```
In [1]:
```

```
import numpy as np
import pandas as pd
```

In [4]:

```
data=pd.read_csv("C:/Users/wit12/Downloads/skin cancer.csv")
```

In [5]:

data

Out[5]:

	lesion_id	image_id	dx	dx_type	age	sex	localization
0	HAM_0000118	ISIC_0027419	bkl	histo	0.08	male	scalp
1	HAM_0000118	ISIC_0025030	bkl	histo	0.08	ma l e	scalp
2	HAM_0002730	ISIC_0026769	bkl	histo	0.08	ma l e	scalp
3	HAM_0002730	ISIC_0025661	bkl	histo	0.08	ma l e	scalp
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	ma l e	ear
10010	HAM_0002867	ISIC_0033084	akiec	histo	40.0	ma l e	abdomen
10011	HAM_0002867	ISIC_0033550	akiec	histo	40.0	ma l e	abdomen
10012	HAM_0002867	ISIC_0033536	akiec	histo	40.0	ma l e	abdomen
10013	HAM_0000239	ISIC_0032854	akiec	histo	0.08	ma l e	face
10014	HAM_0003521	ISIC_0032258	mel	histo	70.0	female	back

10015 rows × 7 columns

In [6]:

```
# check if there is any null values in the data
```

In [9]:

```
data.isnull().sum()
```

Out[9]:

lesion_id	0
image_id	0
dx	0
dx_type	0
age	57
sex	0
localization	0
dtype: int64	

```
In [11]:
```

data.size

Out[11]:

70105

In [14]:

```
data.dropna()
```

Out[14]:

	lesion_id	image_id	dx	dx_type	age	sex	localization
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp
2	HAM_0002730	ISIC_0026769	bkl	histo	0.08	male	scalp
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear
10010	HAM_0002867	ISIC_0033084	akiec	histo	40.0	ma l e	abdomen
10011	HAM_0002867	ISIC_0033550	akiec	histo	40.0	ma l e	abdomen
10012	HAM_0002867	ISIC_0033536	akiec	histo	40.0	ma l e	abdomen
10013	HAM_0000239	ISIC_0032854	akiec	histo	0.08	ma l e	face
10014	HAM_0003521	ISIC_0032258	mel	histo	70.0	female	back

9958 rows × 7 columns

In [29]:

```
val=int(data['age'].mean())
data['age'].fillna(val,inplace=True)
```

In [30]:

```
data.isnull().sum()
```

Out[30]:

```
lesion_id 0
image_id 0
dx 0
dx_type 0
age 0
sex 0
localization 0
dtype: int64
```

In [31]:

```
data.shape
```

Out[31]:

(10015, 7)

```
In [32]:
```

```
data.columns
Out[32]:
Index(['lesion_id', 'image_id', 'dx', 'dx_type', 'age', 'sex', 'localizatio
n'], dtype='object')
In [36]:
# count no of male cancers and female cancers
cntmale=0;
cntfemale=0;
for i in data['sex']:
    if i== "male":
        cntmale+=1
    elif i== 'female':
        cntfemale+=1
print("No.of male cancers are :",cntmale,"No.of female cancers are:",cntfemale)
No. of male cancers are: 5406 No. of female cancers are: 4552
In [39]:
print(len(data[data['sex']=='male']))
print(len(data[data['sex']=='female']))
5406
4552
In [40]:
data['dx']
Out[40]:
           bkl
0
1
           bkl
2
           bkl
3
           bkl
4
           bkl
10010
         akiec
10011
         akiec
10012
         akiec
10013
         akiec
10014
           mel
Name: dx, Length: 10015, dtype: object
```

```
In [38]:
dx = data['dx'].value_counts().sort_index()
print(dx)
akiec
           327
           514
bcc
bkl
          1099
df
           115
          1113
mel
          6705
nν
           142
vasc
Name: dx, dtype: int64
In [41]:
data.head()
Out[41]:
       lesion_id
                     image_id dx dx_type
                                                 sex localization
                                           age
0 HAM_0000118 ISIC_0027419
                              bkl
                                     histo
                                           0.08
                                                male
                                                            scalp
1 HAM_0000118 ISIC_0025030
                              bk
                                     histo
                                           0.08
                                                male
                                                            scalp
2 HAM_0002730 ISIC_0026769
                              bk
                                     histo
                                           0.08
                                                male
                                                            scalp
3 HAM_0002730 ISIC_0025661
                                     histo
                                           0.08
                                                            scalp
                              bk
                                                male
  HAM_0001466 ISIC_0031633 bkl
                                     histo 75.0
                                                male
                                                             ear
In [47]:
```

```
data['dx_type'].unique()
```

Out[47]:

array(['histo', 'consensus', 'confocal', 'follow_up'], dtype=object)

In [49]:

```
categories = dx.index.values
counts = dx.values
print(categories)
print(counts)
```

```
['akiec' 'bcc' 'bkl' 'df' 'mel' 'nv' 'vasc']
[ 327 514 1099 115 1113 6705 142]
```

In [50]:

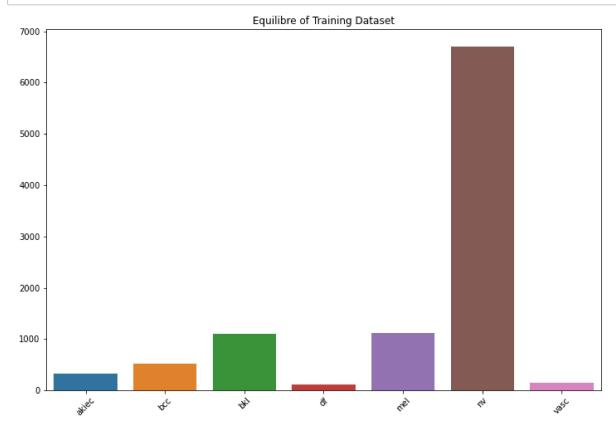
```
import matplotlib.pyplot as plt
import seaborn as sns
#sns.set_style("whitegrid")

def plot_equilibre(categories, counts):
    plt.figure(figsize=(12, 8))

    sns_bar = sns.barplot(x=categories, y=counts)
    sns_bar.set_xticklabels(categories, rotation=45)
    plt.title('Equilibre of Training Dataset')
    plt.show()
```

In [51]:

plot_equilibre(categories, counts)



In [53]:

```
# training the model
from sklearn.model_selection import train_test_split
df_train, df_tmp = train_test_split(data, test_size=0.2, random_state=101, stratify=data['d
df_val, df_test = train_test_split(df_tmp, test_size=0.5, random_state=101)
```

In []: