# Python for Data Analysis 資料視覺化

講者:楊翔斌

n07061033@mail.ncku.edu.tw

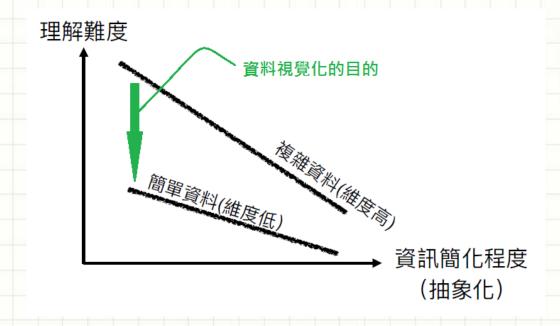
大綱

1. 前言

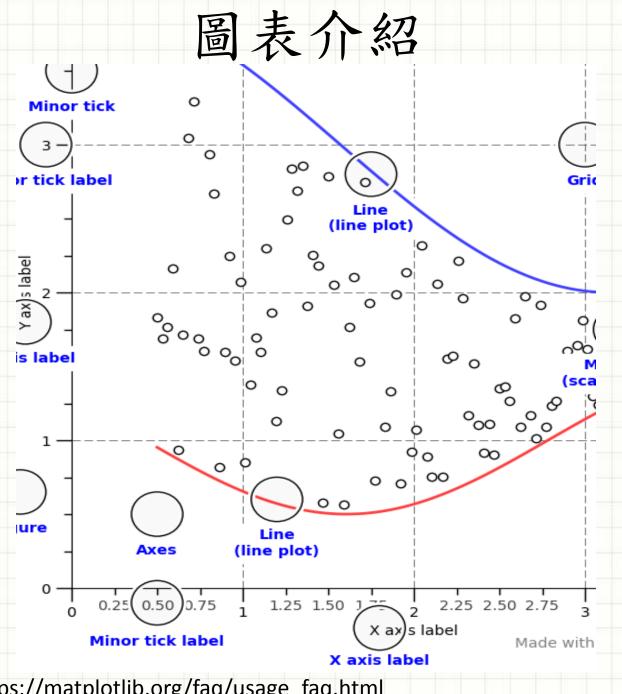
2. 圖表介紹

# 前言

# 文不如表表不如圖



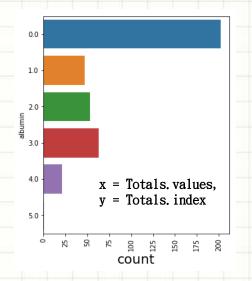
出處:https://www.slideshare.net/tw\_dsconf/ss-60041639

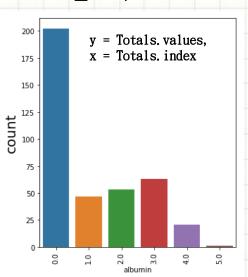


barplot:沿用腎臟病數據

Code:

import pandas as pd import matplotlib.pyplot as plt import seaborn as sns plt.figure(figsize=(5,6))#定義圖大小 Totals=datal\_new["albumin"].value\_counts()#計算albumin各類別的量 sns.barplot(y = Totals.values, x = Totals.index)#繪製barplot plt.xticks(rotation=90)#可調整tick的角度 plt.ylabel("count", size=20)#y軸名稱及字體大小 plt.xlabel("albumin", size=10)#x軸名稱及字體大小 法2:sns.countplot(x="albumin", data=datal\_new)

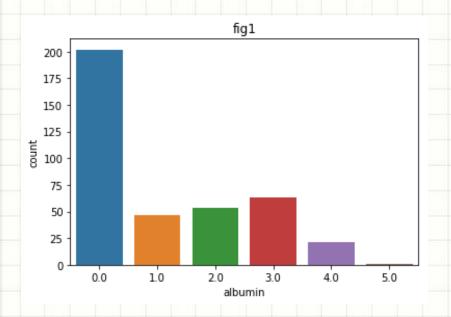


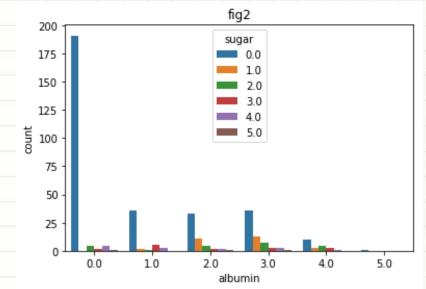


countplot:

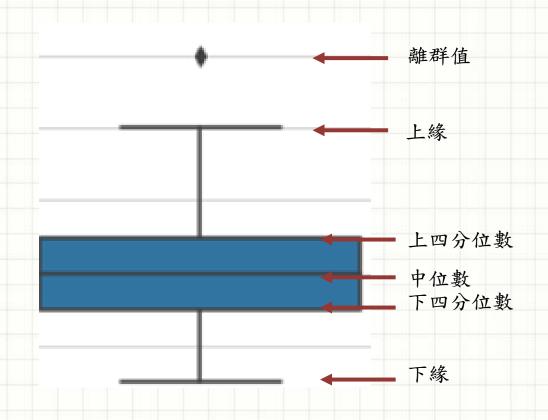
Code:

sns.countplot(x="albumin",data=datal\_new)#依照albumin計數作圖,如figlsns.countplot(x="albumin",hue="sugar",data=datal\_new)
#barplot 畫好後再根據sugar做分類



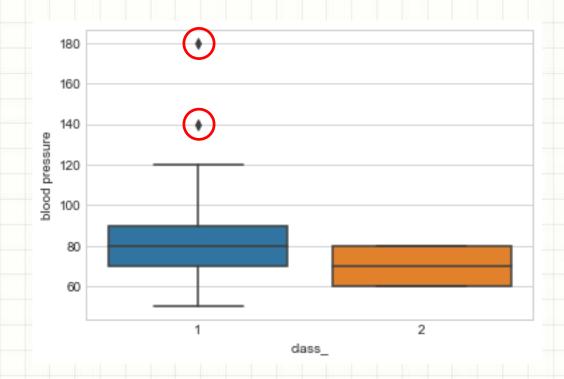


## 



boxplot:顯示一組數據之分散情況,可用來尋找離群值 Code:

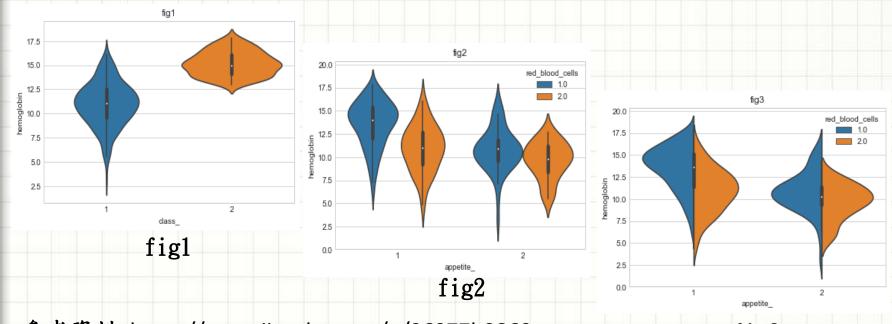
sns.boxplot(x="class\_",y="blood pressure",data=datal\_new) #依照class分類,將blood pressure數據畫出分佈圖



violinplot:定量數據在一個維度分类变量的多个层次上的分布

#### Code:

sns.violinplot(x="class\_",y="hemoglobin",data=datal\_new)#如figl sns.violinplot(x="appetite\_",y="hemoglobin",data=datal\_new,hue="red\_blood\_cells")#引入第三維度變量進來,fig2 sns.violinplot(x="appetite\_",y="hemoglobin",data=datal\_new,hue="red\_blood\_cells",split="1")



參考資料:https://www.jianshu.com/p/96977b9869ac

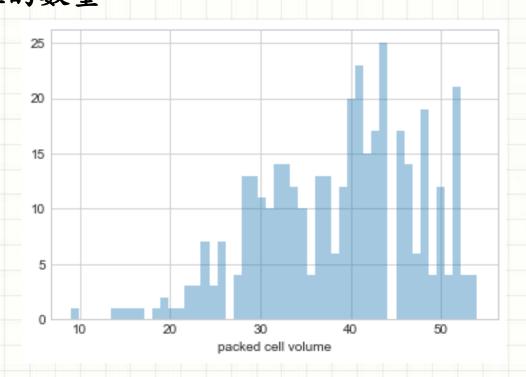
fig3

histogram:

Code:

sns.distplot(data1\_new["packed cell volume"],
kde=False, bins=50)

#kde為False則圖為實際數據,True則圖為機率分佈。 #bin表示柱的數量



pie chart:

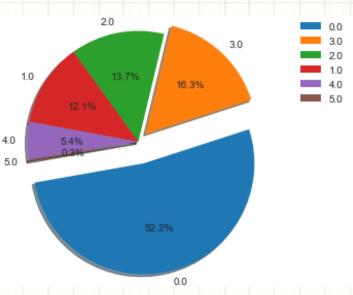
Code:

Totals = datal\_new["albumin"].value\_counts() labels1 =Totals.index#取得label explode = (0.5, 0.1, 0,0, 0,0)#調整圓餅圖間距

plt.pie(Totals, explode=explode, labels=labels1, autopct='%1.1f%', shadow=True, startangle=190) plt.legend(labels1, loc="best")

plt.axis("equal")

plt. tight\_layout()



## Scatter plot:

### Code:

法一:plt.plot(datal\_new["..."], datal\_new["..."], 'ro')

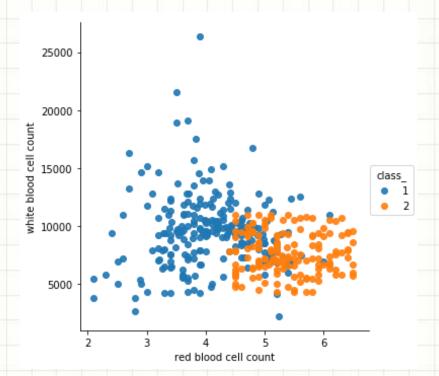
法二:g=sns.FacetGrid(data1\_new, hue="class\_", size=5)

#要畫散布圖的

g. map(plt. scatter, "red blood cell count",

"white blood cell count", alpha=.9)

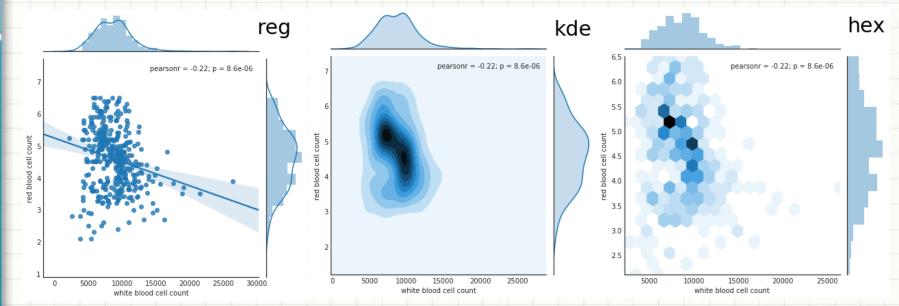
g. add\_legend()



## jointplot:

## Code:

```
with sns.axes_style("white"):
    sns.jointplot("white blood cell count", "red blood cell count",
    data=datal_new, kind=" scatter ")
plt.text(30000, 8.5, "reg", size=30)#size可以調整字體大小
#kind可以選reg、kde、hex
```



## 其他技巧:subplot

#### Code:

fig, axes=plt. subplots(2, 3, figsize=(15, 5))
sns. boxplot(x="sugar", y="blood glucose random",
data=datal\_new, ax=axes[0, 1])
sns. boxplot(x="sugar", y="age", data=datal\_new, ax=axes[0, 0])
sns. boxplot(x="sugar", y="blood urea", data=datal\_new, ax=axes[0, 2])
sns. boxplot(x="sugar", y="serum creatinine",
data=datal\_new, ax=axes[1, 0])
sns. boxplot(x="sugar", y="sodium", data=datal\_new, ax=axes[1, 1])
sns. boxplot(x="sugar", y="hemoglobin", data=datal\_new, ax=axes[1, 2])

