Aggregation Stats Query Syntax

In OpenCGA, *stats* refers to the arrangement of search results into categories based on indexed field. Results are presented as a list of buckets, where each bucket is composed of 1) the field value and 2) a numerical count of how many matching documents were found for that field. In literature, this *stats* c oncept is known as facet or faceting as well. In fact, OpenCGA stats are based on Solr faceted search.

In addtion, stats allows users to query:

- Ranges to count how many documents are in an interval of a numerical field.
- Aggregation functions such as average, maximum, minimum, percentiles,...
- Nested faceted search.

The basic syntax for stats (or facets) is:

Basic facet specification
`field_name[value1,value2,value3...]:limit`

Parameters:

Parameter	Description
field_name	The field name to produce buckets from. Mandatory.
value1,value2,value3...	They are the values of the field name you want to count. They have to be enclosed in square brackets. Optional.
limit	Number of counts to show, i.e., number of buckets. Optional.

E.g.: *...&fields=chromosome[1,2]*

Users can query multiple *stats* by separating field names by semicolons.

E.g.: *...&fields=chromosome[1,2];types*

Ranges

When asking for ranges, the result contains multiple buckets over a numeric field. You must specify the field name, the lower and upper bounds and the step or bucket size.

Range specification
`field_name[start..end]:step`

Range parameters:

Parameter	Description
field_name	The numeric field name to produce range buckets from. Mandatory
start	Lower bound of the ranges. Mandatory.
end	Upper bound of the ranges. Mandatory.
step	Size of each range bucket produced. Mandatory.

E.g.: *...&fields=gerp[0..10]:0.5*

Aggregation functions

Aggregation functions, also called **facet functions, analytic functions,** or **metrics**, calculate something interesting over a domain (each facet bucket).

Aggregation specification
`aggregation_function(field_name)`

List of aggregation functions:

Aggregation function	Description	Example
avg	Average of numeric values	avg(gerp)
min	Minimum value	min(sift)
max	Maximum value	max(caddScaled)
unique	Number of unique values	unique(biotypes)
hll	Distributed cardinality estimate via hyper-log-log algorithm	hll(type)
percentile	Percentile estimates via t-digest algorithm. Calculate the percentiles: 1, 10, 25, 50, 75, 90 and 99th.	percentile(gerp)

sumsq	Sum of squares of field or function	sumsq(caddRaw)

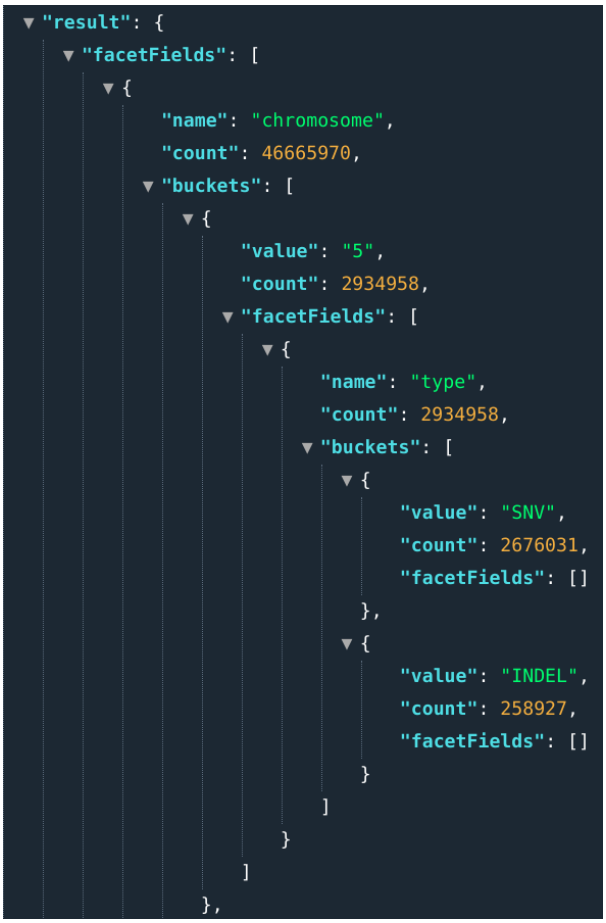
E.g.: *...&fields=percentile(gerp);max(caddScaled)*


```
"result": {
  "facetFields": [
    {
      "name": "gerp",
      "count": 0,
      "aggregationName": "percentile",
      "aggregationValues": [
        -7.32916103966793,
        -3.2598138856785384,
        -1.1872542298684619,
        0,
        0.6023076581836967,
        1.8404930558210097,
        4.551321522141655
      ]
    },
    {
      "name": "caddScaled",
      "count": 0,
      "aggregationName": "max",
      "aggregationValues": [
        58
      ]
    }
  ]
}
```


Nested facets

Nested facets allow users to nest bucketing terms, ranges or aggregations. In order to specify nested facets you must use the symbols **>>**

E.g.: *...&fields=chromosome[5,6]>>type*



Field types: categorical and numeric

Categorical field names

Field name	Description	Facet example
id	Variant ID	List of values
names	Names	List of `<chromosome>:<start>-<end>`
chromosome		
reference		
alternate		
strand		
type	Variant type, e.g.: INDEL, SNV, SNP,...	List of values. Accepted values: [SNV, MNV, INDEL, SV, CNV]
reference	Reference	List of values
alternate	Allternate	List of values
study	Matches with variants that are in the specified studies	List of values. Accept negations.
file		

genotype	Samples with a specific genotype e.g. HG0097:0/0;HG0098:0/1,1/1. Genotype aliases accepted: HOM_REF, HOM_ALT, HET, HET_REF, HET_ALT and MISS e.g. HG0097:HOM_REF;HG0098:HET_REF,HOM_ALT. This will automatically set 'includeSample' parameter when not provided	{samp_1}:{gt_1}(,{gt_n})*(;{samp_n}:{gt_1}(,{gt_n})*)*
sample	Filter variants where ALL the provided samples are mutated (HET or HOM_ALT)	List of samples.
filter	Specify the FILTER for any of the files. If "files" filter is provided, will match the file and the filter.	List of values.
qual	Specify the QUAL for any of the files. If 'file' filter is provided, will match the file and the qual	
info	Filter by INFO attributes from file. If no file is specified, will use all files from "file" filter. e.g. AN>200 or file_1.vcf:AN>200;file_2.vcf:AN<10 . Many INFO fields can be combined. e.g. file_1.vcf:AN>200;DB=true;file_2.vcf:AN<10	[{file}:]{key}{op}{value}[,;]*
format	Filter by any FORMAT field from samples. If no sample is specified, will use all samples from "sample" or "genotype" filter. e.g. DP>200 or HG0097:DP>200,HG0098:DP<10 . Many FORMAT fields can be combined. e.g. HG0097:DP>200;GT=1/1,0/1,HG0098:DP<10	[{sample}:]{key}{op}{value}[,;]*
release	Return variants that were present in that specific release	Release number
geneTraitId	Gene trait association ID	umls:C0007222 , OMIM:269600
geneTraitName	Gene trait association name	Cardiovascular Diseases
clinVarTrait	ClinVar trait name	
gwasTrait	GWAS trait name	
hpo	List of HPO terms.	HP:0000545
go	List of GO (Genome Ontology) terms.	GO:0002020,GO:0006508
expression	List of tissues of interest	
proteinKeywords	List of protein variant annotation keywords	
drug	List of drug names	

Numeric field names

Numeric field names can be used to compute range facets and aggregation functions.

Field name	Description	Facet range example
start	List of genes	
end		
length	Consequence type SO term list.	SO:0000045,SO:0000046
xref	External references	
biotype	List of biotypes	

polyphen	*polyphen* protein substitution score	polyphen>0.1 , sift=tolerant
sift	*sift* protein substitution score	phastCons>0.5 , phylop<0.1 , gerp>0.1
phastCons	*phastCons* conservation score	
phylop	*phylop* conservation score	
gerp	*gerp* conservation score	
cadd_raw	*Raw CADD* functional score	
cadd_scaled	*Scaled CADD* functional score	
maf	Minor allele frequency	
populationFrequencyAlt	Alternate Population Frequency	1000GENOMES_phase_3:AFR>0.2
populationFrequencyRef	Reference Population Frequency	ESP_6500:AA<0.2
populationFrequencyMaf	Population minor allele frequency	EXAC:AES>=0.6
transcriptionFlags	List of transcript annotation flags	CCDS, basic, cds_end_NF, mRNA_end_NF, cds_start_NF, mRNA_start_NF, seleno
geneTraitId	List of gene trait association ids	umls:C0007222 , OMIM:269600
geneTraitName	List of gene trait association names	Cardiovascular Diseases
trait	List of traits, based on ClinVar, HPO, COSMIC	
hpo	List of HPO terms.	HP:0000545
go	List of GO (Genome Ontology) terms.	GO:0002020,GO:0006508
expression	List of tissues of interest	
proteinKeywords	List of protein variant annotation keywords	
drug	List of drug names	

Variant Fields

The parameters **include** and **exclude** accepts a list of Variant Fields. This is a list with all the accepted values. Some short alias to those fields are listed in *italic*.

- id
- chromosome
- start
- end
- reference
- alternate
- length
- type
- studies
    - studies.samplesData | *samples* | *samplesData*
    - studies.files | *files*
    - studies.stats | *stats*
    - studies.secondaryAlternates
    - studies.studyId
- annotation
    - annotation.ancestralAllele
    - annotation.id
    - annotation.xrefs
    - annotation.hgvs
    - annotation.displayConsequenceType
    - annotation.consequenceTypes
    - annotation.populationFrequencies
    - annotation.minorAllele
    - annotation.minorAlleleFreq
    - annotation.conservation
    - annotation.geneExpression
    - annotation.geneTraitAssociation
    - annotation.geneDrugInteraction

- annotation.variantTraitAssociation
- annotation.functionalScore
- annotation.additionalAttributes

GroupBy and Rank

Histogram