**Data Description**

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# **Syntax**

* For the attribute enclosed with double quotation marks, it must be named as shown.
* For the attribute not enclosed with double quotation marks, it can be named according to the user as the attribute would only be shown as a tooltip in the visualization.
* For the attribute shown in blue colour, it is an optional
* For the attribute shown in green colour, it can be multiple children

# **Gene**

## “gene” object structure

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| gene : JSON Object   |  | | --- | | “end” : Integer | | “symbol” : String | | “start” : Integer | | “chr” : String | | “id” : String | | “strand” : String | | “transcripts” : JSON Object   |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | | Transcript ID : JSON Object   |  | | --- | | “start” : Integer | | “end” : Integer | | “id” : String | | “exons” : Array   |  |  |  |  | | --- | --- | --- | --- | | 0 : Array Index, JSON Object   |  | | --- | | “start” : Integer | | “end” : Integer | | “id” : String | | | | | |

## “gene” attributes description

|  |  |
| --- | --- |
| **Attribute** | **Description** |
| “end” | End position of the gene |
| “symbol” | Gene Symbol |
| “start” | Start position of the gene |
| “chr” | Chromosome pairs |
| “id” | Gene ID |
| “strand” | Gene’s strand could be minus or positive |
| “transcripts” | Gene Transcripts which is a JSON object storing the attributes of the transcript. Each transcript represents a line in the visualization of gene plot |
| Transcript ID | Transcript ID e.g. ENSTXXXX |
| “start” | Start position of transcript |
| “end” | End position of a transcript |
| “id” | ID of transcript |
| “exons” | Array of JSON Object containing, end (end position of an exon), id (ID of an exon), start (start position of an exon) |
| “start” | Start position of exon |
| “end” | End position of exon |
| “id” | Exon ID |

# **eQTLs**

## “eqtls” object structure

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| eqtls : JSON Object   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | eQTLs studies : Array   |  |  |  |  |  | | --- | --- | --- | --- | --- | | 0 : Array Index, JSON Object   |  | | --- | | “fdr” : Float | | “p” : Float | | “pos” : Integer | | “snp” : String | | | |

## “eqtls” attribute description

|  |  |
| --- | --- |
| **Attribute** | **Description** |
| “fdr” | False Discovery Rate or the adjusted p value |
| “p” | Probability value of the association showing the strength of variation |
| “pos” | Position of SNP |
| “snp” | SNP ID |

# **SNPs**

## “snps” object structure

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| snps : JSON Object   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | SNP ID : JSON Object   |  | | --- | | “alt\_allele” : String | | “rsid” : String | | “pos” : Integer | | “chr” : String | | “maf” : Integer | | “ref\_allele” : String | | |

## “snps” attribute description

|  |  |
| --- | --- |
| **Attribute** | **Description** |
| SNP ID | SNP ID e.g. “chr19:54539554:A:G” |
| “alt\_allele” | The alternative allele |
| “rsid” | dbSNP ID |
| “pos” | Position of SNP |
| “chr” | Chromosome |
| “maf” | Minor allele frequency |
| “ref\_allele” | The reference allele |

# **LD**

## “ld” object structure

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ld : Array   |  |  |  |  | | --- | --- | --- | --- | | 0 : Array Index, Array   |  | | --- | | 0 : Array Index, String | | 1 : Array Index, String | | 2 : Array Index, Float | | |

## “ld” attribute description

|  |  |
| --- | --- |
| **Attribute** | **Description** |
| 0,1 (String) | SNPs ID |
| 2 (Float) | The r^2 distance between the two SNPs |

# **mQTLs**

## “mqtls” object structure

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| mqtls : Array   |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | | 0 : Array Index, JSON Object   |  | | --- | | “beta” : Float | | “chrom” : String | | “fdr” : Float | | “p\_value” : Float | | “probe” : String | | “probe\_position” : Integer | | “snp” : String | | “snp\_position” : Integer | | |

## “mqtls” attribute description

|  |  |
| --- | --- |
| **Attribute** | **Description** |
| “beta” | numerical number showing an effect size of methylation level of that particular SNP |
| “chrom” | Chromosome pair in human |
| “fdr” | false discovery rate where showing the probability of false positives (incorrectly reject the null hypothesis) in the significant results |
| “p\_value” | probability value where the null hypothesis is there is no methylation occurs while the alternative hypothesis is there is methylation occurs. |
| “probe” | Name of the probe |
| “probe\_position” | Position of the probe |
| “snp” | Name of the SNP |
| “snp\_position” | Position of the SNP |

# **Methylation**

## “methylation\_data” object structure

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| methylation\_data : JSON Object   |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | Methylation data sample : JSON Object   |  | | --- | | “description” : String | | “probes” : JSON Object   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | Probes ID : JSON Object   |  | | --- | | “average\_beta” : Float | | “beta” : Array   |  | | --- | | 0 : Array Index, Float | | | “chromosome” : String | | “position” : Integer | | “samples” : Array   |  | | --- | | 0 : Array Index, String | | | | | |

## “methylation\_data” attribute description

|  |  |
| --- | --- |
| **Attribute** | **Description** |
| Methylation data sample | JSON Object contains ‘description’ and JSON Object ‘probes’ as keys e.g. PMBC 112 Samples |
| “description” | String contains a description of the sample |
| “probes” | JSON object contains JSON Objects where probe name is the key |
| Probes ID | Probes ID e.g. cg01718139 |
| “average Beta” | Average value from ‘beta’ attribute |
| “beta” | An array of numerical value showing methylation intensity which are corresponding to the ‘samples’ attribute |
| “chromosome” | chromosome pairs in human |
| “position” | position of methylation occurs |
| “samples” | an array of samples’ name which corresponding to ‘beta’ attribute |