

General

All the configuration settings are in [config.js](#) and [tools.js](#) file.

config.js

CellBase Configuration

The host and version of CellBase are configured in the section below

CellBase

```
var cellbase = {
  hosts: ["bioinfodev.hpc.cam.ac.uk/cellbase-4.5.0-beta"],
  version: "v4"
};
```

OpenCGA Configuration

The below section in [config.js](#) allows to do the following:

- OpenCGA Host and version can be configured.
- There is a section called projects which allows to browse public projects without any login.
- Cookies section is useful when the application expects users to login and their cookie names that store the actual user name and session ID can be configured here.

OpenCGA

```
var opencga = {
  host: "bioinfodev.hpc.cam.ac.uk/opencga-1.0.0-rc3",
  version: "v1",
  projects: [
    {
      name: "Project A",
      alias: "proj_a",
      studies : [
        {
          name: "Study 1",
          alias: "std_1"
        }
      ]
    }
  ],
  cookies: {
    userName: "iva_userId",
    sessionId: "iva_sid"
  }
};
```

Visual Settings

Consequence Type, Population frequency and Protein Substitution Scores which can be found in [config.js](#) are enabled to have colors in web application. They can be modified to your needs.

Table of Contents:

- [config.js](#)
 - [CellBase Configuration](#)
 - [OpenCGA Configuration](#)
 - [Visual Settings](#)
- [tools.js](#)

Consequence Type

```
var consequenceTypes = {
  // This is the impact color. It allows to customise both the impact
  categories and desired colors
  color: {
    high: "red",
    moderate: "orange",
    low: "blue",
    modifier: "green"
  },
  /* 'Title' is optional. if there is no title provided then 'name' is
  going to be used.
  There are two more optional properties - 'checked' and 'color'. They
  can be set to display them default in web application.
  Similarly 'description' is optional as well.
  */
  categories: [
    {
      id: "",
      name: "",
      title: "Intergenic",
      description: "",
      terms: [
        {
          id: "SO:0001631",
          name: "upstream_gene_variant",
          title: "upstream gene variant",
          description: "A sequence variant located 5' of a gene",
          impact: "modifier"
        }
      ],
      .
      .
      .
    },
    .
    .
  ]
};
```

Population Frequency

```
var populationFrequencies = {
  color: {
    veryRare: "red",
    rare: "yellow",
    average: "orange",
    common: "blue"
  },
  studies: [
    {
      id: "1kG_phase3",
      title: "1000 Genomes",
      populations: [
        {
          id: "ALL",
          title: "All populations [ALL]",
          active: true
        },
        {
          id: "EUR",
          title: "European [EUR]"
        },
        .
        .
        .
      ]
    },
    :
    .
  ]
};
```

Protein Substitution Score

```
var proteinSubstitutionScores = {
  // This is to show the predictions in respective colors
  sift: {
    deleterious: "red",
    tolerated: "green"
  },
  polyphen: {
    probablyDamaging: "red",
    possiblyDamaging: "orange",
    benign: "green",
    unknown: "black"
  }
};
```

tools.js