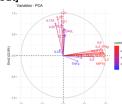
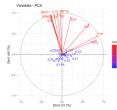
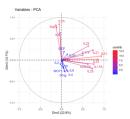
# # ELF\_Cytokine Principal Component Analysis # Apr 23, 2024 R (v.4.3.2) PCA by Teiji Sawa, MD, PhD # Kyoto Prefectural University of Medicine, Japan # For the analyses of the following publication: # Authors: Sazuki Sudo, others & Teiji Sawa. # Title: Case study observational research: inflammatory # cytokines in the bronchial epithelial lining fluid of COVID-19 # patients with acute hypoxemic respiratory failure. # Journal: Critical Care volume 28: 134, 2024. # DOI: doi:10.1186/s13054-024-04921-3 #-[R Code #1]install.packages("FactoMineR") install.packages("factoextra") library(ggplot2) library(GGally) library(FactoMineR) library(factoextra) library(tidyverse) #-[END]-#-[R Code #2]--data1 <- read\_csv("pMOL\_ELF4\_r25\_p27\_20240301\_PCA2.csv", show\_col\_types = FALSE) data2 <-read\_csv("pMOL\_Plasma4\_r25\_p27\_20240301\_PCA2.csv", show\_col\_types = FALSE) fviz\_screeplot(pca\_d1, addlabels =TRUE, ylim =c(0, 50)) #-[END]------[out] #-[R Code #5]fviz\_pca\_var(pca\_d1,axes= c(1,2), col.var = "contrib", repel =TRUE) #-[END]------[out]

# ELF\_Cytokine\_Analysis PCA, Apr 23, 2024. R (v.4.3.2)

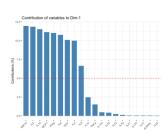
# #-[END]-[out]

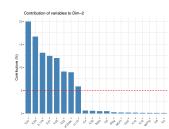


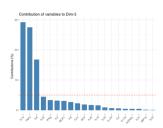


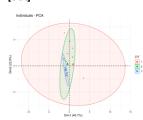


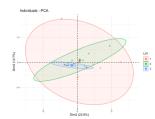
### [out]

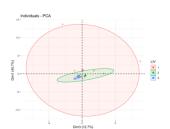






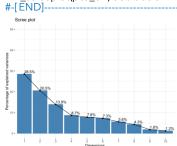






#### #-[R Code #9]-

fviz\_screeplot(pca\_d2, addlabels =TRUE, ylim =c(0, 50)) #-[END]-----

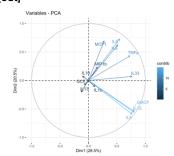


### [out]

#### #-[R Code #10]--

fviz\_pca\_var(pca\_d2,axes= c(1,2), col.var = "contrib", repel =TRUE)

#### [out]

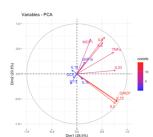


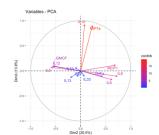
#### #-[R Code #11]-

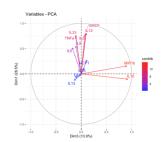
fviz\_pca\_var(pca\_d2, axes= c(1,2), col.var ="contrib", repel =TRUE) + scale\_color\_gradient2(low="white", mid="blue",

high="red", midpoint=0.6)
fviz\_pca\_var(pca\_d2, axes= c(2,3), col.var = "contrib", repel =TRUE) + scale\_color\_gradient2(low="white", mid="blue", high="red", midpoint=0.6)

#### [out]



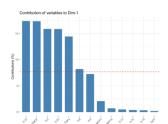


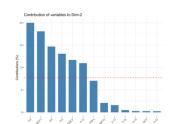


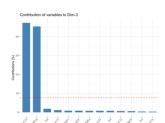
#### #-[R Code #12]-

#-[K-Code #12]
fviz\_contrib(pca\_d2, choice = "var", axes = 1)
fviz\_contrib(pca\_d2, choice = "var", axes = 2)
fviz\_contrib(pca\_d2, choice = "var", axes = 3)
#-[END]

[out]

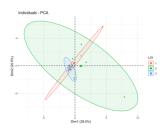


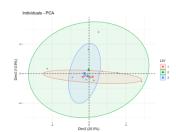


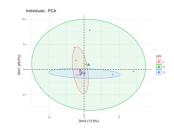


### #-[R Code #13]---

### [out]

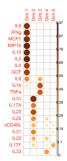






```
#-[R Code #14]-
library(corrplot)
corrplot 0.92 loaded
#-[END]---
#-[R Code #15]--
var1 <- get_pca_var(pca_d1)
#-[END]-----
[out]
#-[R Code #17]-----var1$cos2 %>% round(4)
#-[END]-----
[out]
             Dim.1 Dim.2 Dim.3 Dim.4 Dim.5 0.8750 0.0179 0.0661 0.0051 0.0056 0.8956 0.0075 0.0829 0.0030 0.0001
IL6
IFNg
MCP1
             0.8956 0.0075 0.0829 0.0030 0.0001
0.9046 0.0049 0.0759 0.0017 0.0022
0.9718 0.0014 0.0022 0.0014 0.0160
0.9362 0.0019 0.0388 0.0025 0.0150
0.9634 0.0010 0.0129 0.0003 0.0138
0.8124 0.0240 0.0783 0.0001 0.0448
0.8201 0.0039 0.0458 0.0048 0.0001
MIP1b
IL10
IL2
IL4
GCF
             0.8201 0.0039 0.0458 0.0048 0.0035
0.5395 0.0011 0.4235 0.0185 0.0035
0.1986 0.0033 0.7375 0.0483 0.0035
0.1210 0.0181 0.6948 0.1233 0.0061
0.0016 0.9055 0.0089 0.0072 0.0380
0.0362 0.5964 0.0092 0.1284 0.0575
0.0171 0.7562 0.0004 0.0307 0.1268
IL8
IL1b
TNFa
IL31
IL17A
IL23
IL22
IL17F
IL33
             0.0001 0.4101 0.1111 0.3238 0.0056
0.0016 0.2636 0.0148 0.1539 0.4360
0.0073 0.0220 0.0213 0.4929 0.0001
#-[R Code #18]----var1$cos2 %>% corrplot(is.corr = FALSE)
#-[END]-
[out]
#-[R Code #19]---
var2 <- get_pca_var(pca_d2)
#-[END]-----
```

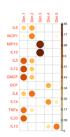
#### [out]



#-[R Code #21]-----var2\$cos2 %>% round(4) #-[END]-----

#### [out]

[out]



#### ELF\_Cytokine\_統計解析 PCA, Apr 23, 2024 Python 3.18

```
#-[Python Code #1]---
from sklearn.preprocessing import StandardScaler
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from matplotlib.colors import ListedColormap
#pip install pca
#-[END]-
#-[Python Code #2]------data_ELF_all = pd.read_csv('Data5_ELF_PCA_20240426_selected.csv') data_plasma_all = pd.read_csv('Data6_Plasma_PCA_20240426_selected.csv')
#-[Python Code #3]-
data_all_ELF = data_all[data_all.source=='elf']
data_all_plasma = data_all[data_all.source=='plasma']
data_ELF = data_all_ELF.iloc[:,3:23]
data_plasma = data_all_plasma.iloc[:,3:16]
data_LIV = data_all.iloc[0:27,2]
#-[END]--
#-[Python Code #5]--
scaler1 = StandardScaler(with_mean=True, with_std=True) scaler2 = StandardScaler(with_mean=True, with_std=True) ELF_std = scaler1.fit_transform(ELF) plasma_std = scaler2.fit_transform(plasma) #-[END]
#-[Python Code #6]-
#-[END]---
#-[Python Code #7]-
from pca import pca
model = pca(normalize = True)
#-[END]-----
#-[Python Code #8]-
from pca import pca
# Initialize
model2 = pca(normalize = True)
#-[END]--
row_labels=LIV_group)
#-[END]--
#-[Python Code #10]--
# Fit transform and include the column labels and row labels
results_plasma = model2.fit_transform(plasma_std, col_labels=cytokines_plasma, \
row_labels=LIV_group)
#-[END]--
#-[Python Code #11]-
'color_strong': 'red', 'color_weak': 'blue'}, s=500, cmap="rainbow", density= True)
ax.set_xlim(-5, 5)
ax.set_ylim(-5, 5)
ax.set_zlim(-5, 5)
```

```
ax.legend(loc=1)
plt.savefig('Fig1_3D_ELF.svg')
plt.savefig('Fig1_3D_ELF.png')
plt.show()
#-[END]------
```

#### [out]

