLogFiles= -XX:GCLogFileSize=`.

Solr and HDFS - the Block Cache

Cloudera Search enables Solr to store indexes in an HDFS filesystem. To maintain performance, an HDFS block cache has been implemented using Least Recently Used (LRU) semantics. This enables Solr to cache HDFS index files on read and write, storing the portions of the file in JVM "direct memory" (meaning off heap) by default or optionally in the JVM heap. Direct memory is preferred as it is not affected by garbage collection.

Batch jobs typically do not make use of the cache, while Solr servers (when serving queries or indexing documents) should. When running indexing using MapReduce, the MR jobs themselves do not make use of the block cache. Block caching is turned off by default and should be left disabled.

Tuning of this cache is complex and best practices are continually being refined. In general, allocate a cache that is about 10-20% of the amount of memory available on the system. For example, when running HDFS and Solr on a host with 50 GB of memory, typically allocate 5-10 GB of memory using `solr.hdfs.blockcache.slab.count`. As index sizes grow you may need to tune this parameter to maintain optimal performance.

- **Note:** Block cache metrics are currently unavailable.

Configuration

The following parameters control caching. They can be configured at the Solr process level by setting the respective system property or by editing the `solrconfig.xml` directly.

Parameter	Default	Description
`solr.hdfs.blockcache.enabled`	true	Enable the block cache.
`solr.hdfs.blockcache.read.enabled`	true	Enable the read cache.
`solr.hdfs.blockcache.write.enabled`	false	Enable the write cache.
`solr.hdfs.blockcache.direct.memory.allocation`	true	Enable direct memory allocation. If this is false, heap is used.
`solr.hdfs.blockcache.slab.count`	1	Number of memory slabs to allocate. Each slab is 128 MB in size.
`solr.hdfs.blockcache.global`	true	If enabled, a single HDFS block cache is used for all SolrCores on a host. If `blockcache.global` is disabled, each SolrCore on a host creates its own private HDFS block cache. Enabling this parameter simplifies managing HDFS block cache memory.

- **Note:**

  Increasing the direct memory cache size may make it necessary to increase the maximum direct memory size allowed by the JVM. Add the following to `/etc/default/solr` to do so. You must also replace *MAXMEM* with a reasonable upper limit. A typical default JVM value for this is 64 MB. When using *MAXMEM*, you must specify a unit such as `g` for gigabytes or `m` for megabytes. If *MAXMEM* were set to 2, the following command would set *MaxDirectMemorySize* to 2 GB:

  ```
  CATALINA_OPTS="-XX:MaxDirectMemorySize=MAXMEMg -XX:+UseLargePages"
  ```

  Restart Solr servers after editing this parameter.

Solr HDFS optimizes caching when performing NRT indexing using Lucene's `NRTCachingDirectory`.

Lucene caches a newly created segment if both of the following conditions are true:

- The segment is the result of a flush or a merge and the estimated size of the merged segment is <= `solr.hdfs.nrtcachingdirectory.maxmergesizemb`.
- The total cached bytes is <= `solr.hdfs.nrtcachingdirectory.maxcachedmb`.

The following parameters control NRT caching behavior:

Parameter	Default	Description
`solr.hdfs.nrtcachingdirectory.enable`	true	Whether to enable the NRTCachingDirectory.
`solr.hdfs.nrtcachingdirectory.maxcachedmb`	192	Size of the cache in megabytes.
`solr.hdfs.nrtcachingdirectory.maxmergesizemb`	16	Maximum segment size to cache.

Here is an example of `solrconfig.xml` with defaults:

```
 <directoryFactory name="DirectoryFactory">
   <bool name="solr.hdfs.blockcache.enabled">${solr.hdfs.blockcache.enabled:true}</bool>

    <int
name="solr.hdfs.blockcache.slab.count">${solr.hdfs.blockcache.slab.count:1}</int>
    <bool
name="solr.hdfs.blockcache.direct.memory.allocation">${solr.hdfs.blockcache.direct.memory.allocation:true}</bool>

    <int
name="solr.hdfs.blockcache.blocksperbank">${solr.hdfs.blockcache.blocksperbank:16384}</int>

    <bool
name="solr.hdfs.blockcache.read.enabled">${solr.hdfs.blockcache.read.enabled:true}</bool>

    <bool
name="solr.hdfs.blockcache.write.enabled">${solr.hdfs.blockcache.write.enabled:true}</bool>

    <bool
name="solr.hdfs.nrtcachingdirectory.enable">${solr.hdfs.nrtcachingdirectory.enable:true}</bool>

    <int
name="solr.hdfs.nrtcachingdirectory.maxmergesizemb">${solr.hdfs.nrtcachingdirectory.maxmergesizemb:16}</int>

    <int
name="solr.hdfs.nrtcachingdirectory.maxcachedmb">${solr.hdfs.nrtcachingdirectory.maxcachedmb:192}</int>
</directoryFactory>
```

The following example illustrates passing Java options by editing the `/etc/default/solr` configuration file:

```
CATALINA_OPTS="-Xmx10g -XX:MaxDirectMemorySize=20g -XX:+UseLargePages
-Dsolr.hdfs.blockcache.slab.count=100"
```

For better performance, Cloudera recommends setting the Linux swap space on all Solr server hosts to 10 or less as shown below:

```
# set swappiness
sudo sysctl vm.swappiness=10
sudo bash -c 'echo "vm.swappiness=10">> /etc/sysctl.conf'
# disable swap space until next reboot:
sudo /sbin/swapoff -a
```

Cloudera previously recommended a setting of 0, but in recent kernels (such as those included with RedHat 6.4 and higher, and Ubuntu 12.04 LTS and higher) a setting of 0 might lead to out of memory issues per this blog post: http://www.percona.com/blog/2014/04/28/oom-relation-vm-swappiness0-new-kernel/.

Threads

Configure the Tomcat server to have more threads per Solr instance. Note that this is only effective if your hardware is sufficiently powerful to accommodate the increased threads. 10,000 threads is a reasonable number to try in many cases.

To change the maximum number of threads, add a `maxThreads` element to the Connector definition in the Tomcat server's `server.xml` configuration file. For example, if you installed Search for CDH 5 using parcels installation, you would modify the Connector definition in the `<parcel path>/CDH/etc/solr/tomcat-conf.dist/conf/server.xml` file so this:

```
    <Connector port="${solr.port}" protocol="HTTP/1.1"
               connectionTimeout="20000"
               redirectPort="8443" />
```

Becomes this:

```
    <Connector port="${solr.port}" protocol="HTTP/1.1"
               maxThreads="10000"
               connectionTimeout="20000"
               redirectPort="8443" />
```

Garbage Collection

Choose different garbage collection options for best performance in different environments. Some garbage collection options typically chosen include:

- **Concurrent low pause collector**: Use this collector in most cases. This collector attempts to minimize "Stop the World" events. Avoiding these events can reduce connection timeouts, such as with ZooKeeper, and may improve user experience. This collector is enabled using `-XX:+UseConcMarkSweepGC`.
- **Throughput collector**: Consider this collector if raw throughput is more important than user experience. This collector typically uses more "Stop the World" events so this may negatively affect user experience and connection timeouts. This collector is enabled using `-XX:+UseParallelGC`.

You can also affect garbage collection behavior by increasing the Eden space to accommodate new objects. With additional Eden space, garbage collection does not need to run as frequently on new objects.

Replicas

If you have sufficient additional hardware, add more replicas for a linear boost of query throughput. Note that adding replicas may slow write performance on the first replica, but otherwise this should have minimal negative consequences.

Shards

In some cases, oversharding can help improve performance including intake speed. If your environment includes massively parallel hardware and you want to use these available resources, consider oversharding. You might increase the number of replicas per host from 1 to 2 or 3. Making such changes creates complex interactions, so you should continue to monitor your system's performance to ensure that the benefits of oversharding do not outweigh the costs.

Commits

Changing commit values may improve performance in some situation. These changes result in tradeoffs and may not be beneficial in all cases.

- For hard commit values, the default value of 60000 (60 seconds) is typically effective, though changing this value to 120 seconds may improve performance in some cases. Note that setting this value to higher values, such as 600 seconds may result in undesirable performance tradeoffs.
- Consider increasing the auto-commit value from 15000 (15 seconds) to 120000 (120 seconds).

- Enable soft commits and set the value to the largest value that meets your requirements. The default value of 1000 (1 second) is too aggressive for some environments.

Other Resources

- General information on Solr caching is available on the SolrCaching page on the Solr Wiki.
- Information on issues that influence performance is available on the SolrPerformanceFactors page on the Solr Wiki.
- Resource Management describes how to use Cloudera Manager to manage resources, for example with Linux cgroups.
- For information on improving querying performance, see ImproveSearchingSpeed.
- For information on improving indexing performance, see ImproveIndexingSpeed.

Troubleshooting Cloudera Search

After installing and deploying Cloudera Search, use the information in this section to troubleshoot problems.

Troubleshooting

The following table contains some common troubleshooting techniques.

Note: In the URLs in the following table, you must replace entries such as `<server:port>` with values from your environment. The port defaults value is 8983, but see `/etc/default/solr` for the port if you are in doubt.

Symptom	Explanation	Recommendation
All	Varied	Examine Solr log. By default, the log can be found at `/var/log/solr/solr.out`.
No documents found	Server may not be running	Browse to http://*server:port*/solr to see if the server responds. Check that cores are present. Check the contents of cores to ensure that numDocs is more than 0.
No documents found	Core may not have documents	Browsing `http://server:port/solr/[collection name]/select?q=*:*&wt=json&indent=true` should show `numFound`, which is near the top, to be more than 0.
The secure Solr Server fails to respond to Solrj requests, but other clients such as curl can communicate successfully	This may be a version compatibility issue. `Httpclient` 4.2.3, which ships with solrj in Search 1.x, has a dependency on `commons-codec` 1.7. If an earlier version of `commons-codec` is on the classpath, `httpclient` may be unable to communicate using Kerberos.	Ensure your application is using `commons-codec` 1.7 or later. Alternatively, use `httpclient` 4.2.5 instead of version 4.2.3 in your application. Version 4.2.3 behaves correctly with earlier versions of `commons-codec`.

Dynamic Solr Analysis

Any JMX-aware application can query Solr for information and display results dynamically. For example, Zabbix, Nagios, and many others have been used successfully. When completing Static Solr Log Analysis, many of the items related to extracting data from the log files can be seen from querying Solr, at least the last value (as opposed to the history which is available from the log file). These are often useful for status boards. In general,

anything available from the Solr admin page can be requested on a live basis from Solr. Some possibilities include:

- `numDocs/maxDoc` per core. This can be important since the difference between these numbers indicates the number of deleted documents in the index. Deleted documents take up disk space and memory. If these numbers vary greatly, this may be a rare case where optimizing is advisable.
- Cache statistics, including:
  - Hit ratios
  - Autowarm times
  - Evictions
- Almost anything available on the admin page. Note that drilling down into the "schema browser" can be expensive.

Other Troubleshooting Information

Since the use cases for Solr and search vary, there is no single solution for all cases. That said, here are some common challenges that many Search users have encountered:

- Testing with unrealistic data sets. For example, a users may test a prototype that uses faceting, grouping, sorting, and complex schemas against a small data set. When this same system is used to load of real data, performance issues occur. Using realistic data and use-cases is essential to getting accurate results.
- If the scenario seems to be that the system is slow to ingest data, consider:
  - Upstream speed. If you have a SolrJ program pumping data to your cluster and ingesting documents at a rate of 100 docs/second, the gating factor may be upstream speed. To test for limitations due to upstream speed, comment out only the code that sends the data to the server (for example, `SolrHttpServer.add(doclist)`) and time the program. If you see a throughput bump of less than around 10%, this may indicate that your system is spending most or all of the time getting the data from the system-of-record.
  - This may require pre-processing.
  - Indexing with a single thread from the client. `ConcurrentUpdateSolrServer` can use multiple threads to avoid I/O waits.
  - Too-frequent commits. This was historically an attempt to get NRT processing, but with SolrCloud hard commits this should be quite rare.
  - The complexity of the analysis chain. Note that this is rarely the core issue. A simple test is to change the schema definitions to use trivial analysis chains and then measure performance.
  - When the simple approaches fail to identify an issue, consider using profilers.

SolrCloud and ZooKeeper

SolrCloud is relatively new and relies on ZooKeeper to hold state information. There are not yet best practices related to SolrCloud. Monitoring ZooKeeper is valuable in this case and is available through Cloudera Manager.

Static Solr Log Analysis

To do a static analysis, inspect the log files, schema files, and the actual index for issues. If possible, connect to the live Solr instance while simultaneously examining log files so you can compare the schema with the index. The schema and the index can be out of sync in situations where the schema is changed, but the index was never rebuilt. Some hints are:

- A high number or proportion of 0-match queries. This indicates that the user-facing part of the application is making it easy for users to enter queries for which there are no matches. In Cloudera Search, given the size of the data, this should be an extremely rare event.
- Queries that match an excessive number of documents. All documents that match a query have to be scored, and the cost of scoring a query goes up as the number of hits increases. Examine any frequent queries that

match millions of documents. An exception to this case is “constant score queries”. Queries, such as those of the form ":" bypass the scoring process entirely.

- Overly complex queries. Defining what constitutes overly complex queries is difficult to do, but a very general rule is that queries over 1024 characters in length are likely to be overly complex.
- High autowarm times. Autowarming is the process of filling caches. Some queries are executed before a new searcher serves the first live user request. This keeps the first few users from having to wait. Autowarming can take many seconds or can be instantaneous. Excessive autowarm times often indicate excessively generous autowarm parameters. Excessive autowarming usually has limited benefit, with longer runs effectively being wasted work.
  - Cache autowarm. Each Solr cache has an autowarm parameter. You can usually set this value to an upper limit of 128 and tune from there.
  - `FirstSearcher/NewSearcher`. The `solrconfig.xml` file contains queries that can be fired when a new searcher is opened (the index is updated) and when the server is first started. Particularly for `firstSearcher`, it can be valuable to have a query that sorts relevant fields.

    > **Note:** The aforementioned flags are available from `solrconfig.xml`

- Exceptions. The Solr log file contains a record of all exceptions thrown. Some exceptions, such as exceptions resulting from invalid query syntax are benign, but others, such as Out Of Memory, require attention.
- Excessively large caches. The size of caches such as the filter cache are bounded by maxDoc/8. Having, for instance, a filterCache with 10,000 entries is likely to result in Out Of Memory errors. Large caches occurring in cases where there are many documents to index is normal and expected.
- Caches with low hit ratios, particularly filterCache. Each cache takes up some space, consuming resources. There are several caches, each with its own hit rate.
  - `filterCache`. This cache should have a relatively high hit ratio, typically around 80%.
  - `queryResultCache`. This is primarily used for paging so it can have a very low hit ratio. Each entry is quite small as it is basically composed of the raw query as a string for a key and perhaps 20-40 `ints`. While useful, unless users are experiencing paging, this requires relatively little attention.
  - `documentCache`. This cache is a bit tricky. It’s used to cache the document data (stored fields) so various components in a request handler don’t have to re-read the data from the disk. It’s an open question how useful it is when using `MMapDirectory` to access the index.
- Very deep paging. It is uncommon for user to go beyond the first page and very rare to go through 100 pages of results. A `&start=<pick your number>` query indicates unusual usage that should be identified. Deep paging may indicate some agent is completing scraping.

  > **Note:** Solr is not built to return full result sets no matter how deep. If returning the full result set is required, explore alternatives to paging through the entire result set.

- Range queries should work on `trie` fields. `Trie` fields (numeric types) store extra information in the index to aid in range queries. If range queries are used, it’s almost always a good idea to be using `trie` fields.
- `fq` clauses that use bare NOW. `fq` clauses are kept in a cache. The cache is a map from the `fq` clause to the documents in your collection that satisfy that clause. Using bare NOW clauses virtually guarantees that the entry in the filter cache is not be re-used.
- Multiple simultaneous searchers warming. This is an indication that there are excessively frequent commits or that autowarming is taking too long. This usually indicates a misunderstanding of when you should issue commits, often to simulate Near Real Time (NRT) processing or an indexing client is improperly completing commits. With NRT, commits should be quite rare, and having more than one simultaneous autowarm should not happen.
- Stored fields that are never returned (`fl=` clauses). Examining the queries for `fl=` and correlating that with the schema can tell if stored fields that are not used are specified. This mostly wastes disk space. And `fl=*` can make this ambiguous. Nevertheless, it’s worth examining.

- Indexed fields that are never searched. This is the opposite of the case where stored fields are never returned. This is more important in that this has real RAM consequences. Examine the request handlers for "edismax" style parsers to be certain that indexed fields are not used.
- Queried but not analyzed fields. It's rare for a field to be queried but not analyzed in any way. Usually this is only valuable for "string" type fields which are suitable for machine-entered data, such as part numbers chosen from a pick-list. Data that is not analyzed should not be used for anything that humans enter.
- String fields. String fields are completely unanalyzed. Unfortunately, some people confuse `string` with Java's `String` type and use them for text that should be tokenized. The general expectation is that string fields should be used sparingly. More than just a few string fields indicates a design flaw.
- Whenever the schema is changed, re-index the entire data set. Solr uses the schema to set expectations about the index. When schemas are changed, there's no attempt to retrofit the changes to documents that are currently indexed, but any new documents are indexed with the new schema definition. So old and new documents can have the same field stored in vastly different formats (for example, `String` and `TrieDate`) making your index inconsistent. This can be detected by examining the raw index.
- Query stats can be extracted from the logs. Statistics can be monitored on live systems, but it is more common to have log files. Here are some of the statistics you can gather:
  - Longest running queries
  - 0-length queries
  - average/mean/min/max query times
  - You can get a sense of the effects of commits on the subsequent queries over some interval (time or number of queries) to see if commits are the cause of intermittent slowdowns
- Too-frequent commits have historically been the cause of unsatisfactory performance. This is not so important with NRT processing, but it is valuable to consider.
- Optimizing an index, which could improve search performance before, is much less necessary now. Anecdotal evidence indicates optimizing may help in some cases, but the general recommendation is to use `expungeDeletes`, instead of committing.
  - Modern Lucene code does what `optimize` used to do to remove deleted data from the index when segments are merged. Think of this process as a background optimize. Note that merge policies based on segment size can make this characterization inaccurate.
  - It still may make sense to optimize a read-only index.
  - `Optimize` is now renamed `forceMerge`.

Cloudera Search Glossary

commit

An operation that forces documents to be made searchable.

- **hard** - A commit that starts the autowarm process, closes old searchers and opens new ones. It may also trigger replication.
- **soft** - New functionality with NRT and SolrCloud that makes documents searchable without requiring the work of hard commits.

embedded Solr

The ability to execute Solr commands without having a separate servlet container. Generally, use of embedded Solr is discouraged because it is often used due to the mistaken belief that HTTP is inherently too expensive to go fast. With Cloudera Search, and especially if the idea of some kind of MapReduce process is adopted, embedded Solr is probably advisable.

faceting

"Counting buckets" for a query. For example, suppose the search is for the term "shoes". You might want to return a result that there were various different quantities, such as "X brown, Y red and Z blue shoes" that matched the rest of the query.

filter query (fq)

A clause that limits returned results. For instance, "fq=sex:male" limits results to males. Filter queries are cached and reused.

Near Real Time (NRT)

The ability to search documents very soon after they are added to Solr. With SolrCloud, this is largely automatic and measured in seconds.

replica

In SolrCloud, a complete copy of a shard. Each replica is identical, so only one replica has to be queried (per shard) for searches.

sharding

Splitting a single logical index up into some number of sub-indexes, each of which can be hosted on a separate machine. Solr (and especially SolrCloud) handles querying each shard and assembling the response into a single, coherent list.

SolrCloud

ZooKeeper-enabled, fault-tolerant, distributed Solr. This is new in Solr 4.0.

SolrJ

A Java API for interacting with a Solr instance.

Cloudera Search Frequently Asked Questions

General

The following are general questions about Cloudera Search and the answers to those questions.

What is Cloudera Search?

Cloudera Search is Apache Solr integrated with CDH, including Apache Lucene, Apache SolrCloud, Apache Flume, Apache Tika, and Apache Hadoop MapReduce and HDFS. Cloudera Search also includes valuable integrations that make searching more scalable, easy to use, and optimized for both near-real-time and batch-oriented indexing. These integrations include Cloudera Morphlines, a customizable transformation chain that simplifies loading any type of data into Cloudera Search.

What is the difference between Lucene and Solr?

Lucene is a low-level search library that is accessed by a Java API. Solr is a search server that runs in a servlet container and provides structure and convenience around the underlying Lucene library.

What is Apache Tika?

The Apache Tika toolkit detects and extracts metadata and structured text content from various documents using existing parser libraries. Using the `solrCell` morphline command, the output from Apache Tika can be mapped to a Solr schema and indexed.

How does Cloudera Search relate to web search?

Traditional web search engines crawl web pages on the Internet for content to index. Cloudera Search indexes files and data that are stored in HDFS and HBase. To make web data available through Cloudera Search, it needs to be downloaded and stored in Cloudera's Distribution, including Apache Hadoop (CDH).

How does Cloudera Search relate to enterprise search?

Enterprise search connects with different backends (such as RDBMS and filesystems) and indexes data in all those systems. Cloudera Search is intended as a full-text search capability for data in CDH. Cloudera Search is a tool added to Cloudera's data processing platform and does not aim to be a stand-alone search solution, but rather a user-friendly interface to explore data in Hadoop and HBase.

How does Cloudera Search relate to custom search applications?

Custom and specialized search applications are an excellent complement to Cloudera's data-processing platform. Cloudera Search is not designed to be a custom application for niche vertical markets. However, Cloudera Search does include a simple search GUI through a plug-in application for Hue. It is based on the Solr API and allows for easy exploration, along with all of the other Hadoop frontend applications in Hue.

Do Search security features use Kerberos?

Yes, Cloudera Search includes support for Kerberos authentication. Search continues to use simple authentication with the anonymous user as the default configuration, but Search now supports changing the authentication scheme to Kerberos. All required packages are installed during the installation or upgrade process. Additional configuration is required before Kerberos is available in your environment.

Do I need to configure Sentry restrictions for each access mode, such as for the admin console and for the command line?

Sentry restrictions are consistently applied regardless of the way users attempt to complete actions. For example, restricting access to data in a collection consistently restricts that access, whether queries come from the command line, from a browser, or through the admin console.

Does Search support indexing data stored in JSON files and objects?

Yes, you can use the `readJson` and `extractJsonPaths` morphline commands that are included with the CDK to access JSON data and files. For more information, see cdk-morphlines-json.

How can I set up Cloudera Search so that results include links back to the source that contains the result?

You can use stored results fields to create links back to source documents. For information on data types, including the option to set results fields as stored, see the Solr Wiki page on SchemaXml.

For example, with `MapReduceIndexerTool` you can take advantage of fields such as `file_path`. See MapReduceIndexerTool Metadata on page 60 for more information. The output from the MapReduceIndexerTool includes file path information that can be used to construct links to source documents.

If you use the Hue UI, you can link to data in HDFS by inserting links of the form:

```
<a href="/filebrowser/download/{{file_path}}?disposition=inline">Download</a>
```

Performance and Fail Over

The following are questions about performance and fail over in Cloudera Search and the answers to those questions.

How large of an index does Cloudera Search support per search server?

There are too many variables to provide a single answer to this question. Typically, a server can host from 10 to 300 million documents, with the underlying index as large as hundreds of gigabytes. To determine a reasonable maximum document quantity and index size for servers in your deployment, prototype with realistic data and queries.

What is the response time latency I can expect?

Many factors affect how quickly responses are returned. Some factors that contribute to latency include whether the system is also completing indexing, the type of fields you are searching, whether the search results require aggregation, and whether there are sufficient resources for your search services.

With appropriately-sized hardware, if the query results are found in memory, they may be returned within milliseconds. Conversely, complex queries requiring results aggregation over huge indexes may take a few seconds.

The time between when Search begins to work on indexing new data and when that data can be queried can be as short as a few seconds, depending on your configuration.

This high performance is supported by custom caching optimizations that Cloudera has added to the Solr/HDFS integration. These optimizations allow for rapid read and writes of files in HDFS, performing at or above the speeds of stand-alone Solr reading and writing from local disk.

What happens when a write to the Lucene indexer fails?

Cloudera Search provides two configurable, highly available, and fault-tolerant data ingestion schemes: near real-time ingestion using the Flume Solr Sink and MapReduce-based batch ingestion using the MapReduceIndexerTool. These approaches are discussed in more detail in Search High Availability on page 99.

What hardware or configuration changes can I make to improve Search performance?

Search performance can be constrained by CPU limits. If you're seeing bottlenecks, consider allocating more CPU to Search.

Schema Management

The following are questions about schema management in Cloudera Search and the answers to those questions.

If my schema changes, will I need to re-index all of my data and files?

When you change the schema, Cloudera recommends re-indexing. For example, if you add a new field to the index, apply the new field to all index entries through re-indexing. Re-indexing is required in such a case because existing documents do yet not have the field. Cloudera Search includes a MapReduce batch-indexing solution for re-indexing and a GoLive feature that assures updated indexes are dynamically served.

Note that, you should typically re-index after adding a new field, this is not necessary if the new field applies only to new documents or data. This is because, were indexing to be completed, existing documents would still have no data for the field, making the effort unnecessary.

For schema changes that only apply to queries, re-indexing is not necessary.

Can I extract fields based on regular expressions or rules?

Cloudera Search supports limited regular expressions in Search queries. For details, see Lucene Regular Expressions.

On data ingestion, Cloudera Search supports easy and powerful extraction of fields based on regular expressions. For example the `grok` morphline command supports field extraction using regular expressions.

Cloudera Search also includes support for rule directed ETL with an extensible rule engine, in the form of the `tryRules` morphline command.

Can I use nested schemas?

Cloudera Search does not support nesting documents in this release. Cloudera Search assumes documents in the Cloudera Search repository have a flat structure.

What is Apache Avro and how can I use an Avro schema for more flexible schema evolution?

To learn more about Avro and Avro schemas, see the Avro Overview page and the Avro Specification page.

To see examples of how to implement inheritance, backwards compatibility, and polymorphism with Avro, see this InfoQ article.

Supportability

The following are questions about supportability in Cloudera Search and the answers to those questions.

Does Cloudera Search support multiple languages?

Cloudera Search supports approximately 30 languages, including most Western European languages, as well as Chinese, Japanese, and Korean.

Which file formats does Cloudera Search support for indexing? Does it support searching images?

Cloudera Search uses the Apache Tika library for indexing many standard document formats. In addition, Cloudera Search supports indexing and searching Avro files and a wide variety of other file types such as log files, Hadoop Sequence Files, and CSV files. You can add support for indexing custom file formats using a morphline command plug-in.

Cloudera Search Release Notes

These release notes provide information on known issues, limitations, and fixed issues for Cloudera Search.

Cloudera Search Incompatible Changes

Incompatible changes between Cloudera Search for CDH 5.2 and Cloudera Search for CDH 5.3

Some packaging changes were made that have consequences for CrunchIndexerTool start-up scripts. If those startup scripts include the following line:

```
export myDriverJar=$(find $myDriverJarDir -maxdepth 1 -name \
'*.jar' ! -name '*-job.jar' ! -name '*-sources.jar')
```

That line in those scripts should be changed as follows:

```
export myDriverJar=$(find $myDriverJarDir -maxdepth 1 -name \
'search-crunch-*.jar' ! -name '*-job.jar' ! -name '*-sources.jar')
```

Incompatible changes between Cloudera Search for CDH 5 beta 2 and older versions of Cloudera Search:

The following incompatible changes occurred between Cloudera Search for CDH 5 beta 2 and older versions of Cloudera Search including both earlier versions of Cloudera Search for CDH 5 and Cloudera Search 1.x:

- Supported values for the `--reducers` option of the `MapReduceIndexer` tool change with the release of Search for CDH 5 beta 2. To use one reducer per output shard, 0 is used in Search 1.x and Search for CDH 5 beta 1. With the release of Search for CDH 5 beta 2, -2 is used for one reducer per output shard. Because of this change, commands using `--reducers 0` that were written for previous Search releases do not continue to work in the same way after upgrading to Search for CDH 5 beta 2. After upgrading to Search for CDH 5 beta 2, using `--reducers 0` results in an exception stating that zero is an illegal value.

New Features in Cloudera Search Version 1.3.0

- Cloudera Search 1.3.0 is a bug fix release, so there are no new features provided with Cloudera Search 1.3.0. For information on resolved issues, see Known Issues Fixed in Cloudera Search Version 1.3.0 on page 124.
- Search 1.3.0 ships with a version of CDK 0.9.2. For more information on changes included in CDK 0.9.2, see the Cloudera Development Kit Release Notes.

New Features in Cloudera Search Version 1.2.0

- MapReduce jobs support YARN.
- Search 1.2.0 ships with CDK 0.9.1. For more information on changes included in CDK 0.9.1, see the Cloudera Development Kit Release Notes.
- Cloudera Search Version 1.2.0 includes all updates that were included in New Features in Cloudera Search Version 1.1.0 on page 118.

New Features in Cloudera Search Version 1.1.0

- HBase Batch Indexing:
  - Cloudera Search supports batch indexing of HBase tables using MapReduce jobs. Such batch indexing does not use the HBase replication feature, the Lily HBase Indexer Service, nor does it require registering

a Lily HBase Indexer configuration with the Lily HBase Indexer Service. For more information, see Using the Lily HBase Batch Indexer for Indexing on page 75.

- Search supports emitting zero or more Solr documents for each HBase input row or HBase input cell. Previously, exactly one Solr document had to be emitted.
- Search supports using dynamic output fields when indexing HBase using the `extractHBaseCells` morphline command. `outputField` parameters ending with a * wildcard enable dynamic output fields.

  For example:

  ```
  inputColumn : "m:e:*"
  outputField : "belongs_to_*"
  ```

  For these puts in HBase:

  ```
  put 'table_name' , 'row1' , 'm:e:1' , 'foo'
  put 'table_name' , 'row1' , 'm:e:9' , 'bar'
  ```

  The fields of the Solr document are as follows:

  ```
  belongs_to_1 : foo
  belongs_to_9 : bar
  ```

- The Cloudera CDK has been updated to CDK 0.8.1. For information on changes included in this release, see the Release Notes. This new version includes updates to Cloudera Morphlines functionality. For the latest Cloudera CDK documentation, see Cloudera Development Kit.
- Tika has been upgraded to tika-1.4.
- Lily HBase Indexer supports Kerberos authentication. Search can use the Lily HBase Indexer to index data stored on HBase servers that require Kerberos authentication.
- Search supports Sentry for providing authorization control. For more information, see Enabling Sentry Authorization for Search on page 93.

Cloudera Search Known Issues

The current release includes the following known limitations:

— Solr, Oozie and HttpFS fail when KMS and SSL are enabled using self-signed certificates

When the KMS service is added and SSL is enabled, Solr, Oozie and HttpFS are not automatically configured to trust the KMS's self-signed certificate and you might see the following error.

```
org.apache.oozie.service.AuthorizationException: E0501: Could not perform authorization
 operation,
sun.security.validator.ValidatorException: PKIX path building failed:
sun.security.provider.certpath.SunCertPathBuilderException:
unable to find valid certification path to requested target
```

Severity: Medium

Workaround: You must explicitly load the relevant truststore with the KMS certificate to allow these services to communicate with the KMS.

Solr, Oozie: Add the following arguments to their environment safety valve so as to load the truststore with the required KMS certificate.

```
CATALINA_OPTS="-Djavax.net.ssl.trustStore=/etc/path-to-truststore.jks
-Djavax.net.ssl.trustStorePassword=<password>"
```

HttpFS: Add the following arguments to the **Java Configuration Options for HttpFS** property.

```
-Djavax.net.ssl.trustStore=/etc/path-to-truststore.jks
-Djavax.net.ssl.trustStorePassword=<password>
```

— CrunchIndexerTool which includes Spark indexer requires specific input file format specifications

If the `--input-file-format` option is specified with CrunchIndexerTool then its argument must be `text`, `avro`, or `avroParquet`, rather than a fully qualified class name.

Severity: Low

— Previously deleted empty shards may reappear after restarting the leader host

It is possible to be in the process of deleting a collection when hosts are shut down. In such a case, when hosts are restarted, some shards from the deleted collection may still exist, but be empty.

Severity: Low

Workaround: To delete these empty shards, manually delete the folder matching the shard. On the hosts on which the shards exist, remove folders under `/var/lib/solr/` that match the collection and shard. For example, if you had an empty shard 1 and empty shard 2 in a collection called `MyCollection`, you might delete all folders matching `/var/lib/solr/MyCollection{1,2}_replica*/`.

— The `quickstart.sh` file does not validate ZooKeeper and the NameNode on some operating systems

The `quickstart.sh` file uses the timeout function to determine if ZooKeeper and the NameNode are available. To ensure this check can be complete as intended, the `quickstart.sh` determines if the operating system on which the script is running supports timeout. If the script detects that the operating system does not support timeout, the script continues without checking if the NameNode and ZooKeeper are available. If your environment is configured properly or you are using an operating system that supports timeout, this issue does not apply.

Severity: Low

Workaround: This issue only occurs in some operating systems. If timeout is not available, a warning if displayed, but the quickstart continues and final validation is always done by the MapReduce jobs and Solr commands that are run by the quickstart.

— Using Solr with Sentry may consume more memory than required

The sentry-enabled `solrconfig.xml.secure` configuration file does not enable the hdfs global block cache. This does not cause correctness issues, but it can greatly increase the amount of memory that solr requires.

Severity: Medium

Workaround: Enable the hdfs global block cache, by adding the following line to `solrconfig.xml.secure` under the `directoryFactory` element:

```
<str name="solr.hdfs.blockcache.global">${solr.hdfs.blockcache.global: true}</str>
```

— Enabling blockcache writing may result in unusable indexes

It is possible to create indexes with `solr.hdfs.blockcache.write.enabled` set to `true`. Such indexes may appear corrupt to readers, and reading these indexes may irrecoverably corrupt indexes. Blockcache writing is disabled by default.

Severity: Medium

Workaround: Do not enable blockcache writing.

— Solr fails to start when Trusted Realms are added for Solr into Cloudera Manager

Cloudera Manager generates name rules with spaces as a result of entries in the Trusted Realms, which do not work with Solr. This causes Solr to not start.

Severity: Medium

Workaround: Do not use the Trusted Realm field for Solr in Cloudera Manager. To write your own name rule mapping, add an environment variable `SOLR_AUTHENTICATION_KERBEROS_NAME_RULES` with the mapping. See the Cloudera Manager Security Guide for more information.

— Lily HBase batch indexer jobs fail to launch

A symptom of this issue is an exception similar to the following:

```
Exception in thread "main" java.lang.IllegalAccessError: class
com.google.protobuf.ZeroCopyLiteralByteString cannot access its superclass
com.google.protobuf.LiteralByteString
 at java.lang. ClassLoader.defineClass1(Native Method)
 at java.lang. ClassLoader.defineClass( ClassLoader.java:792)
 at java.security.SecureClassLoader.defineClass(SecureClassLoader.java:142)
 at java.net.URLClassLoader.defineClass(URLClassLoader.java:449)
 at java.net.URLClassLoader.access$100(URLClassLoader.java:71)
 at java.net.URLClassLoader$1.run(URLClassLoader.java:361)
 at java.net.URLClassLoader$1.run(URLClassLoader.java:355)
 at java.security.AccessController.doPrivileged(Native Method)
 at java.net.URLClassLoader.findClass(URLClassLoader.java:354)
 at java.lang. ClassLoader.loadClass( ClassLoader.java:424)
 at java.lang. ClassLoader.loadClass( ClassLoader.java:357)
 at org.apache.hadoop.hbase.protobuf.ProtobufUtil.toScan(ProtobufUtil.java:818)
 at
org.apache.hadoop.hbase.mapreduce.TableMapReduceUtil.convertScanToString(TableMapReduceUtil.java:433)

 at
org.apache.hadoop.hbase.mapreduce.TableMapReduceUtil.initTableMapperJob(TableMapReduceUtil.java:186)

 at
org.apache.hadoop.hbase.mapreduce.TableMapReduceUtil.initTableMapperJob(TableMapReduceUtil.java:147)

 at
org.apache.hadoop.hbase.mapreduce.TableMapReduceUtil.initTableMapperJob(TableMapReduceUtil.java:270)

 at
org.apache.hadoop.hbase.mapreduce.TableMapReduceUtil.initTableMapperJob(TableMapReduceUtil.java:100)

 at
com.ngdata.hbaseindexer.mr.HBaseMapReduceIndexerTool.run(HBaseMapReduceIndexerTool.java:124)

 at
com.ngdata.hbaseindexer.mr.HBaseMapReduceIndexerTool.run(HBaseMapReduceIndexerTool.java:64)

 at org.apache.hadoop.util.ToolRunner.run(ToolRunner.java:70)
 at
com.ngdata.hbaseindexer.mr.HBaseMapReduceIndexerTool.main(HBaseMapReduceIndexerTool.java:51)

 at sun.reflect.NativeMethodAccessorImpl.invoke0(Native Method)
 at sun.reflect.NativeMethodAccessorImpl.invoke(NativeMethodAccessorImpl.java:57)
 at sun.reflect.DelegatingMethodAccessorImpl.invoke(DelegatingMethodAccessorImpl.java:43)

 at java.lang.reflect.Method.invoke(Method.java:606)
 at org.apache.hadoop.util.RunJar.main(RunJar.java:212)
```

This is because of an optimization introduced in HBASE-9867 that inadvertently introduced a classloader dependency. In order to satisfy the new classloader requirements, `hbase-protocol.jar` must be included in Hadoop's classpath. This can be resolved on a per-job launch basis by including it in the HADOOP_CLASSPATH environment variable when you submit the job.

Severity: High

Workaround: Run the following command before issuing Lily HBase MapReduce jobs. Replace the .jar file names and filepaths as appropriate.

```
$ export HADOOP_CLASSPATH=</path/to/hbase-protocol>.jar; hadoop jar <MyJob>.jar
<MyJobMainClass>
```

— Users may receive limited error messages on requests in Sentry-protected environment.

Users submit requests which are received by a host. The host that receives the request may be different from the host with the relevant information. In such a case, Solr forwards the request to the appropriate host. Once the correct host receives the request, Sentry may deny access.

Because the request was forwarded, available information may be limited. In such a case, the user's client display the error message `Server returned HTTP response code: 401 for URL:` followed by the Solr machine reporting the error.

Severity: Low

Workaround: For complete error information, review the contents of the Solr logs on the machine reporting the error.

— Users with insufficient Solr permissions may receive a "Page Loading" message from the Solr Web Admin UI

Users who are not authorized to use the Solr Admin UI are not given page explaining that access is denied, and instead receive a web page that never finishes loading.

Severity: Low

Workaround: None

— Mapper-only HBase batch indexer fails if configured to use security.

Attempts to complete an HBase batch indexing jobs fail when Kerberos authentication is enabled and reducers is set to 0.

Workaround: Either disable Kerberos authentication or use one or more reducers.

— Spark indexer fails if configured to use security.

Spark indexing jobs fail when Kerberos authentication is enabled.

Workaround: Disable Kerberos authentication or use another indexer.

— Using MapReduceIndexerTool or HBaseMapReduceIndexerTool multiple times may produce duplicate entries in a collection.

Repeatedly running the MapReduceIndexerTool on the same set of input files can result in duplicate entries in the Solr collection. This occurs because the tool can only insert documents and cannot update or delete existing Solr documents.

Severity: Medium

Workaround: To avoid this issue, use HBaseMapReduceIndexerTool with zero reducers. This must be done without Kerberos.

— Deleting collections may fail if hosts are unavailable.

It is possible to delete a collection when hosts that host some of the collection are unavailable. After such a deletion, if the previously unavailable hosts are brought back online, the deleted collection may be restored.

Severity: Low

Workaround: Ensure all hosts are online before deleting collections.

— Lily HBase Indexer is slow to index new data after restart.

After restarting the Lily HBase Indexer, you can add data to one of the HBase tables. There may be a delay of a few minutes before this newly added data appears in Solr. This delay only occurs with a first HBase addition after a restart. Similar subsequent additions are not subject to this delay.

Severity: Low

Workaround: None

— Some configurations for Lily HBase Indexers cannot be modified after initial creation.

Newly created Lily HBase Indexers define their configuration using the properties in `/etc/hbase-solr/conf/hbase-indexer-site.xml`. Therefore, if the properties in the `hbase-indexer-site.xml` file are incorrectly defined, new indexers do not work properly. Even after correcting the contents of `hbase-indexer-site.xml` and restarting the indexer service, old, incorrect content persists. This continues to create non-functioning indexers.

Severity: Medium

Workaround:

- **Warning:** This workaround involves completing destructive operations that delete all of your other Lily HBase Indexers.

To resolve this issue:

1. Connect to each machine running the Lily HBase Indexer service using the NGdata and stop the indexer:

   ```
   service hbase-solr-indexer stop
   ```

   - **Note:** You may need to stop the service on multiple machines.

2. For each indexer machine, modify the `/etc/hbase-solr/conf/hbase-indexer-site.xml` file to include valid settings.
3. Connect to the ZooKeeper machine, invoke the ZooKeeper CLI, and remove all contents of the `/ngdata` chroot:

   ```
   $ /usr/lib/zookeeper/bin/zkCli.sh
   [zk: localhost:2181( CONNECTED) 0] rmr /ngdata
   ```

4. Connect to each indexer machine and restart the indexer service.

   ```
   service hbase-solr-indexer start
   ```

After restarting the client services, ZooKeeper is updated with the correct information stored on the updated clients.

— Saving search results is not supported in this release.

This version of Cloudera Search does not support the ability to save search results.

Severity: Low

Workaround: None

— HDFS Federation is not supported in this release.

This version of Cloudera Search does not support HDFS Federation.

Severity: Low

Workaround: None

— Block Cache Metrics are not supported in this release.

This version of Cloudera Search does not support block cache metrics.

Severity: Low

Workaround: None

— Shard splitting support is experimental.

Shard splitting was added with the recent release of Solr 4.4. Cloudera anticipates shard splitting to function as expected with Cloudera Search, but this interaction has not been thoroughly tested. Therefore, Cloudera cannot guarantee issues will not arise when shard splitting is used with Search.

Severity: Low

Workaround: Use shard splitting for test and development purposes, but be aware of the risks of using shard splitting in production environments. To avoid using shard splitting, use the source data to create a new index with a new sharding count by re-indexing the data to a new collection. You can enable this using the MapReduceIndexerTool.

— User with `update` access to the administrative collection can elevate the access.

Users are granted access to collections. Access to several collections can be simplified by aliasing a set of collections. Creating an alias requires `update` access to the administrative collection. Any user with `update` access to the administrative collection is granted `query` access to all collections in the resulting alias. This is true even if the user with `update` access to the administrative collection otherwise would be unable to `query` the other collections that have been aliased.

Severity: Medium

Workaround: None. Mitigate the risk by limiting the users with `update` access to the administrative collection.

Known Issues Fixed in Cloudera Search Version 1.3.0

— Cloudera Search Version 1.3.0 includes all updates that were included in Search for CDH 5.0.0.

Cloudera Search 1.3.0 includes all fixes that were included in Cloudera Search for CDH 5. Those fixed issues are described in Known Issues Fixed in CDH 5.0.0.

— Documents may not replicate with forwarded batch update on a secure cluster.

Documents are now properly replicated on secure clusters, regardless of whether requests are forwarded from replicas to the shard leader. In the past, on secure clusters, if a batch update request was received by a shard replica and then forwarded to the shard leader, the request might not complete as expected.

— On a secure cluster, proxied updates may not complete.

Proxied updates now complete as expected.

Known Issues Fixed in Cloudera Search Version 1.2.0

— Cloudera Search Version 1.2.0 includes all updates that were included in Search for CDH 5 Beta 2.

Cloudera Search 1.2.0 includes all fixes that were included in Known Issues Fixed in Cloudera Search Version 1.1.0 on page 125.

Known Issues Fixed in Cloudera Search Version 1.1.0

— SolrJ fails to update or delete SolrCloud documents inserted using MapReduceIndexerTool.

When importing documents, if the number of MapReduce reducers was greater than the number of Solr shards, then MapReduceIndexerTool assigned documents to shards in a way that did not follow SolrJ SolrCloud sharding semantics. As a result, SolrJ would relay updates to a shard different from the one chosen by MapReduceIndexerTool. MapReduceIndexerTool and SolrCloud API now assign shards in the same way. Updating and deleting documents in SolrCloud using solrj now works for documents that have been inserted using MapReduceIndexerTool. This is true regardless of the number of MapReduce reducers and Solr shards.

Known Issues Fixed in Cloudera Search Version 1.0.0

— Cloudera Search cannot search HBase data in this Beta release.

Cloudera Search is integrated with and can search data stored in HBase.

— Search does not support Kerberos Authentication in a Cloudera Managed environment.

Kerberos authentication can be used with Search using a configuration that uses Cloudera Manager.

— Hue is not supported with secure Solr.

This version of Cloudera Search supports using Hue with secure solr.

— Flume ingestion is not supported with secure Solr in this release.

This version of Cloudera Search supports Flume ingestion with secure Solr.