

Operating Manual

Made by:

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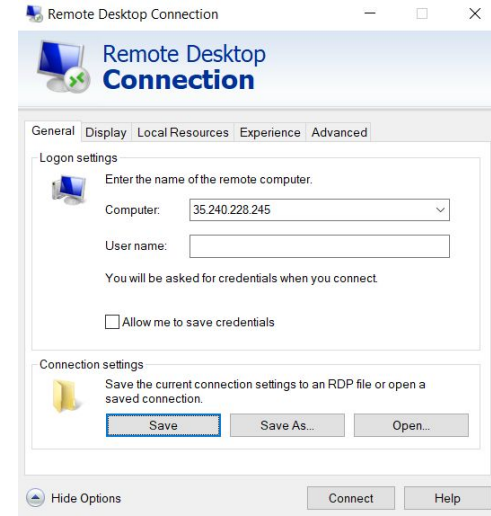
Dikshant Oswal

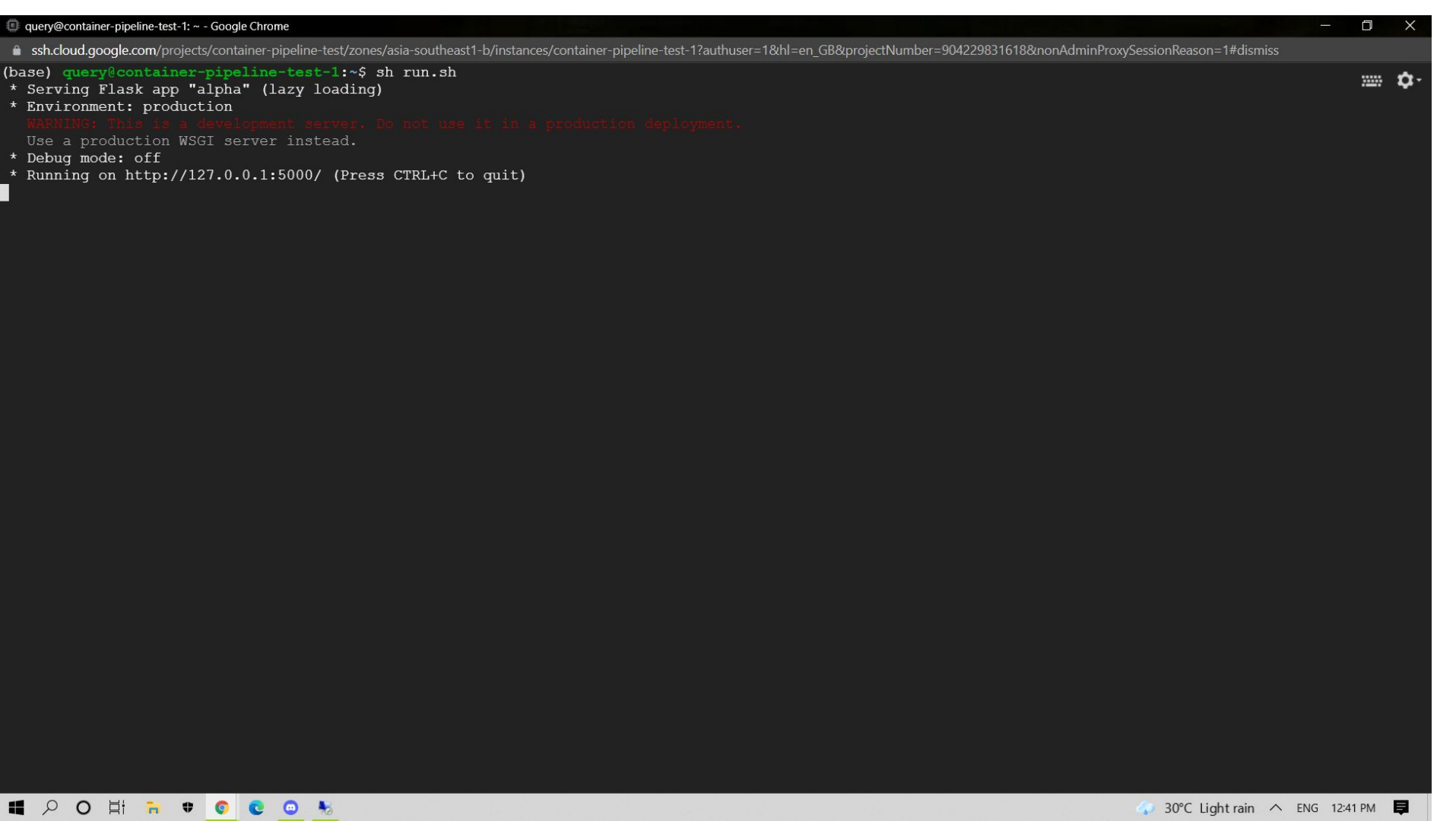
Shivani Dangi

Instructions to start the VM

- Start the VM using GCP.
- Copy the **External IP** address.
- Open remote desktop connection and type the address with the login credentials for the virtual machine.
- You should now be connected to the Virtual Machine.
- Use only **Google Chrome** browser to operate this software.

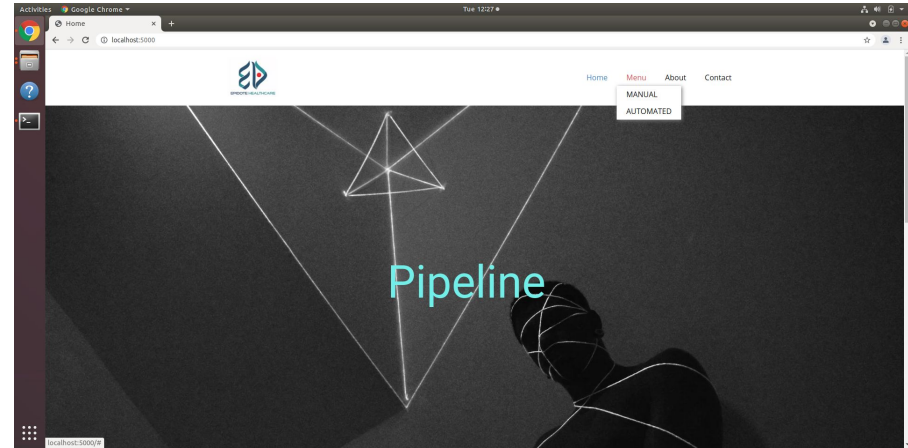
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How to operate the software

- Enter the query '**sh run.sh**' inside the GCP terminal.
- After the software opens up, there are two modes to operate the software named Manual and Automated mode.
- The manual mode can be used to operate each Bio-container individually.
- The automate mode can be used to operate the pipeline containing Hisat2, and Stringtie containers.
- There is a default query prebuilt, with option to add parameters in the provided text-box.



How to add input files and get the Output files

- There is no need to explicitly add files for the automation pipeline. As per the naming nomenclature, just add the **folder name or project name** to the project name text box.
- The folder containing the files should be stored at location
‘/home/query/’ compulsorily.
- If the folder is not present at this location, files will not be found.
- The folder must contain a **‘.fna’** and a **‘.fastq’** file.
- The output files will be stored in a new folder named **‘Output’** created inside the input files folder itself (No need to create the Output folder, it will be created by the pipeline).
- For **manual mode** execution, you need to **type entire query** as per the requirements of the tool. **No folder structure** is created in this instance.

