

Introduction

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Overview

This installation guide provides the necessary instructions to install the Non-Coding Variation Browser package. The subsection [dependencies](#) specify the technical requirements for this website. To begin working with this guide please have your current directory be within the cloned repository file. (If you type `ls` or `dir` you should see a file called `manage.py`, if not please navigate to the appropriate directory)

Dependencies

At least three gigabytes of space.

python 2.7.X - needs to have python 2.7

tqdm - downloaded via pip

pandas - download via pip

django - download via pip

sqlite3 - should already be installed

gzip - should already be installed

Install Django

The quickest way to install Django is to use python's package manager pip. If you haven't heard of pip or pip is not installed, please refer to this following source for information about installing pip: <https://pip.pypa.io/en/stable/installing/#do-i-need-to-install-pip>. After pip is installed, type the following command to install Django:

OS-X or Linux Systems

```
sudo pip install django
```

Windows Systems

```
pip install django
```

If everything goes according to plan, Django should be successfully installed. You can test the installation by typing python into the console. After the python interpreter has been open type: import django to import the Django package. If an error doesn't occur then the package has been successfully installed. After install Django, you can refer to [Set Up the Django Server](#) for information about setting up the server. At this point you can close the python console by typing in exit() and pressing enter. Before moving onto the next section please note that If any other dependency modules are missing you can use this method to install them. Just replace django with the desired module to install.//

Set Up the Django Server

In this section we will be setting up the django server and database. To begin type the following command into the console line: python manage.py makemigrations. This command tells django to create a database schema, that specifies what kind of information each database table will hold. After creating the schema file, type this command to install it: python manage.py migrate. Once this command executes successfully, the database has been successfully installed and you can refer to the [Loading Database Data](#) section to load the data.

Loading the Data Into the Database

Use this link to download the track, LD and other necessary information: [Download Here](#). Once you downloaded the files, please put the file within the same folder as the cloned repository and unzip the data. Next step utilizes the production_database_inserter.py file to decode/insert everything. Before executing the file, execute in this command: python production_database_inserter.py -h. This will show you the arguments this program uses for execution. Using the appropriate arguments, the program will insert all the data into the database. Once the program finishes execution, the final step will be to start the server and use it. Refer to the [Running Django Server](#) section for the last step.

Running Django Server

After the insertion has finished the next step is to actually run the server. To do that open a console and then type the following command: python manage.py runserver. If everything has gone according to plan you should see the following output:

```
Performing system checks...
```

```
System check identified no issues (0 silenced).  
April 18, 2016 - 15:51:15  
Django version 1.9.2, using settings 'gwas_seq.settings'  
Starting development server at http://127.0.0.1:8000/  
Quit the server with CONTROL-C.
```

Once you see this output open a browser and type in the url bar: local-host:8000/NCVB. If successful you will see a welcome screen on your browser that contains a slider, trait selector and a table for selected regions. this is where you select the intervals that you want to take a look at. The next screen that shows is the actual region view, which contains the SNPS within that regions overlapping the CHIP-S/DNAse data. At this point everything should be straight forward to play around with.