

Filters Viral Beacon

All metadata/data fields are to be used as filters to narrow down query to only results meeting certain conditions, e.g, only a certain variant type: "indels", or a certain sequencing platform "Oxford Nanopore", or a certain variant molecular consequence "nonsynonymous", or a certain geographic origin "Spain" or "Sevilla", as well as lists or combinations thereof.

This is a selection of most important filters for Viral Beacon for now:

1. Variant Basic variantType
2. Variant Basic variant frequency (as quartiles?)
3. Variant Annotation molecularConsequence
4. Variant Annotation genomicRegion
5. Biosample sample collectionDate
6. Biosample sampleOriginDetail
7. Individual sex
8. Individual geographicOrigin
9. Individual diseases.ageOfOnset
10. Run platform

The options available for each field could appear as checkboxes allowing to select one or more of each (AND).

For this, what is necessary:

- Variant annotation from VCF (done)
- Harmonization of values (done)