Supplemental Tutorial: cellxgene VIP unleashes full power of interactive visualization, plotting and analysis of scRNA-seq data in the scale of millions of cells

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Supplementary Materials: cellxgene VIP unleashes full power of interactive visualization, plotting and analysis of scRNA-seq data in the scale of millions of cells

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1 Getting started with cellxgene VIP

This is a cellxgene VIP tutorial book written in **Markdown**.

1.1 Why use cellxgene VIP?

To meet the growing demands from scientists to effectively extract deep insights from single cell RNA-seq datasets, we developed cellxgene VIP, a frontend interactive visualization plugin to cellxgene framework, which directly interacts with in-memory data to generate a comprehensive set of plots in high resolution, perform advanced analysis, and make data downloadable for further analysis. It makes large scale scRNA-seq data visualization and analysis more accessible and reproducible with the potential to become an ecosystem for the scientific community to contribute even more modules to the Swiss knife of scRNA-seq data exploration tool.

1.2 Getting Set up

1.2.1 Execute anaconda

```
bash ~/Downloads/Anaconda3-2020.02-Linux-x86_64.sh
```

If anaconda is not installed on server, you can install it following anaconda documentation (https://docs.anaconda.com/anaconda/install/linux/) ### Create and enable conda environment

```
# clone repo from cellxgene VIP github
git clone https://github.com/interactivereport/cellxgene_VIP.git
cd cellxgene_VIP

# conda environment
source <path to Anaconda3>/etc/profile.d/conda.sh (Default:
 ↪  /opt/anaconda3/etc/profile.d/conda.sh)
conda config --set channel_priority flexible
conda env create -n <env name, such as: VIP> -f VIP.yml (system-wide R) or
 ↪  VIP_conda_R.yml (local R under conda, no root privilege needed)
```

Activate conda environment

```
conda activate <env name, such as: VIP>
```

or

```
source activate <env name>
```

1.2.2 Cellxgene installation

Install cellxgene by running config.sh in "cellxgene_VIP" directory

```
./config.sh
```

1.2.3 R dependencies

Install all required R packages on linux:

```
export LIBARROW_MINIMAL=false
#  ensure that the right instance of R is used. e.g. system-wide: /bin/R or /usr/bin/R
 ↪  ; local R under conda: ~/.conda/envs/VIP_conda_R/bin/R
which R

R -q -e 'if(!require(devtools)) install.packages("devtools",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(Cairo)) devtools::install_version("Cairo",version="1.5-12",repos
 ↪  = "http://cran.us.r-project.org")'
R -q -e 'if(!require(foreign))
 ↪  devtools::install_version("foreign",version="0.8-76",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(ggpubr)) devtools::install_version("ggpubr",version="0.3.0",repos
 ↪  = "http://cran.us.r-project.org")'
R -q -e 'if(!require(ggrastr))
 ↪  devtools::install_version("ggrastr",version="0.1.9",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(arrow)) devtools::install_version("arrow",version="2.0.0",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(Seurat)) devtools::install_version("Seurat",version="3.2.3",repos
 ↪  = "http://cran.us.r-project.org")'
R -q -e 'if(!require(rmarkdown))
 ↪  devtools::install_version("rmarkdown",version="2.5",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(tidyverse))
 ↪  devtools::install_version("tidyverse",version="1.3.0",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(viridis))
 ↪  devtools::install_version("viridis",version="0.5.1",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(BiocManager))
 ↪  devtools::install_version("BiocManager",version="1.30.10",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(fgsea)) BiocManager::install("fgsea")'

# These should be already installed as dependencies of above packages
R -q -e 'if(!require(dbplyr)) devtools::install_version("dbplyr",version="1.0.2",repos
 ↪  = "http://cran.us.r-project.org")'
```

```
R -q -e 'if(!require(RColorBrewer))
 ↪  devtools::install_version("RColorBrewer",version="1.1-2",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(glue)) devtools::install_version("glue",version="1.4.2",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(gridExtra))
 ↪  devtools::install_version("gridExtra",version="2.3",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(ggrepel))
 ↪  devtools::install_version("ggrepel",version="0.8.2",repos =
 ↪  "http://cran.us.r-project.org")'
R -q -e 'if(!require(MASS)) devtools::install_version("MASS",version="7.3-51.6",repos
 ↪  = "http://cran.us.r-project.org")'
R -q -e 'if(!require(data.table))
 ↪  devtools::install_version("data.table",version="1.13.0",repos =
 ↪  "http://cran.us.r-project.org")'
```

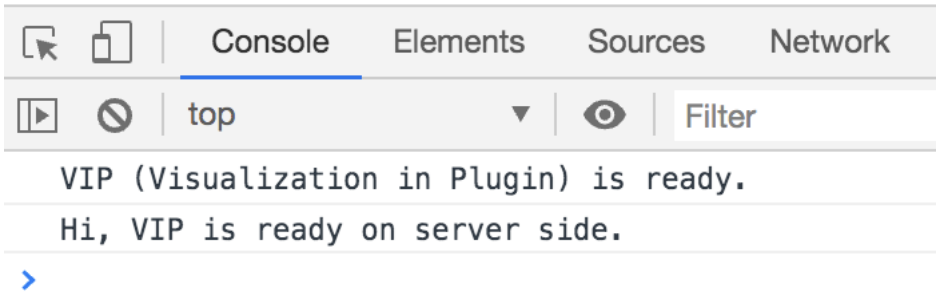
1.2.4 Run cellxgene by h5ad file

You can aslo run cellxgene by specifying a h5ad file, which stores scRNA-seq data along with a host and a port. Use 'ps' to find used ports to spare. Please see https://chanzuckerberg.github.io/cellxgene/posts/launch for details

```
ps -ef | grep cellxgene
Rscript -e 'reticulate::py_config()'
# Run the following command if the output of the above command doesn't point to the
 ↪  Python in your env.
export RETICULATE_PYTHON=`which python`
cellxgene launch --host <xxx> --port <xxx> --disable-annotations --verbose <h5ad file>
```

1.2.5 Cellxgene on web browser

chrome is preferred, version 87.0.4280.88 or 87.0.4280.141 is used. Users can access **http(s)://host:port**. Following screenshot is what you should be able to see in console of chrome developer tools.



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