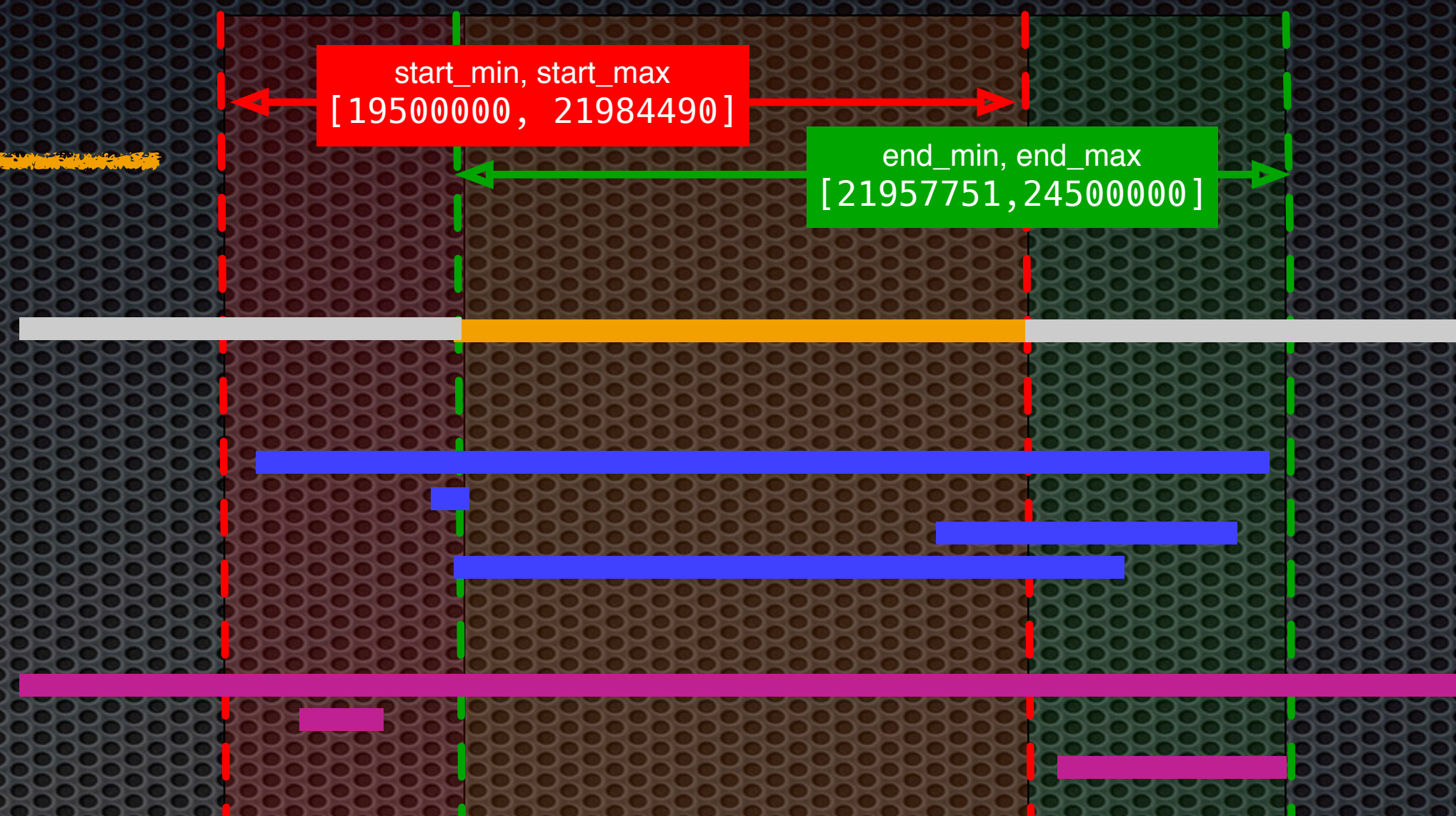```
{
    "allele_request" : {
        "$and" : [
            { "reference_name" : "9" },
            { "variant_type" : "DEL" },
            { "start" : { "$gte" : 19500000 } },   start_min
            { "start" : { "$lte" : 21984490 } },   start_max
            { "end" : { "$gte" : 21957751 } },   end_min
            { "end" : { "$lte" : 24500000 } }   end_max
        ]
    },
    "api_version" : "0.4",
    "beacon_id" : "org.progenetix:progenetix-beacon",
    "exists" : true,
    "info" : {
        "query_string" :
"dataset_id=arraymap&variants.reference_name=chr9&assembly_id=GRCh36&va
riants.variant_type=DEL&variants.start_max=19000000&variants.start_min=
21984490&variants.end_min=21900000&variants.end_max=25000000&biosamples
.bio_characteristics.ontology_terms.term_id=pgx:icdom:9440_3",
        "version" : "Beacon+ implementation based on a development branch
of the beacon-team project: https://github.com/ga4gh/beacon-team/pull/
94"
    },
    "url" : "http://progenetix.org/beacon/info/",
    "dataset_allele_responses" : [
        {
            "dataset_id" : "arraymap",
            "error" : null,
            "exists" : true,
            "external_url" : "http://arraymap.org",
            "sample_count" : 584,
            "call_count" : 3781,
            "variant_count" : 3244,
            "frequency" : 0.0094,
            "info" : {
                "description" : "The query was against database
\"arraymap_ga4gh\", variant collection \"variants_cnv_grch36\". 3781 /
59428 matched callsets for 3602919 variants. Out of 62105 biosamples in
the database, 2047 matched the biosample query; of those, 584 had the
variant.",
                "ontology_ids" : [
                    "ncit:C3058",
                    "pgx:icdom:9440_3",
                    "pgx:icdot:C71.9",
                    "pgx:icdot:C71.0"
                ]
            },
        }
```

start_min, start_max [19500000, 21984490]

end_min, end_max [21957751,24500000]

Match using query ranges "at least one base in interval affected"

Region of Interest, e.g. CDR of Gene (here: CDKN2A)

Example "focal" matches (overlap w/ size limit)

Mismatches
- too large
- end outside
- start outside

- Beacon+ **range queries** allow the definition of a genome region of interest, containing a specified variant (or other mappable feature)

- "fuzzy" matching of region ends is essential for features without base specific positions

- current Beacon implementation addresses CNV (<DUP>, <DEL>), as are specified in VCF && GA4GH variant schema