PCDLPicasso

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Plasma Cell Disorder Library - Picasso (PCDLPicasso)

This ShinyApp will help users search for available lab sequencing datasets and clinical data. Explore available lab seq datasets and count patient samples per clinical data type

Plasma Cell Disorder Library - Picasso was built on R version 4.4.1 (2024-06-15) – "**Race for Your Life**" This means you need to install R version >= 4.4.1

A. Introduction

The lab has so many sequencing datasets. So, we need a tool to navigate the datasets and count the number of patient samples per disease type or sequencing type.

$List of Morgan - Davies lab datasets$ - **These names will be revised by unique names.**

No.1 UK myeloma (463) exome data - Patrick
No.2 MGP data exomes and expression (1273) - Patrick
No.3 GEP datasets Little rock (?) - Patrick
No.4 SMM sequential WGS (Eileen)
No.5 WGS Ancestry/ncPaper (307-294) - Patrick
No.6 WGS next set - Sanghoon
No.7 COMMPASS low pass WGS (794?)
No.8 COMMPASS exomes
No.9 COMMPASS expression
No.10 scATAC, scRNAseq Waldenstrom (13) Dylan
No.11 WGS Waldenstrom - Dylan
No.12 MM cell line ATAC, HiC - Patrick
No.13 PDX mice HiC, RNAseq, - Patrick
No.14 scATAC, scRNA, WGS (MM, SMM, MGUS) - Di
No.15 micropinocytosis resistant cells RNA - Dylan

No.16 NSD2 dTAG cut and tag; SLAMseq - Sanxiong
No.17 Cody structural paper - Patrick
No.18 Chromosome 1 paper Eileen - Patrick
No.19 dbMP - Patrick
No.20 External Datasets – Patrick
No.21 scDatasets – Dylan
No.22 Foundation 1 data/Caleb paper

B. Basic requirements

Step1. Download R and Rstudio, and install them.

You can just Google or Youtube for "R download and install" and "Rstudio download" to complete this step. It is not that difficult. Youtube clip for Mac

If you have some experience already, you can go install R from CRAN

You can install a user-friendly interface, R-Studio, from rstudio.com

Step2. Start Rstudio

What does 'start Rstudio' mean? Visit the Youtube lecture I introduced in Step1.

Step3. In the R console, install necessary R packages first.

If you have some experience already, just go below the code line. Just copy the lines, paste them to console, and hit enter key.

If you don't much experience yet; What are 'R console' and 'R package'? Try to what this 3min Youtube lecture Or, you can find more in Youtube by searching "How to install R packages?"

```
utils :: install.packages ( "pacman", repos= "http://cran.us.r-project.org" )
```

```
library  (pacman)

### Install and load multiple packages at a time.
### This will take 10~15 min if you are installing any packages for the first time.
utils :: install.packages ( c( "data.table" , "BiocManager" , "dplyr" , "stringr" , "tidyverse" ,
  "EnvStats" , "ggbeeswarm" , "htmltools" , "ggplot2" , "ggpubr" , "purrr" , "rstatix" , "shiny" ,
  "plotrix" , "shinyWidgets" ),  repos= "http://cran.us.r-project.org" )
```

```
pacman:  p_load (devtools,usethis)
```

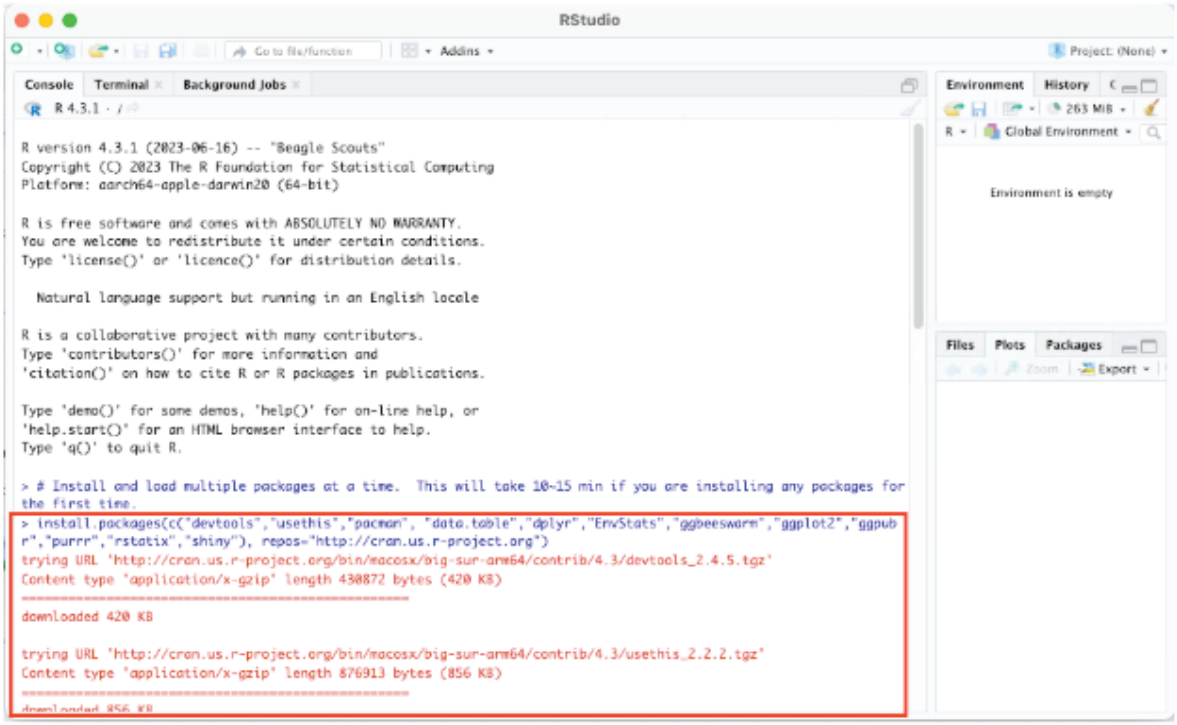

Figure 1: Installing R packages

C. Install PCDLPicasso R package

Step4. Install PCDLPicasso R package and load it

```
### Install PCDLPicasso R package
install_github("Sanghoon-Lee_NYULH/PCDLPicasso")
```

```
Using GitHub PAT from the git credential store.
```

```
Skipping install of 'PCDLPicasso' from a github remote, the SHA1 (44a3f117) has not changed s
  Use `force = TRUE` to force installation
```

```
### Load the R package. Note you DON'T need quotation.
### The package name is PCDLPicasso, not Sanghoon-Lee_NYULH/PCDLPicasso
library(PCDLPicasso)
```

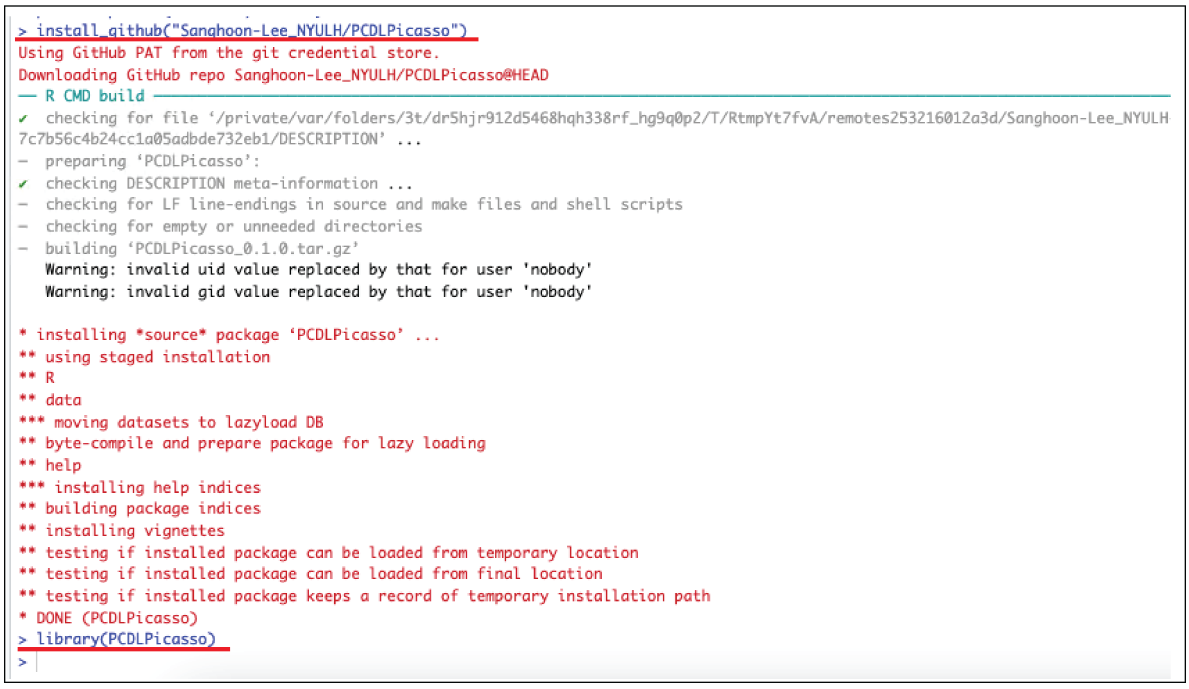

Figure 2: Installing PCDLPicasso packages

D. Play with PCDLPicasso

Step5. Run ShinyApp and Play

In R console, run the command below.

```
shiny::shinyApp(ui=PCDD_UserInterface, server=PCDD_Server)
```

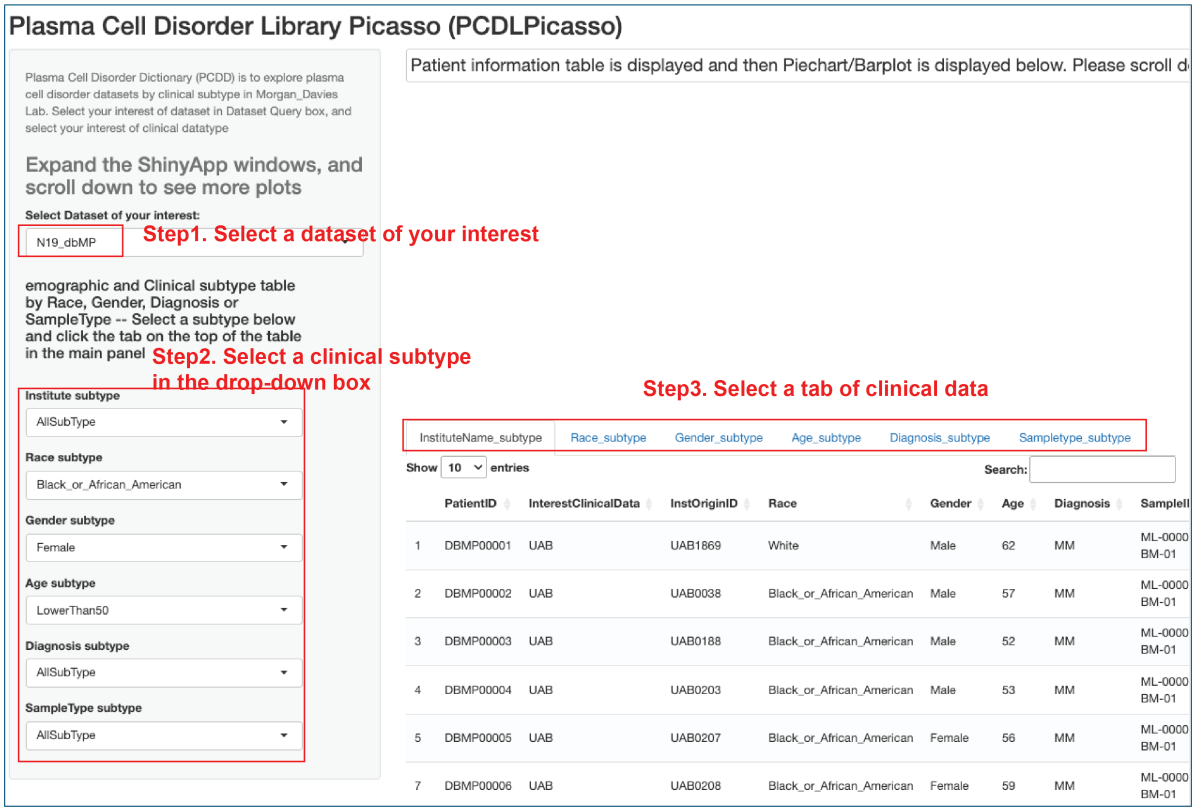

Figure 3: PCDLPicasso ShinyApp - ClinicalData Tables

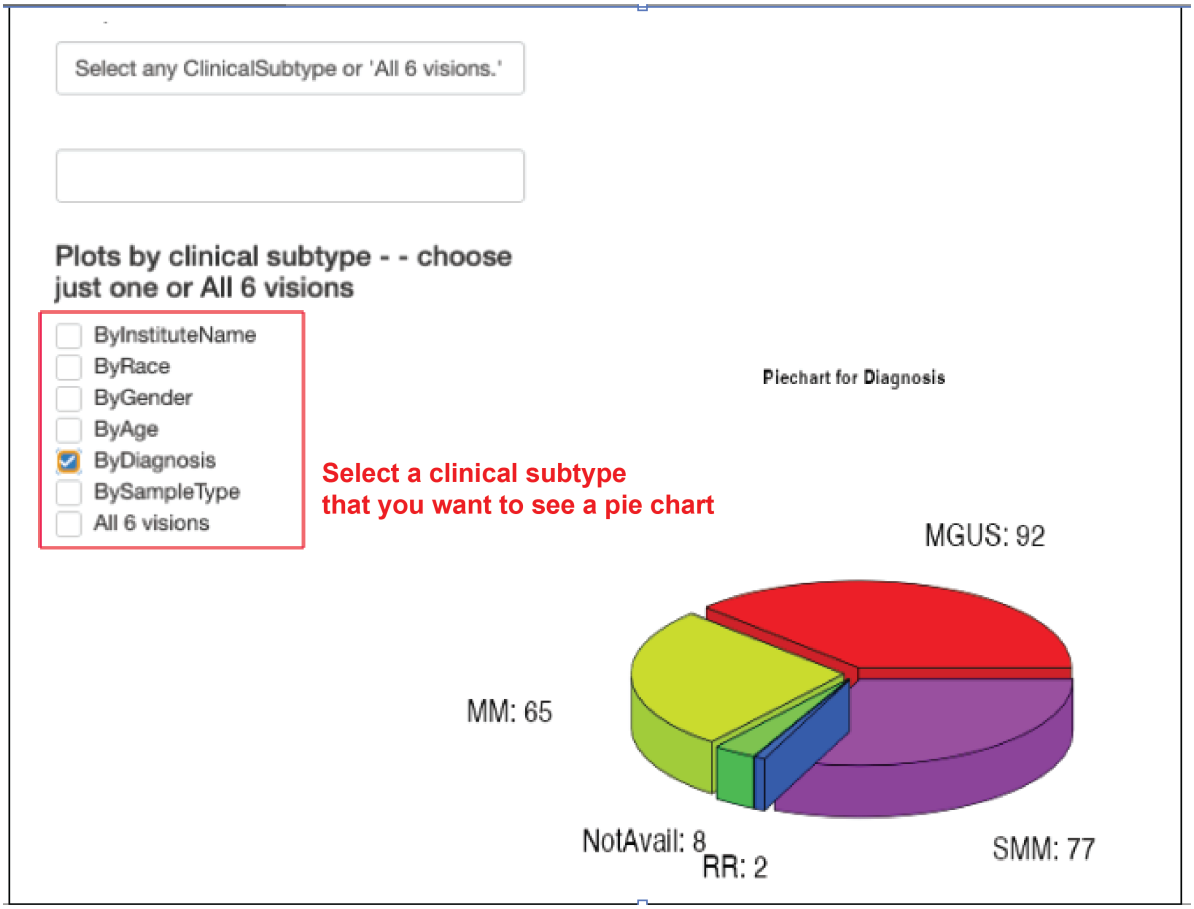

Figure 4: PCDLPicasso ShinyApp - ClinicalData Piechart