

# Sample Queries of Metadata and Variants Services

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# Metadata Services

This includes all of the endpoints under Clinical and Pipeline Metadata Services.

Even though some of the sample queries below are made to specific endpoint, the same format applies to any pipeline or clinical metadata endpoint. Typically you will need to change the *field* in your *filters*, depending on which table you are querying on.

## Fetch Datasets

**Description:** To fetch all of the datasets, make a query to *datasets/search* endpoint with an empty body. You need *dataset\_id* for subsequent queries to other endpoints.

**Query:**

```
{}
```

## Sample Query I

**Description:** Fetch all of the items from the specified dataset from *any* clinical or pipeline metadata service endpoint.

**Query:**

```
{  
  "dataset_id": "WyIxa2dlbm9tZSJd",  
}
```

## Sample Query II

**Description:** Fetch all of the items from the *patients/search* endpoint, whose gender is female.

**Important:** We support a number of operators in the filters, which include: >, <, >=, <=, =, !=, and *contains*.

Query:

```
{
  "dataset_id": "WyIxa2dlbm9tZSJd",
  "filters": [
    {
      "field": "gender",
      "operator": "=",
      "value": "female"
    }
  ]
}
```

## Sample Query III

**Description:** Fetch all of the items from the *patients/search* endpoint, whose gender is female and whose ethnicity is NOT 'GBR'.

**Important:** You can specify more than one filter under *filters*.

```
{
  "dataset_id": "WyIxa2dlbm9tZSJd",
  "filters": [
    {
      "field": "gender",
      "operator": "=",
      "value": "female"
    },
    {
      "field": "ethnicity",
      "operator": "!=",
      "value": "GBR"
    }
  ]
}
```

## Sample Query IV

**Description:** Fetch all of the items from the *patients/search* endpoint, whose ethnicity is one of GBR, FIN or ESN.

**Important:** Note that this query is very different from the previous ones. To specify a list of values you are interested in, you need to:

- Specify *values* in your filters, instead of *value*.
- Specify a list of values that you are interested in.
- Specify *in* as the operator.

```
{
  "dataset_id": "WyIxa2dlbm9tZSJd",
  "filters": [
    {
      "field": "ethnicity",
      "operator": "in",
      "values": [
        "GBR",
        "FIN",
        "ESN"
      ]
    }
  ]
}
```

# Variants Services

This mainly includes the */variantsets/search*, */variants/search* and */variantsbygene* endpoints.

## Sample Query I

**Description:** Fetch all of the variantsets associated with a particular dataset.

**Endpoint:** *variantsets/search*

**Note:** This query is the same as Sample Query I under Metadata services, but it is the same across metadata, variantSets, referenceSets, etc.

Query:

```
{
  "dataset_id": "WyIxa2dlbm9tZSJd"
}
```

## Sample Query II

**Description:** Search for variants within the range between the *start* and *end* that are on *chromosome 22*, from the *designated variantSets*.

**Endpoint:** *variants/search*

```
{
  "start": "50158561",
  "end": "50158565",
  "reference_name": "22",
  "variant_set_ids": [
    "yourVariantSetId1",
    "yourVariantSetId2"
  ]
}
```

## Sample Query III

**Description:** Search for variants within the range between the *start* and *end* that are on *chromosome 22*, from **all** variantsets that are associated with one particular dataset.

**Endpoint:** *variants/search*

**Important:** You should never attempt to specify both *dataset\_id* and *variant\_set\_ids*.

```
{
  "dataset_id": "WyIxa2dlbm9tZSJd",
  "start": "50158561",
  "end": "50158565",
  "reference_name": "22"
}
```

## Sample Query IV

**Description:** Search for variants that are associated with a particular gene.

**Endpoint:** */variantsbygene*

```
{
  "dataset_id": "WyIxa2dlbm9tZSJd",
  "gene": "ABCD",
}
```