
Arranger Documentation

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overture.bio

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Note: This project is undergoing refactoring work, for what will become version 3+. Covering great feedback we've received from the community, there will be some breaking changes, and an upgrade guide is already in the works.

1.1 What is Arranger?

Arranger is a collection of reusable components for creating “-centric” search portals with **Elasticsearch**. Arranger consists of the

- *Arranger Search API* provides a layer that sits above your Elasticsearch cluster to expose a data-model aware **GraphQL** API, generated from your own Elasticsearch index mapping.
- *Arranger Components* provides a rich set of UI components that are configured to speak to the search API.
- *Arranger Admin* provides the API and UI for configuring the search API and content management for the search portal.

Arranger is one of many products provided by **Overture** and is completely open-source and free for everyone to use.

See also:

For additional information on other products in the Overture stack, please visit <https://overture.bio>

1.2 Features

- GraphQL API for query flexibility.
- **SQON** query filter notation balances between human-interpretability and machine-readability to simply search.
- Admin UI for API configuration and content management.
- Configuration import and export for easy migration.

1.3 License

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The easiest way to understand Arranger, is to simply use it!

Below is a description of how to get Arranger quickly up and running, as well as a description of how Arranger works and some important terms.

2.1 Quick Start

The goal of this quick start is to get a working application quickly up and running.

Using [Docker](#):

1. Download the latest version of Arranger.
2. From the Arranger root directory, run [docker-compose](#):

```
$ docker-compose up -d
```

Arranger should now be deployed locally.

Alternatively, see the [Installation instructions](#).

2.2 How Arranger Works

1. Starting with some Elasticsearch (ES) indices with mappings.

- Arranger makes no assumption about your data model.
- Model your [index mappings](#) and index them.
- For demo convenience, you can follow a [tutorial below](#) to index some test data from our Kids First project.

See also:

The [Overture](#) software suite also provides [Maestro](#) for indexing genomic data to ES

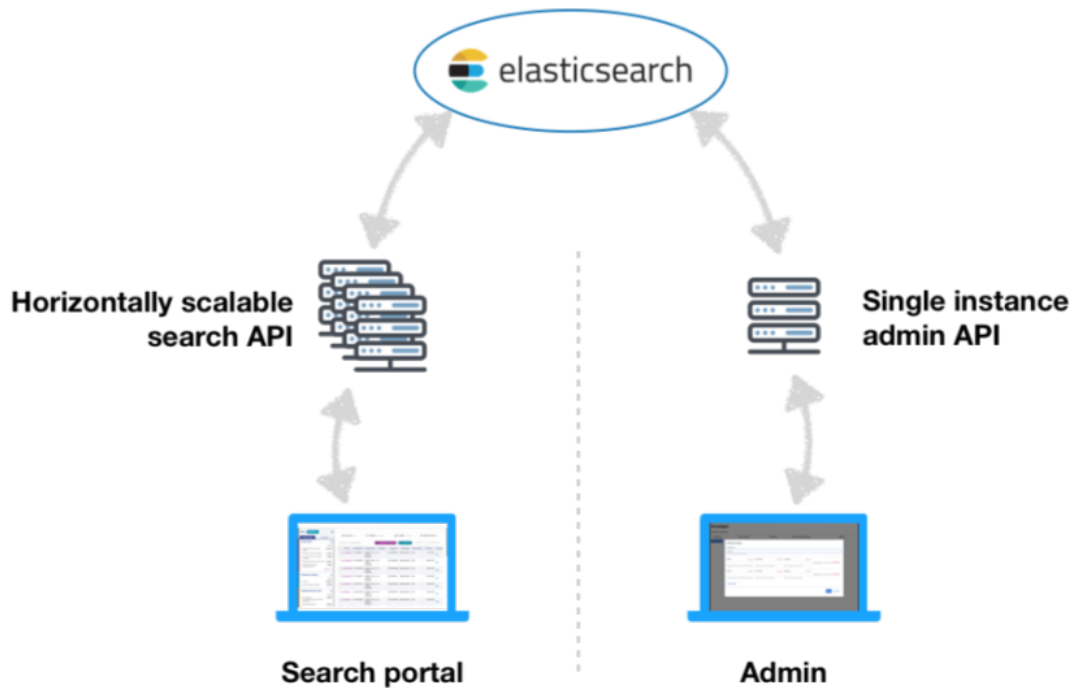
2. Create an API version for your project from Arranger Admin.

- From your browser, navigate to <http://localhost:8080>
- Click “Add Project”
- Input your project id in **snake_case**
- Click “Add Index” for each index you want to expose from ES, with the following fields:
 - “Name”: any name for your index, in **camelCase**
 - “ES Index”: the index that you want to expose
 - “ES Type”: the type that you want to expose
- Click “Add” once finalized.
- Navigate into your newly registered project’s configuration and ensure that “Has Mapping” is “yes” for all indices registered.
- [Configure your project](#) from the API and click “Save” to save as a new project.

3. View your data in a portal.

- From a UI:
 - Go to <http://localhost:8081/?selectedKind=Portal>.
 - Select your project and index from the dropdown.
 - Note: a production-ready white-label portal using UI components provided by Arranger is in our roadmap for Arranger.
- From the GraphQL API:
 - Each Arranger project created through the Admin system in step 2 creates a new GraphQL endpoint.
 - Start a GraphQL IDE (such as [GraphiQL](#) or [GraphQL Playground](#))
 - Point your IDE to http://localhost:5050/<project_id>/graphql to explore the API schema (where `<project_id>` is the project id you have input in step 2).
 - For documentation regarding this API, check out the [Arranger for Application Developers](#) guide

2.3 Architecture



2.4 Indexing Demo Data

- From your browser, visit the locally running Kibana at <http://localhost:5601> and go to Dev Tools
- Creating a `file_centric` index:
 - Run [these commands](#) to create a `file_centric` index and add a mapping then [these commands](#) to index some demo documents into the index
 - Run [these commands](#) to create a `participant_centric` index and add a mapping then [these commands](#) to index some demo documents into the index
- You can run `GET file_centric/_mapping` and `GET participant_centric/_mapping` to confirm that the mapping has been created successfully

3.1 Tutorial

To administer Arranger, the admin must:

1. Install Arranger.

View the [installation instructions](#).

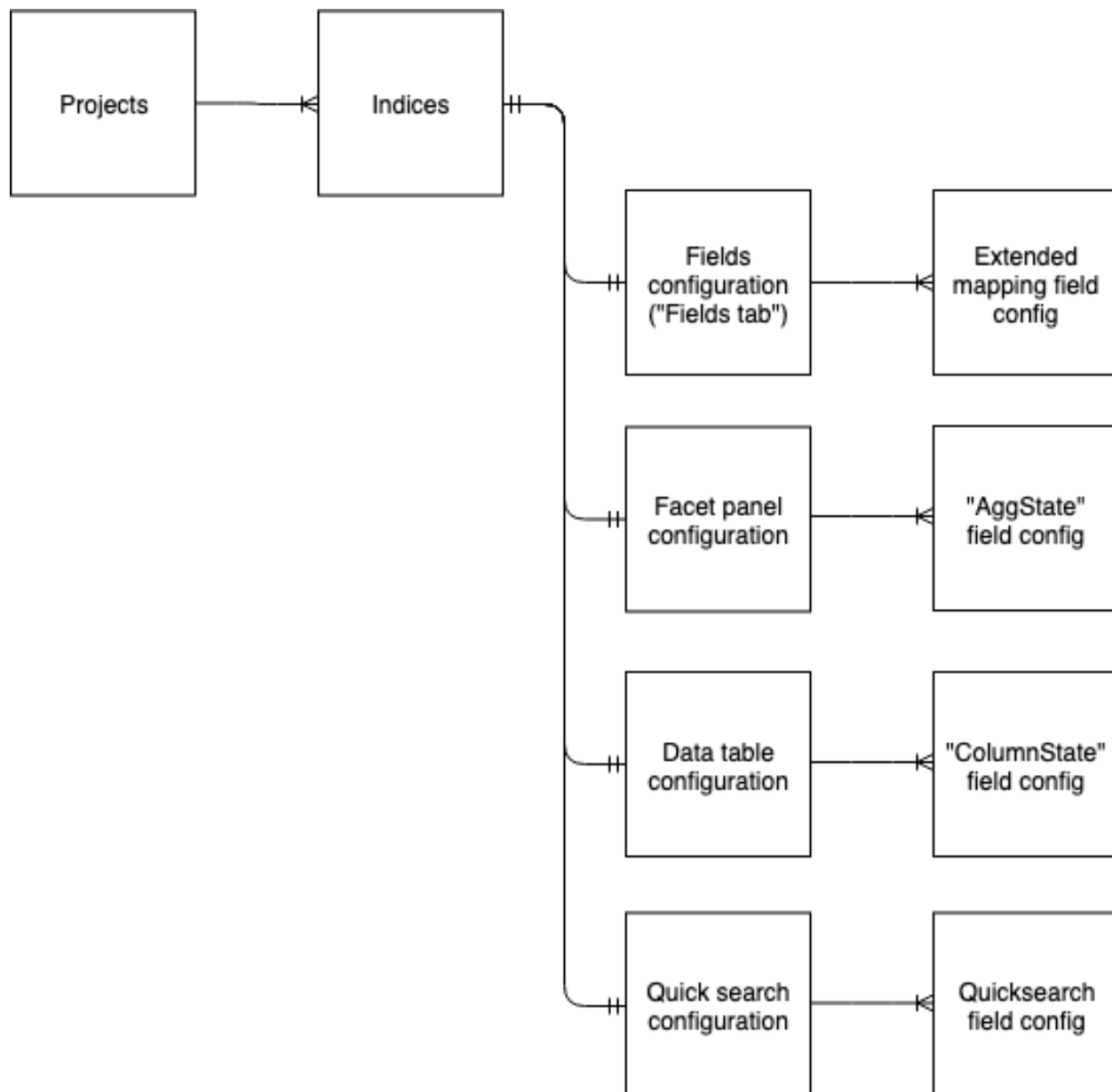
2. Have an Elasticsearch mapping and data indexed to search.

View the [Indexing Demo Data](#) for a demo setup.

3. Admin registers the indices with arranger through the admin UI and apply configurations.

3.2 Using the Admin UI

The arranger UI reflects the following pseudo entity relationship:



1) Projects:

Project versions

Project ID	Index Counts	Created	Export configurations	Delete
project1	2	2019-05-16T19:49:03.429Z	Export	Delete
project2	2	2019-05-16T19:49:33.725Z	Export	Delete

[Add Project](#)

This page lists the available projects and provides an interface for registering new projects

Available functionalities:

- Adding a new project
- Removing existing project
- Export configuration data (exported data can then be imported into new projects to migrate data).

Clicking on a project id will navigate to that project's list of indices.

2) Indices:

Save Project Cancel

Arranger project: project1

Name (aka graphqlField)	ES index	ES type	has mapping
participant	participant_centric	participant_centric	yes
file	file_centric	file_centric	yes

This page lists the indices registered to Arranger under the selected project.

Clicking on an index name will navigate to the configuration page for the index. The following configurations are available:

a) Fields configurations

Fields Aggs Panel Table Quick Search

Field filter

Type

Is active

Is array

Is primary key

Quicksearch enabled

Fields (157)

- acl
- availability
- controlled_access
- created_at
- data_type
- experiment_strategies
- external_id
- file_format
- file_name
- instrument_models
- is_harmonized

Field: acl

Display Name

Aggregation Type

☐ Active
☐ Quicksearch enabled
☐ Is primary key
☐ Is array

This lists all fields available in the index and allows configuration of Arranger metadata for these fields, including:

- **Display Name:** how the field should be displayed to user.
- **Aggregation Type:** lets the search portal know how to display aggregation filters for the field.
- **Active:** this field is **DEPRECATED**
- **Quicksearch enabled:** whether the field is enabled for quicksearch using the *@arranger/components's QuickSearch* component.

- **Is primary key:** check if the field is the unique identifier for the index's main entity.
- **Is array:** check if the field is an array. Elasticsearch's mapping does not specify this information.

For convenience, filtering on the fields can be done through the inputs above the header.

b) Facet panel configurations

The screenshot shows the 'Aggs Panel' in the Arranger interface. At the top, there are tabs for 'Fields', 'Aggs Panel' (selected), 'Table', and 'Quick Search'. Below the tabs, there are three input fields: 'Field filter', 'Active' (a dropdown menu), and 'Show' (a dropdown menu). The main area displays a list of facets, each with a 'Position' dropdown, a field name, and 'Active' and 'Shown' checkboxes. The facets are:

Position	Field Name	Active	Shown
0	affected_status	<input checked="" type="checkbox"/>	<input type="checkbox"/>
1	alias_group	<input checked="" type="checkbox"/>	<input type="checkbox"/>
2	available_data_types	<input checked="" type="checkbox"/>	<input type="checkbox"/>
3	biospecimens_age_at_event_days	<input checked="" type="checkbox"/>	<input type="checkbox"/>
4	biospecimens_analyte_type	<input checked="" type="checkbox"/>	<input type="checkbox"/>
5	biospecimens_composition	<input checked="" type="checkbox"/>	<input type="checkbox"/>
6	biospecimens_concentration_mg_per_ml	<input checked="" type="checkbox"/>	<input type="checkbox"/>

This lists all available aggregations on the fields mentioned. On Arranger's default portal UI, this list is rendered as a facet panel. Each entry on Supported configurations:

- **Ordering the facets:** drag the facet on its "hamberger menu icon" to place the facet at the desired position. Alternatively, the position can also be set through the select menu beside the icon.
- **Shown:** displays the facet in the portal's facet panel.
- **Active:** enables this facet for search. An *Active* facet will appear in the *Advanced-FacetView* component in `@arranger/components`. Only facets that are both *Active* and *Shown* will be shown in the portal's facet panel.

c) Data table configurations

Fields Aggs Panel **Table** Quick Search

Field

Shown

Sortable

Position

affected_status

0

☒ Active

☐ Default

☒ Sortable

Position

alias_group

1

☒ Active

☐ Default

☒ Sortable

Position

available_data_types

2

☒ Active

☐ Default

☒ Sortable

Position

biospecimens.age_at_event_days

3

☐ Active

☐ Default

☐ Sortable

Position

biospecimens.analyte_type

4

☐ Active

☐ Default

☐ Sortable

Position

biospecimens.composition

5

☐ Active

☐ Default

☐ Sortable

Position

biospecimens.concentration_mg_per_ml

6

☐ Active

☐ Default

☐ Sortable

This contains configuration for the data table in the default portal. Each entry in the list represents a column in the data table. Available configurations:

- **Column order:** positioning can be done by dragging or using the select, similar to the facet panel.
- **Active:** enables this column to be viewed in the table. Does not show by default.
- **Default:** shows this column by default. Can only be checked if *Active* is checked.
- **Sortable:** enables sorting of the table on this field.

d) Quick search configurations

Fields	Aggs Panel	Table	Quick Search
--------	------------	-------	--------------

Active

Fields (8)

☒ participant
 ☐ Biospecimens
 ☐ Diagnoses
 ☐ Family Family Compositions
 ☐ Family Family Compositions Family Members
 ☐ Family Family Compositions Family Members Diagnoses
 ☐ Files
 ☐ Files Sequencing Experiments

participant

Display Name

participant

☐ Active

Key Field

Select...

Search Fields

Select...

This contains configuration for the portal's quick-search feature, which allows users to filter indexed entities by text. Currently, Arranger only supports exact match on quicksearch, but free-text search is in our roadmap to support. This feature can be exposed to end-users through the *QuickSearch* UI component from `@arranger/components`.

Only entities (in other words, the root object and its “nested” fields in Elasticsearch) are available for quick search.

Available configurations:

- **Display Name:** the name to display this field as.
- **Active:** check to enable search for this entity.
- **Key Field:** the unique field that identifies each instance of this entity.
- **Search Field:** the properties of the entity to enable search on.

CHAPTER 4

SQON Filters

Arranger uses a custom JSON object format for filtering that is called SQON (Serializable Query Object Notation, pronounced like “Scone”). SQON provides a flexible system for combining many different filters.

A SQON object consists of nested objects of two types: **Operations** and **Values**.

Operation objects apply boolean logic to a list of operation objects. They are of the form:

Combination Operation (aka, Boolean Operation) which groups one or more filters

```
{
  "content":[] // List of Operation objects that the boolean operation will
  ↳ apply to
  "op":"", // Operation to apply to content ["and", "or", "not"]
}
```

OR

Field Operation that applies to a filter to Value Object

```
{
  "content":{} // Value object specifying the field and list of values that
  ↳ the field must be "in" or "not-in"
  "op":"", // Operation to apply to content ["in", "<=", ">="]
}
```

Value objects specify a list the field name and values for it that the wrapping . This filter can specify to include or exclude fields with any of the listed values. It will have the following format:

```
{
  "field":"", // name of the field this operation applies to
  "value":[] // List of values for the field if using the "in" operation, or a
  ↳ scalar value for ">=" and "<=" operations
}
```

The top level of a SQON must always be a Combination Operation, even if only a single filter is being applied.

4.1 Sample

```
{
  content: [
    {
      content: [
        {
          content: {
            field: "id",
            value: [
              "id123"
            ]
          },
          op: "in"
        }
      ],
      op: "or"
    },
    {
      content: {
        field: "id",
        value: [
          "id123"
        ]
      },
      op: "in"
    }
  ],
  op: "and"
}
```

If you'd like to contribute to this project, it's hosted on github.

See <https://github.com/overture-stack/arranger>

5.1 Indices and tables

- [genindex](#)
- [search](#)