



## **LEARN PYTHON & R FOR BIOINFORMATICS**

### **Introduction:**

The Genome Browser at the University of California Santa Cruz (UCSC) provides a uniform graphical interface to sequences, features, and annotations of genomes across a wide spectrum of organisms, from yeast to humans. UCSC is a well known genome browser which is publicly available for the researchers around the globe. It provides Web-based tools for quickly displaying a requested portion of a genome at any scale, accompanied by a series of aligned annotations. If you're intended to work on any organism, e.g., SARS-CoV-2 (a strain of Corona Virus), UCSC provides you with a range of tools according to your research parameters, you can access the data available on UCSC and utilize it for your research without any copyright issues. UCSC researchers are heavily conducting their research on genomics that is why we're exploring UCSC rather than other Genome Browsers like NCBI and Ensembl.

## Steps:

- Enter UCSC Genome Browser on Google search bar and open first link with address [www.genome.ucsc.edu](http://www.genome.ucsc.edu).

[it will open up the homepage of UCSC Genome Browser, it provides us with various tools so that we can select any of them according to our query or research requirements].

- From '*Our Tools*' option click on Genome Browser.

[It might ask you to select a mirror-site according to your continent, like in our case we'll select the link with asian-site, so that it does not create any lapse in our results].

- On the left side of the resulting page it shows '*Browse/Select Specie*' option where it shows:

- The Phylogenetic tree of evolutionary basis of organisms at the bottom.
- At the top it gives the names of some popular species or we can say some model organisms.
- And in the middle it gives a search box, where we can search any specie of our interest even with it's common name.

- Now enter the name of your specie of interest in the search box present at the middle or you can select it from the phylogenetic tree of evolutionary basis.

- It will give you information about the specie you selected on the right side of the page under 'Find Position' domain, as

- On the top it shows '*SARS-CoV-2 assembly*' or the Genome assembly of the specie you've selected, it basically shows the assembly date of that particular genome or the year when that particular genome got available on public domain.

- Then there's a '*position/search term*' box, where you can enter the disease name or gene name or gene position related to that particular specie and it will find that gene/disease in the entire genome.
- Then at the bottom, it shows the the name of the specie along with the assembly ID where it provides us further details related to the genome assembly of our specie, like
  - ◆ UCSC Genome Browser assembly ID
  - ◆ Assembly provider ID
  - ◆ Assembly date
  - ◆ Accession ID
  - ◆ NCBI Genome ID
  - ◆ NCBI Assembly ID
  - ◆ BioProject ID, etc.

## Summary:

In this introductory video we came to know how we can retrieve any genomic information about the specie of our interest from UCSC Genome Browser. Since Corona Virus is a burning issue now a days, we focused our interest mainly on SARS-CoV-2 genome, so that we don't have to go through different tools and literature to conduct our research, rather we can simply go to UCSC Genome Browser to get information about our particular genome.

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