**README**

The repository includes three Jupyter notebooks:

* Neural\_Cell\_Analysis.ipynb
* DENV\_Hepatoma Analysis.ipynb
* PPI\_Analysis.ipynb

**What each notebook does**

* **Neural\_Cell\_Analysis**: Preprocessing of RNA-seq data and comparative transcriptomic analysis of ZIKV- and DENV-infected human neural progenitor cells (hNPC).
* **DENV\_Hepatoma Analysis**: Preprocessing of RNA-seq data and comparative transcriptomic analysis of DENV-infected human hepatoma cells.
* **PPI\_Analysis**: Preprocessing and integration of virus–host protein–protein interaction (PPI) datasets to generate Cytoscape-ready files (tested with Cytoscape 3.10.3).

**Environment**

* **Python:** 3.12 (Jupyter)