Dataset Overview

HAM10000 ("Human Against Machine with 10000 training images") dataset - a large collection of multi-source dermatoscopic images of pigmented lesions

The dermatoscopic images are collected from different populations, acquired and stored by different modalities. The final dataset consists of 10015 dermatoscopic images.

It has 7 different classes of skin cancer which are listed below :

- **Melanocytic nevi**
- **Melanoma**
- **Benign keratosis-like lesions**
- **Basal cell carcinoma**
- **Actinic keratoses**
- **Vascular lesions**
- **Dermatofibroma**

Importing libraries

In [31]:

```
import seaborn as sns
import pandas as pd
import matplotlib.pyplot as plt
from imblearn.over_sampling import RandomOverSampler
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score,KFold

import os, cv2
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Conv2D, Flatten, Dense, MaxPool2D, Activation, Batch
Normalization
from sklearn.metrics import classification_report, accuracy_score
```

Reading the Data

In [32]:

```
data = pd.read_csv('/kaggle/input/skin-cancer-mnist-ham10000/hmnist_28_28_RGB.csv')
data.head()
```

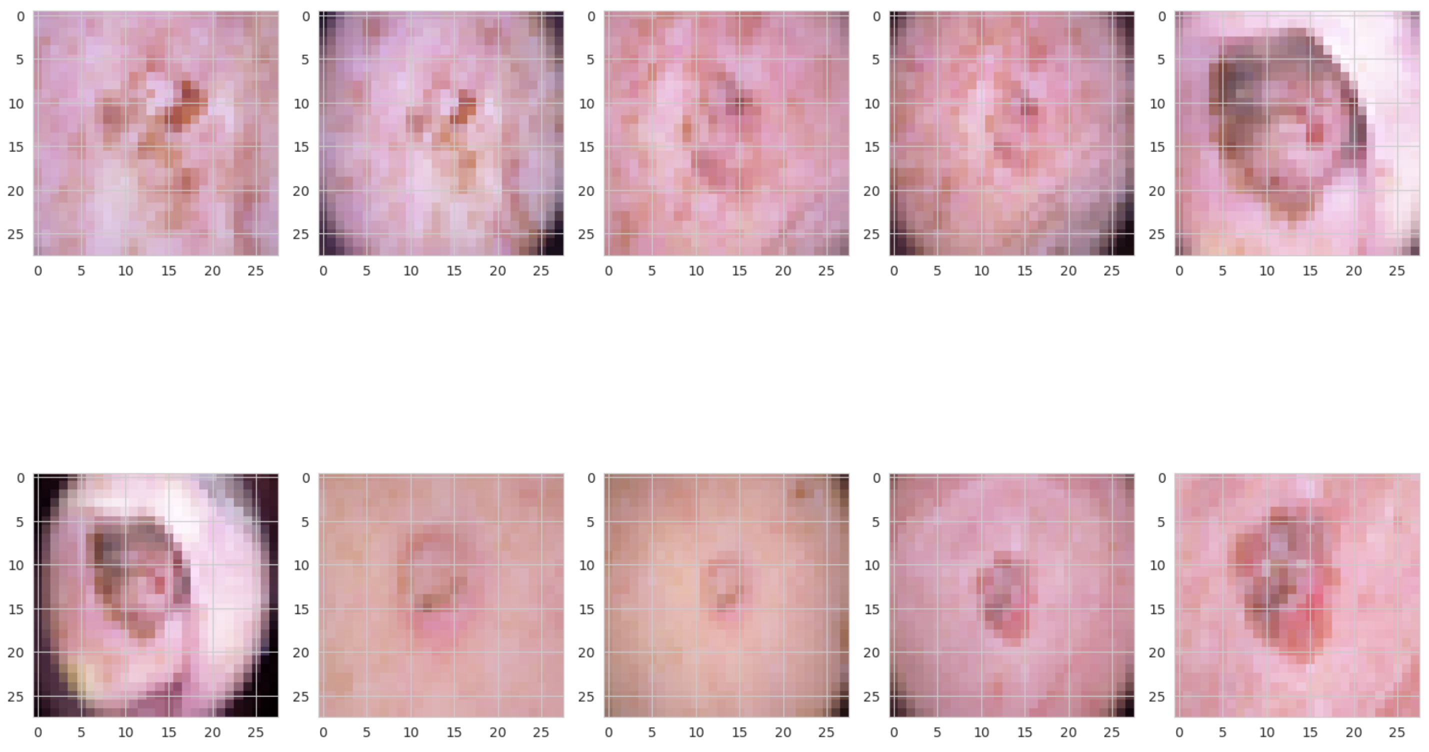
Out[32]:

	pixel0000	pixel0001	pixel0002	pixel0003	pixel0004	pixel0005	pixel0006	pixel0007	pixel0008	pixel0009	...	pixel2343	pix
0	192	153	193	195	155	192	197	154	185	202	...	173	
1	25	14	30	68	48	75	123	93	126	158	...	60	
2	192	138	153	200	145	163	201	142	160	206	...	167	
3	38	19	30	95	59	72	143	103	119	171	...	44	
4	158	113	139	194	144	174	215	162	191	225	...	209	

5 rows × 2353 columns

In [33]:

```
f , ax = plt.subplots(2,5)
f.set_size_inches(15, 15)
k = 0
y1 = data['label']
x1 = data.drop(columns = ['label'])
x1= np.array(x1).reshape(-1,28,28,3)
for i in range(2):
    for j in range(5):
        ax[i,j].imshow(x1[k].reshape(28,28,3))
#           ax[i, j].set_title(f"Image {Y_train[4]}")
        k = k + 1
    plt.tight_layout()
```



Data Preprocessing

Data Cleaning

In [34]:

```
data['label'].unique()
y = data['label']
x = data.drop(columns = ['label'])
data.isnull().sum().sum()  #no null values present
```

Out[34]:

```
0
```

In [35]:

```
meta_data = pd.read_csv('/kaggle/input/skin-cancer-mnist-ham10000/HAM10000_metadata.csv')
meta_data.head()
```

Out[35]:

	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	80.0	male	scalp
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear

In [36]:

```
meta_data['dx'].unique()
```

Out[36]:

```
array(['bkl', 'nv', 'df', 'mel', 'vasc', 'bcc', 'akiec'], dtype=object)
```

In [37]:

```
data.isnull().sum().sum() #no null values present
meta_data.head()
```

Out[37]:

	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	80.0	male	scalp
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear

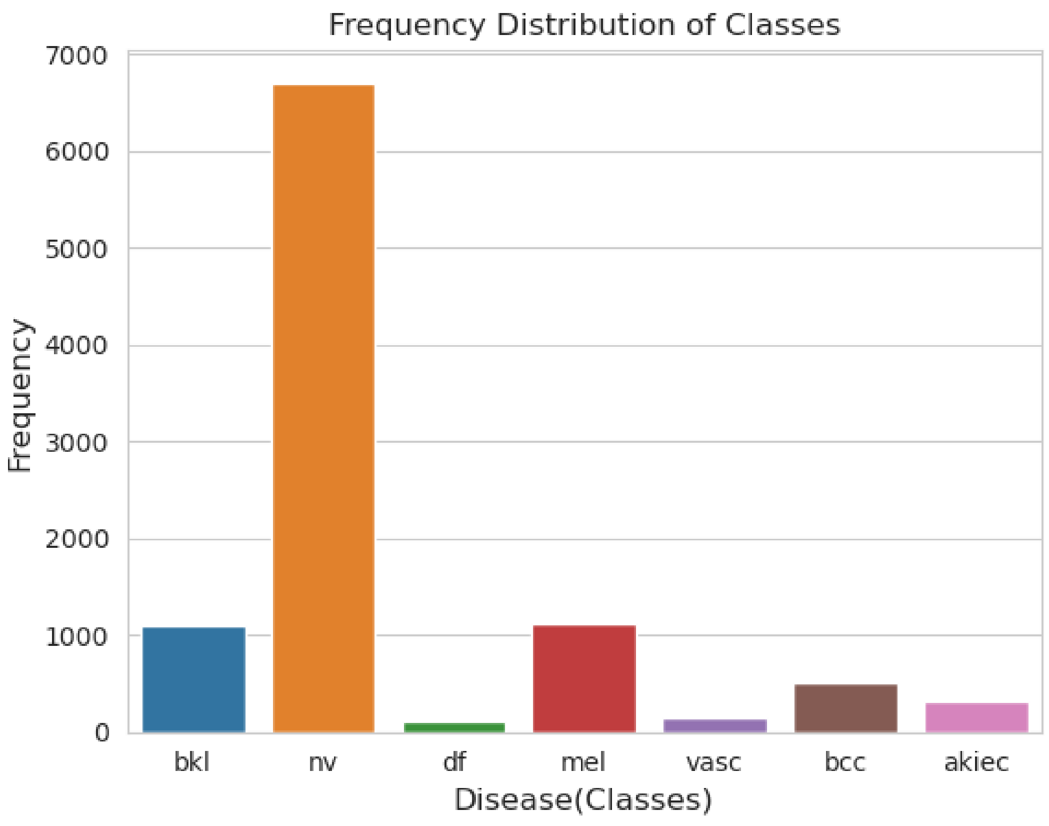
Exploratory Data Analysis

In [38]:

```
sns.countplot(x = 'dx', data = meta_data)
plt.xlabel('Disease(Classes)', size=12)
plt.ylabel('Frequency', size=12)
plt.title('Frequency Distribution of Classes')
```

Out[38]:

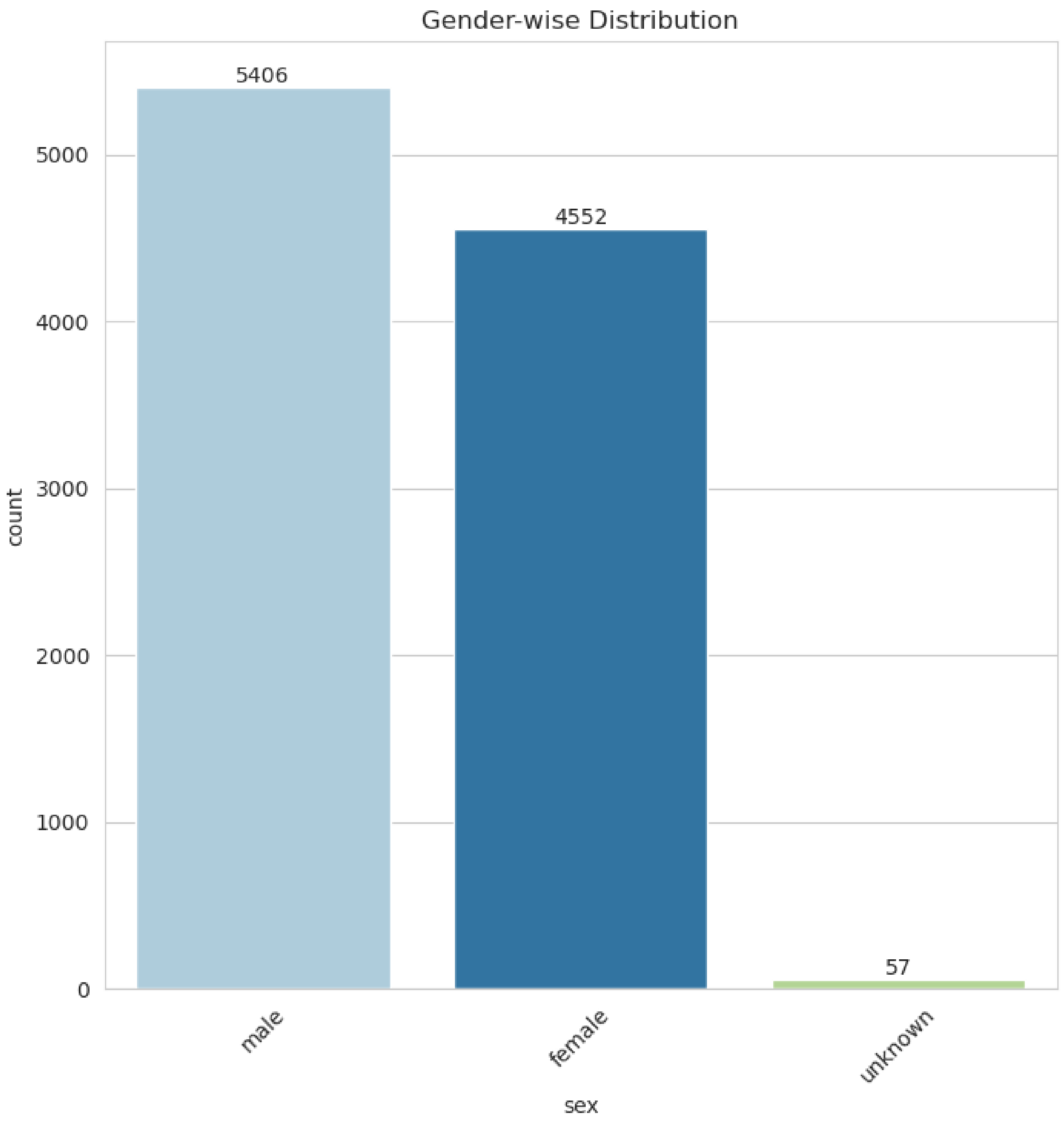
```
Text(0.5, 1.0, 'Frequency Distribution of Classes')
```



In [39]:

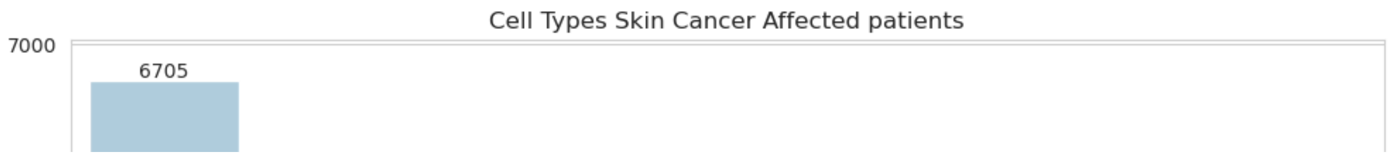
```
sns.set_style('whitegrid')
```

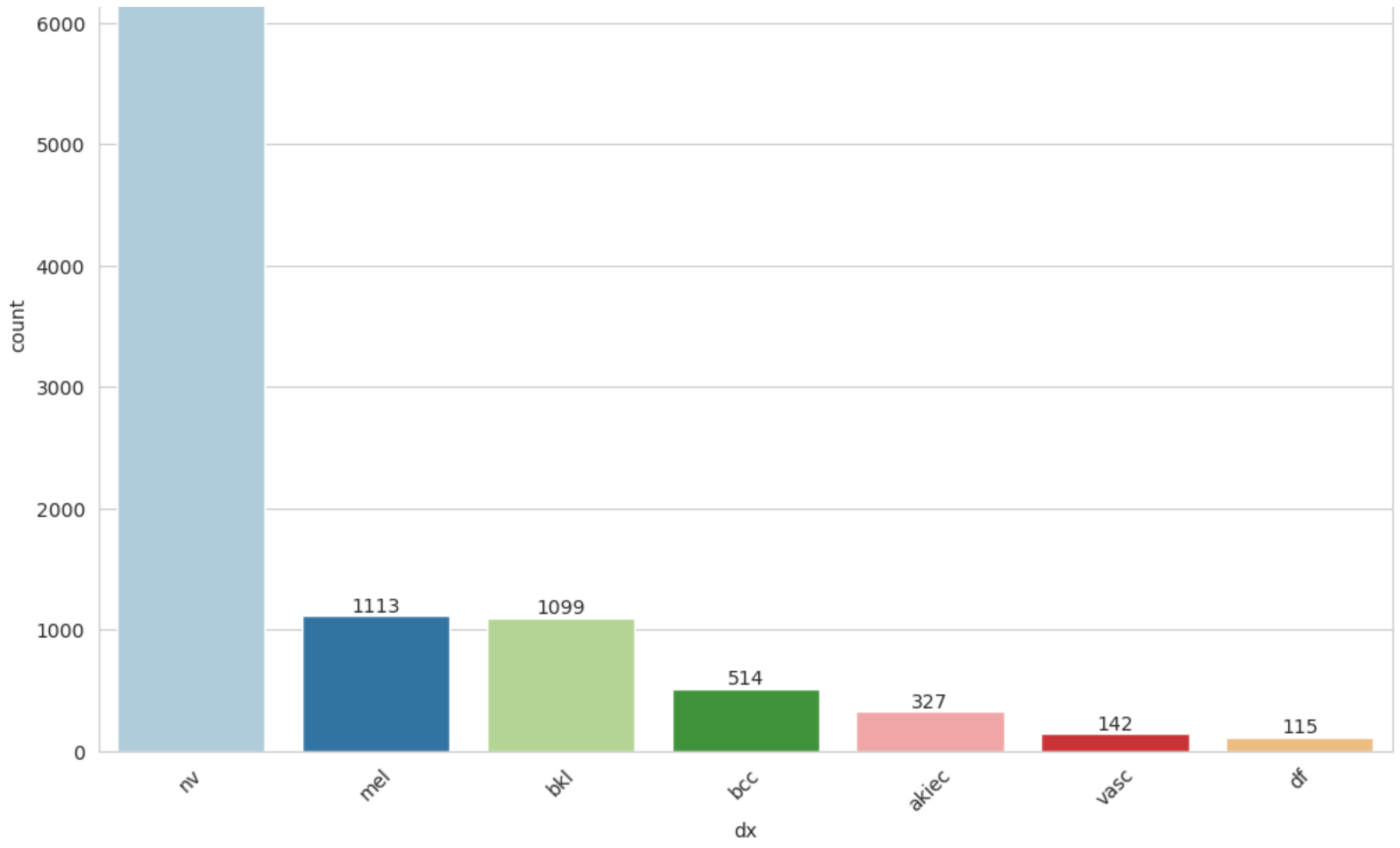
```
colors = ['#87ace8','#e3784d', 'green']
fig,axes = plt.subplots(figsize=(8,8))

ax = sns.countplot(x='sex',data=meta_data, palette = 'Paired')
for container in ax.containers:
    ax.bar_label(container)
plt.title('Gender-wise Distribution')
plt.xticks(rotation=45)
plt.show()
```



In [40]:

```
sns.set_style('whitegrid')
fig,axes = plt.subplots(figsize=(12,8))
ax = sns.countplot(x='dx',data=meta_data, order = meta_data['dx'].value_counts().index,
palette = 'Paired')
for container in ax.containers:
    ax.bar_label(container)
plt.title('Cell Types Skin Cancer Affected patients')
plt.xticks(rotation=45)
plt.show()
```





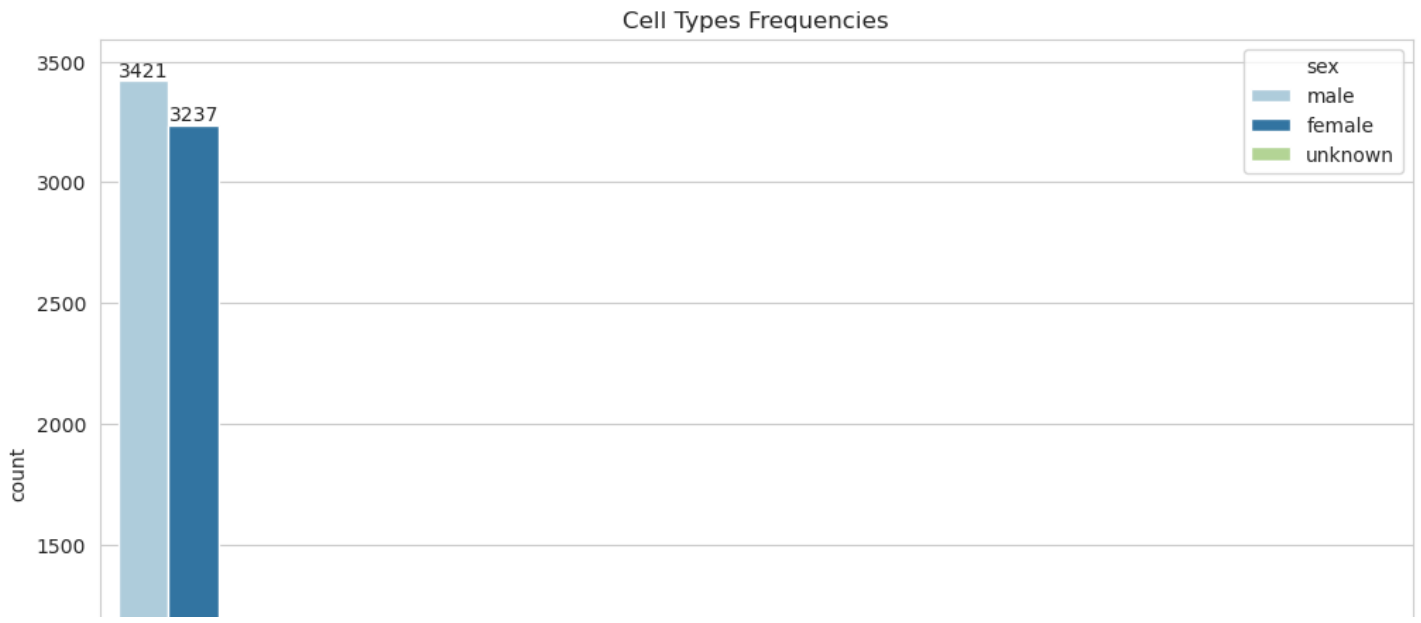
In [41]:

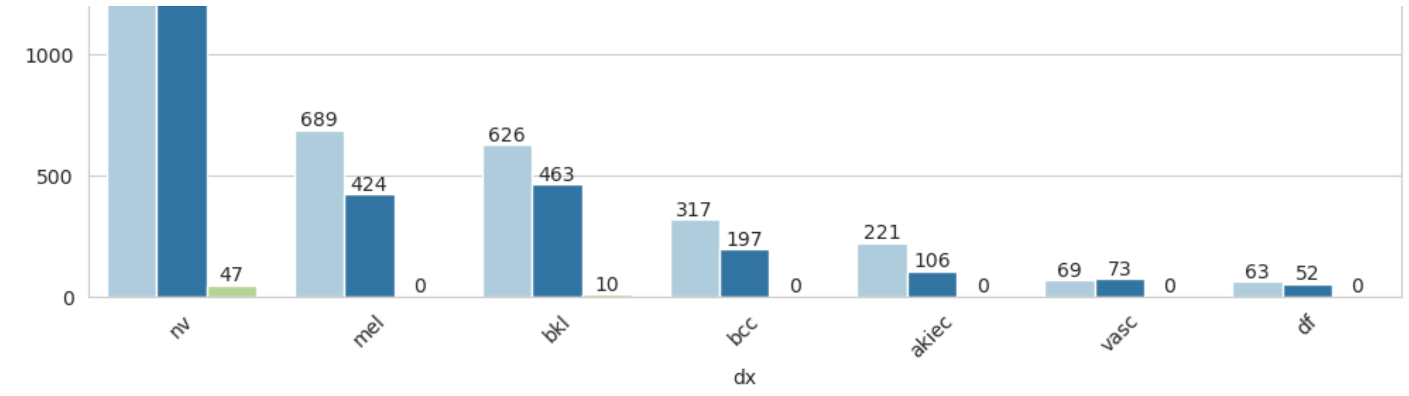
```
classes = {2:'bkl', 4:'nv', 3:'df', 6:'mel', 5:'vasc', 1:'bcc', 0:'akiec'}

classes_labels=[]
for key in classes.keys():
    classes_labels.append(key)
print(classes_labels)
```

```
[2, 4, 3, 6, 5, 1, 0]
```

In [42]:

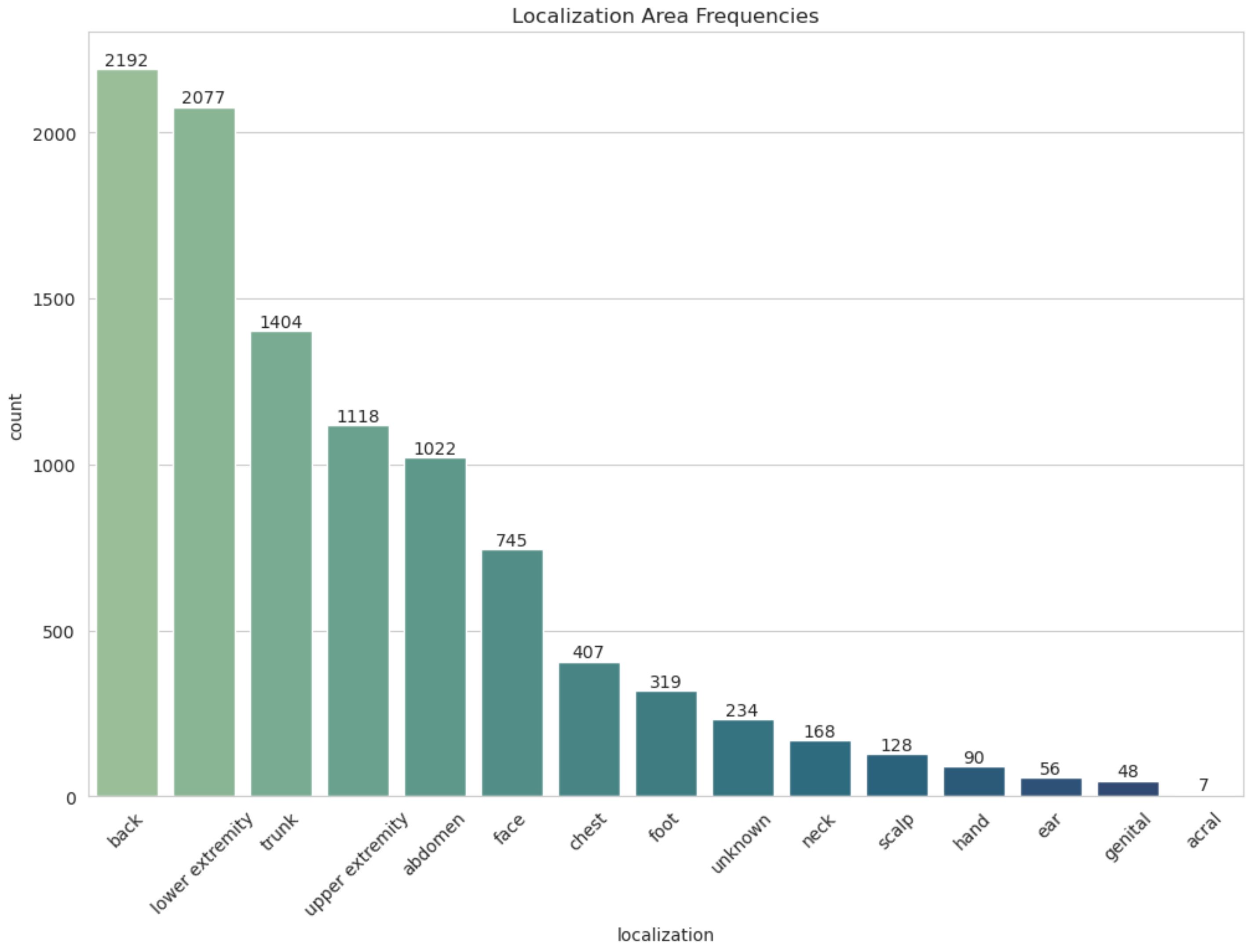
```
sns.set_style('whitegrid')
fig,axes = plt.subplots(figsize=(12,8))
ax = sns.countplot(x='dx',hue='sex', data=meta_data, order = meta_data['dx'].value_count
s().index, palette = 'Paired')
for container in ax.containers:
    ax.bar_label(container)
plt.title('Cell Types Frequencies')
plt.xticks(rotation=45)
plt.show()
```





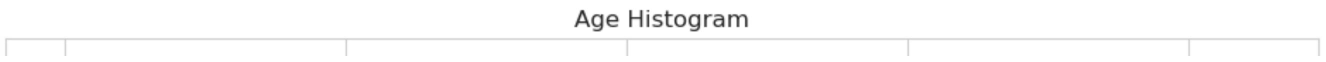
In [43]:

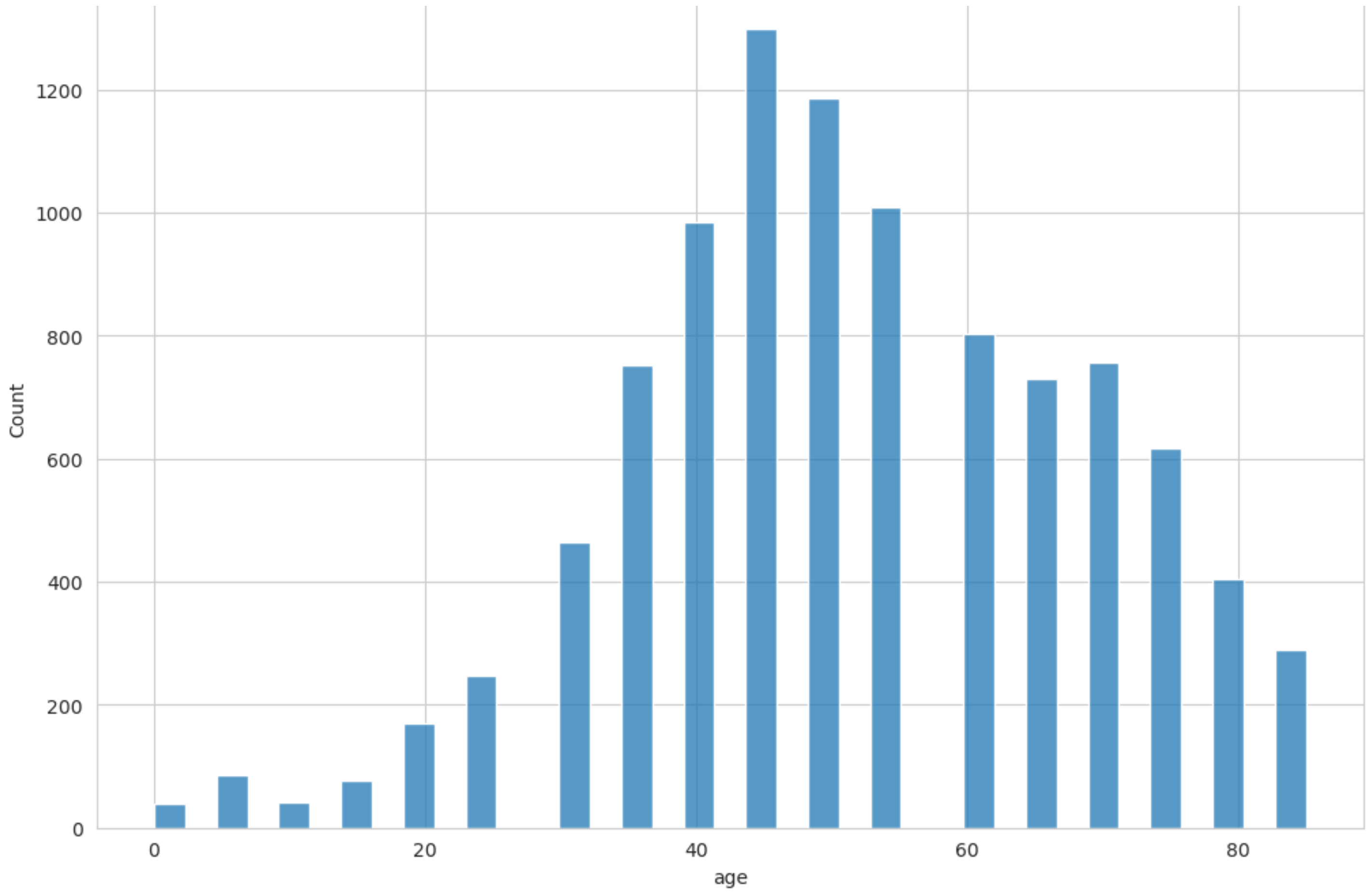
```
sns.set_style('whitegrid')
fig,axes = plt.subplots(figsize=(12,8))
ax = sns.countplot(x='localization',data=meta_data, order = meta_data['localization'].val
ue_counts().index, palette = 'crest')
for container in ax.containers:
    ax.bar_label(container)
plt.title('Localization Area Frequencies')
plt.xticks(rotation=45)
plt.show()
```



In [44]:

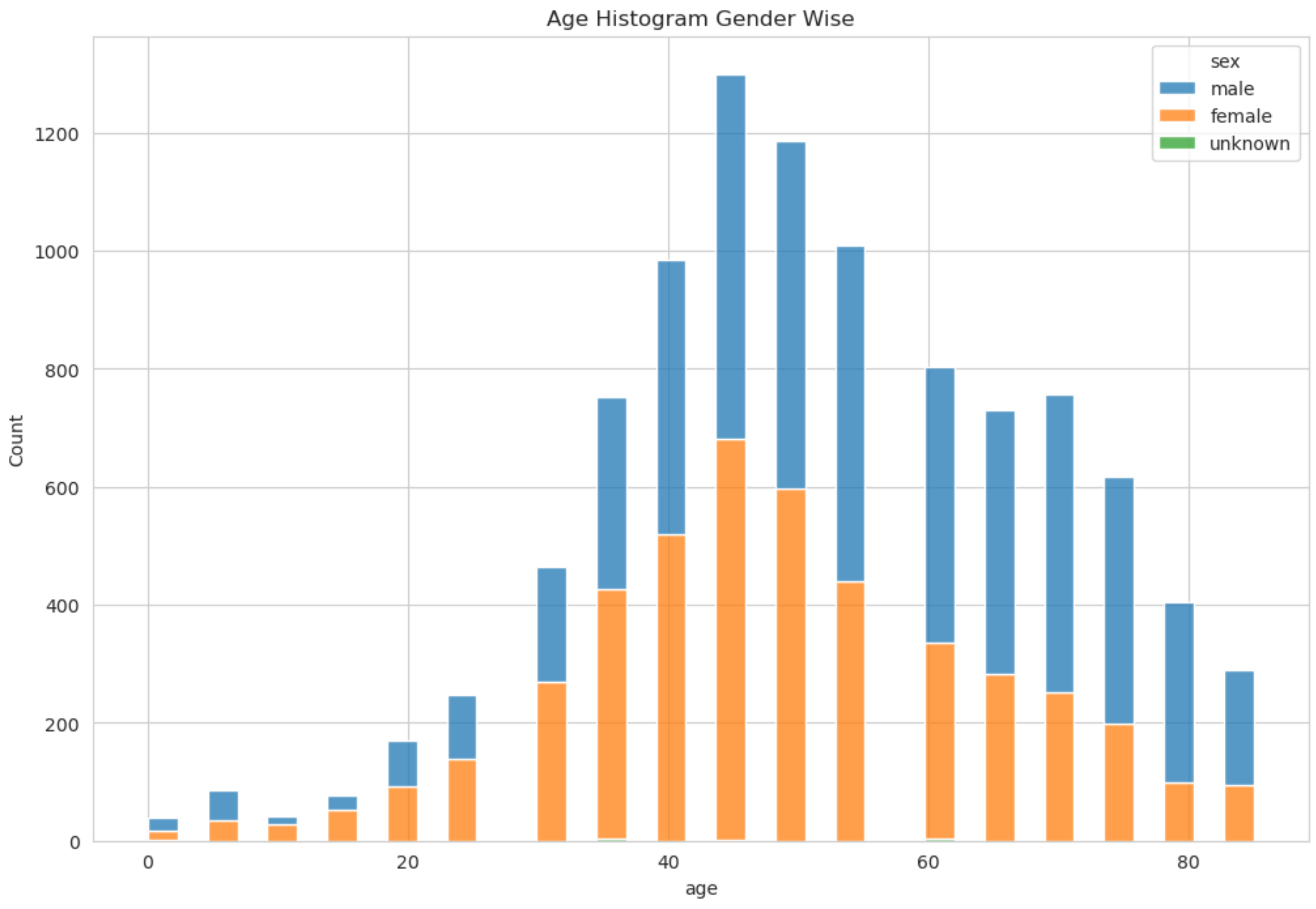
```
sns.set_style('whitegrid')
fig,axes = plt.subplots(figsize=(12,8))
ax = sns.histplot(data=meta_data, x='age')
plt.title('Age Histogram')
plt.show()
```





In [45]:

```
sns.set_style('whitegrid')
fig,axes = plt.subplots(figsize=(12,8))
ax = sns.histplot(data=meta_data, x='age',hue='sex',multiple='stack')
plt.title('Age Histogram Gender Wise')
plt.show()
```



In [46]:

```
print(x.shape,y.shape)
# To overcome class imbalace
oversample = RandomOverSampler()
Data,Label  = oversample.fit_resample(x,y)
print(Data.shape,Label.shape)
```

```
(10015, 2352) (10015,)
(46935, 2352) (46935,)
```

In [47]:

```
# reshaping the data so that it can be taken by convolution neural network(without distur
bing the no. of samples)
Data= np.array(Data).reshape(-1,28,28,3)
print('Shape of X :',Data.shape)
print('Shape of y :',Label.shape)
```

```
Shape of X : (46935, 28, 28, 3)
Shape of y : (46935,)
```

In [48]:

```
print(Label)
```

```
0        2
1        2
2        2
3        2
4        2
        ..
46930    6
46931    6
46932    6
46933    6
46934    6
Name: label, Length: 46935, dtype: int64
```

In [49]:

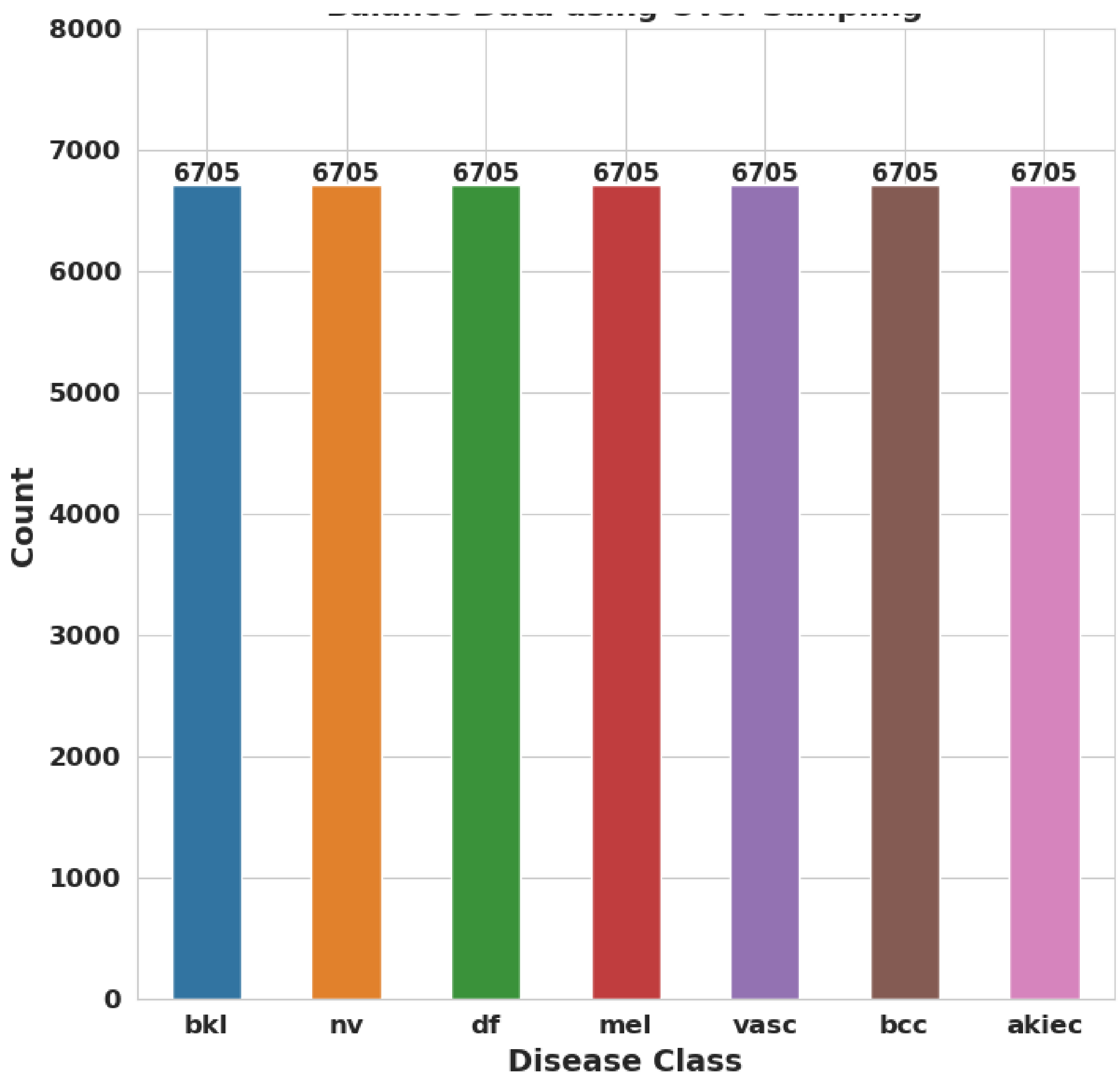
```
newLabel = []

for i in range(len(Label)):
    for key in classes.keys():
        if Label[i] == key:
            newLabel.append(classes[key])

newLabel[46930]
```

Out[49]:

```
'mel'
```

In [50]:

```
sns.set_style('whitegrid')
fig,axes = plt.subplots(figsize=(8,8))
ax = sns.countplot(x=newLabel,data=data,width=0.5)
for container in ax.containers:
    ax.bar_label(container, fontweight='bold', fontsize=11)
plt.title('Balance Data using Over Sampling', fontweight='bold', fontsize=14)
plt.ylim(0, 8000)
plt.xticks(fontweight='bold', fontsize=12)
plt.yticks(fontweight='bold', fontsize=12)
plt.ylabel("Count",fontweight='bold', fontsize=14)
plt.xlabel("Disease Class", fontweight='bold', fontsize=14)

plt.grid(linewidth=0.8)
plt.show()
```



In [51]:

```
Data = np.array(Data).reshape(-1,28,28,3)
print('Shape of X :',Data.shape)
print('Shape of y :',Label.shape)
```

```
Shape of X : (46935, 28, 28, 3)
Shape of y : (46935,)
```

In [52]:

```
# Splitting Data
X_train, X_test, Y_train, Y_test = train_test_split(Data,Label, test_size=0.2, random_st
ate=1)
print(X_train.shape,Y_train.shape)
print(X_test.shape , Y_test.shape)
```

```
(37548, 28, 28, 3) (37548,)
(9387, 28, 28, 3) (9387,)
```

In [53]:

```
classes = {4:'melanocytic nevi',
6: 'melanoma',
2:'benign keratosis-like lesions',
1:'basal cell carcinoma',
5:'pyogenic granulomas and hemorrhage',
0:'Actinic keratoses and intraepithelial carcinomae',
3:'dermatofibroma'}
```

In [54]:

```
Y_train[:10]
```

Out[54]:

```
18033    1
38412    5
26590    2
6910     4
37704    5
15663    0
31556    3
45531    6
24641    2
44902    6
Name: label, dtype: int64
```

In [55]:

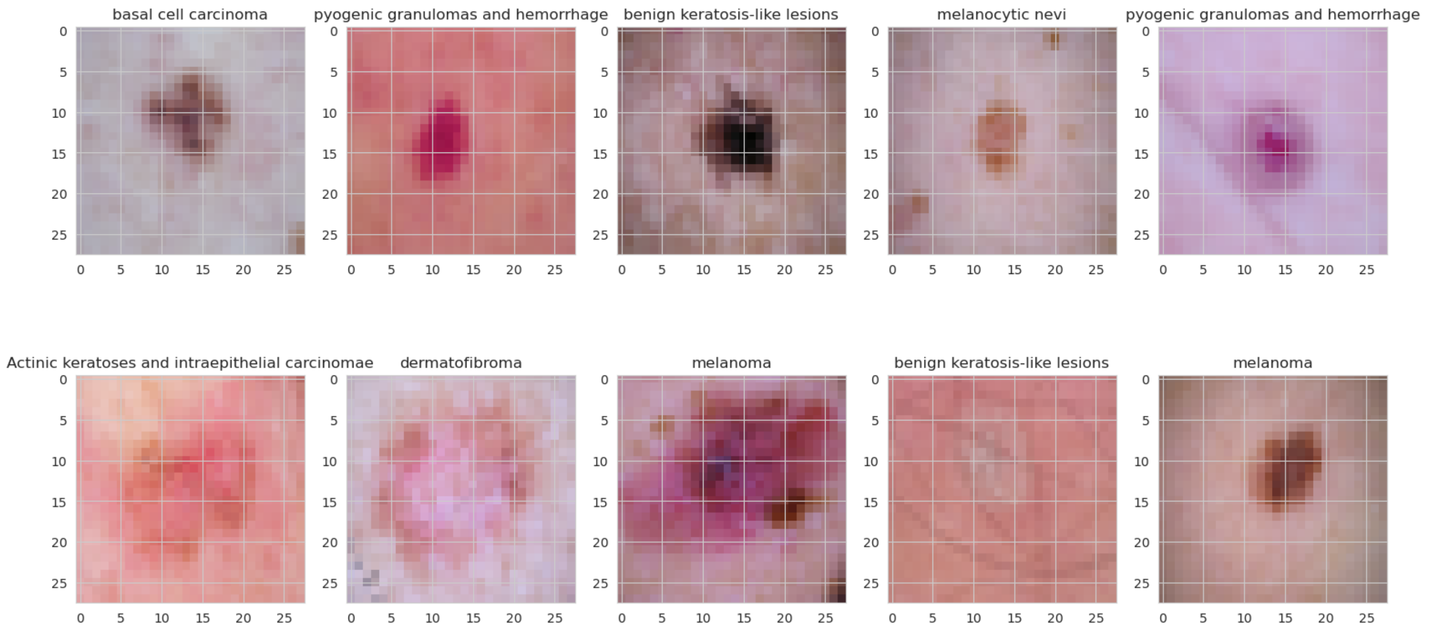
```
l_train = np.array(Y_train)
l_train[1]
```

Out[55]:

```
5
```

In [56]:

```
f , ax = plt.subplots(2,5)
f.set_size_inches(15, 15)
k = 0
l_train = np.array(Y_train)
for i in range(2):
    for j in range(5):
        plt.subplots_adjust(wspace=5)
        ax[i,j].imshow(X_train[k].reshape(28,28,3))
        ax[i, j].set_title(f"{classes[l_train[k]]}")
        k = k + 1

    plt.tight_layout()
```



basal cell carcinoma
pyogenic granulomas and hemorrhage
benign keratosis-like lesions
melanocytic nevi
pyogenic granulomas and hemorrhage
Actinic keratoses and intraepithelial carcinomae
dermatofibroma
melanoma
benign keratosis-like lesions
melanoma
0
5
10
15
20
25

In [57]:

```
model_CNN = Sequential()
model_CNN.add(Conv2D(32, kernel_size = (3,3), input_shape = (28, 28, 3), activation = 'r
elu', padding = 'same'))
model_CNN.add(BatchNormalization())
```

```python
model_CNN.add(MaxPool2D(pool_size = (2,2)))


model_CNN.add(Conv2D(64, kernel_size = (3,3), activation = 'relu', padding = 'same'))
model_CNN.add(BatchNormalization())

model_CNN.add(MaxPool2D(pool_size = (2,2), padding = 'same'))
model_CNN.add(Conv2D(128, kernel_size = (3,3), activation = 'relu', padding = 'same'))
model_CNN.add(BatchNormalization())

model_CNN.add(MaxPool2D(pool_size = (2,2), padding = 'same'))

model_CNN.add(Flatten())


model_CNN.add(Dense(64, activation = 'relu'))
model_CNN.add(BatchNormalization())


model_CNN.add(Dense(32))
model_CNN.add(Activation(activation='relu'))
model_CNN.add(BatchNormalization())

model_CNN.add(Dense(16))
model_CNN.add(Activation(activation='relu'))
model_CNN.add(BatchNormalization())

model_CNN.add(Dense(7))
model_CNN.add(Activation(activation='softmax'))

optimizer = tf.keras.optimizers.Adam(learning_rate = 0.001)

model_CNN.compile(loss = 'sparse_categorical_crossentropy',
                 optimizer = optimizer,
                  metrics = ['accuracy'])
print(model_CNN.summary())
```

```
Model: "sequential_1"
_________________________________________________________________
 Layer (type)                Output Shape              Param #   
=================================================================
 conv2d_3 (Conv2D)           (None, 28, 28, 32)        896       
                                                                 
 batch_normalization_6 (Batc  (None, 28, 28, 32)       128       
 hNormalization)                                                 
                                                                 
 max_pooling2d_3 (MaxPooling  (None, 14, 14, 32)       0         
 2D)                                                             
                                                                 
 conv2d_4 (Conv2D)           (None, 14, 14, 64)        18496     
                                                                 
 batch_normalization_7 (Batc  (None, 14, 14, 64)       256       
 hNormalization)                                                 
                                                                 
 max_pooling2d_4 (MaxPooling  (None, 7, 7, 64)         0         
 2D)                                                             
                                                                 
 conv2d_5 (Conv2D)           (None, 7, 7, 128)         73856     
                                                                 
 batch_normalization_8 (Batc  (None, 7, 7, 128)        512       
 hNormalization)                                                 
                                                                 
 max_pooling2d_5 (MaxPooling  (None, 4, 4, 128)        0         
 2D)                                                             
                                                                 
 flatten_1 (Flatten)         (None, 2048)              0         
                                                                 
 dense_4 (Dense)             (None, 64)                131136    
                                                                 
 batch_normalization_9 (Batc  (None, 64)               256       
 hNormalization)                                                 
 dense_5 (Dense)             (None, 32)                2080

 activation_3 (Activation)   (None, 32)                0

 batch_normalization_10 (Bat  (None, 32)               128
 chNormalization)

 dense_6 (Dense)             (None, 16)                528

 activation_4 (Activation)   (None, 16)                0

 batch_normalization_11 (Bat  (None, 16)               64
 chNormalization)

 dense_7 (Dense)             (None, 7)                 119

 activation_5 (Activation)   (None, 7)                 0

=================================================================
Total params: 228,455
Trainable params: 227,783
Non-trainable params: 672
_________________________________________________________________
None
```

In [58]:

```
from tensorflow.keras.callbacks import ReduceLROnPlateau, EarlyStopping
early_stop = EarlyStopping(monitor='val_loss', patience=10, verbose=1, mode='auto')
reduce_lr = ReduceLROnPlateau(monitor='val_loss', factor=0.1, patience=3, verbose=1, mod
e='auto')
history = model_CNN.fit(X_train,
                    Y_train,
                    validation_split=0.2,
                    batch_size = 64,
                    epochs = 50,
                    callbacks = [reduce_lr, early_stop])
```

```
Epoch 1/50
470/470 [==============================] - 9s 9ms/step - loss: 1.0044 - accuracy: 0.6432
- val_loss: 0.7764 - val_accuracy: 0.7091 - lr: 0.0010
Epoch 2/50
470/470 [==============================] - 4s 8ms/step - loss: 0.4632 - accuracy: 0.8415
- val_loss: 0.8838 - val_accuracy: 0.6871 - lr: 0.0010
Epoch 3/50
470/470 [==============================] - 4s 8ms/step - loss: 0.2989 - accuracy: 0.8958
- val_loss: 0.6778 - val_accuracy: 0.7487 - lr: 0.0010
Epoch 4/50
470/470 [==============================] - 4s 8ms/step - loss: 0.2196 - accuracy: 0.9224
- val_loss: 1.0653 - val_accuracy: 0.6581 - lr: 0.0010
Epoch 5/50
470/470 [==============================] - 4s 8ms/step - loss: 0.1689 - accuracy: 0.9410
- val_loss: 0.3811 - val_accuracy: 0.8569 - lr: 0.0010
Epoch 6/50
470/470 [==============================] - 5s 10ms/step - loss: 0.1274 - accuracy: 0.9568
- val_loss: 0.5980 - val_accuracy: 0.8057 - lr: 0.0010
Epoch 7/50
470/470 [==============================] - 4s 8ms/step - loss: 0.1164 - accuracy: 0.9581
- val_loss: 0.4327 - val_accuracy: 0.8523 - lr: 0.0010
Epoch 8/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0936 - accuracy: 0.9674
- val_loss: 0.2524 - val_accuracy: 0.9142 - lr: 0.0010
Epoch 9/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0931 - accuracy: 0.9677
- val_loss: 0.5019 - val_accuracy: 0.8316 - lr: 0.0010
Epoch 10/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0572 - accuracy: 0.9804
- val_loss: 0.2258 - val_accuracy: 0.9308 - lr: 0.0010
Epoch 11/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0639 - accuracy: 0.9777
- val_loss: 0.6433 - val_accuracy: 0.8142 - lr: 0.0010
Epoch 12/50
```

```
470/470 [==============================] - 4s 8ms/step - loss: 0.0524 - accuracy: 0.9824
- val_loss: 1.0235 - val_accuracy: 0.7035 - lr: 0.0010
Epoch 13/50
467/470 [============================>.] - ETA: 0s - loss: 0.0779 - accuracy: 0.9731
Epoch 13: ReduceLROnPlateau reducing learning rate to 0.00010000000474974513.
470/470 [==============================] - 4s 9ms/step - loss: 0.0779 - accuracy: 0.9731
- val_loss: 0.2557 - val_accuracy: 0.9185 - lr: 0.0010
Epoch 14/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0221 - accuracy: 0.9936
- val_loss: 0.0764 - val_accuracy: 0.9776 - lr: 1.0000e-04
Epoch 15/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0119 - accuracy: 0.9972
- val_loss: 0.0770 - val_accuracy: 0.9779 - lr: 1.0000e-04
Epoch 16/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0082 - accuracy: 0.9984
- val_loss: 0.0731 - val_accuracy: 0.9792 - lr: 1.0000e-04
Epoch 17/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0062 - accuracy: 0.9989
- val_loss: 0.0726 - val_accuracy: 0.9799 - lr: 1.0000e-04
Epoch 18/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0045 - accuracy: 0.9996
- val_loss: 0.0774 - val_accuracy: 0.9804 - lr: 1.0000e-04
Epoch 19/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0038 - accuracy: 0.9995
- val_loss: 0.0765 - val_accuracy: 0.9794 - lr: 1.0000e-04
Epoch 20/50
463/470 [============================>.] - ETA: 0s - loss: 0.0037 - accuracy: 0.9995
Epoch 20: ReduceLROnPlateau reducing learning rate to 1.0000000474974514e-05.
470/470 [==============================] - 4s 9ms/step - loss: 0.0040 - accuracy: 0.9994
- val_loss: 0.0843 - val_accuracy: 0.9784 - lr: 1.0000e-04
Epoch 21/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0028 - accuracy: 0.9997
- val_loss: 0.0740 - val_accuracy: 0.9808 - lr: 1.0000e-05
Epoch 22/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0028 - accuracy: 0.9997
- val_loss: 0.0742 - val_accuracy: 0.9806 - lr: 1.0000e-05
Epoch 23/50
470/470 [==============================] - 4s 9ms/step - loss: 0.0028 - accuracy: 0.9997
- val_loss: 0.0723 - val_accuracy: 0.9811 - lr: 1.0000e-05
Epoch 24/50
470/470 [==============================] - 4s 10ms/step - loss: 0.0023 - accuracy: 0.9999
- val_loss: 0.0749 - val_accuracy: 0.9794 - lr: 1.0000e-05
Epoch 25/50
470/470 [==============================] - 4s 10ms/step - loss: 0.0021 - accuracy: 0.9999
- val_loss: 0.0756 - val_accuracy: 0.9799 - lr: 1.0000e-05
Epoch 26/50
465/470 [============================>.] - ETA: 0s - loss: 0.0021 - accuracy: 0.9999
Epoch 26: ReduceLROnPlateau reducing learning rate to 1.0000000656873453e-06.
470/470 [==============================] - 4s 8ms/step - loss: 0.0022 - accuracy: 0.9999
- val_loss: 0.0763 - val_accuracy: 0.9795 - lr: 1.0000e-05
Epoch 27/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0020 - accuracy: 0.9999
- val_loss: 0.0772 - val_accuracy: 0.9792 - lr: 1.0000e-06
Epoch 28/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0021 - accuracy: 0.9999
- val_loss: 0.0772 - val_accuracy: 0.9792 - lr: 1.0000e-06
Epoch 29/50
469/470 [============================>.] - ETA: 0s - loss: 0.0020 - accuracy: 0.9998
Epoch 29: ReduceLROnPlateau reducing learning rate to 1.0000001111620805e-07.
470/470 [==============================] - 4s 9ms/step - loss: 0.0020 - accuracy: 0.9998
- val_loss: 0.0757 - val_accuracy: 0.9796 - lr: 1.0000e-06
Epoch 30/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0022 - accuracy: 0.9997
- val_loss: 0.0758 - val_accuracy: 0.9798 - lr: 1.0000e-07
Epoch 31/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0021 - accuracy: 0.9999
- val_loss: 0.0760 - val_accuracy: 0.9798 - lr: 1.0000e-07
Epoch 32/50
466/470 [============================>.] - ETA: 0s - loss: 0.0020 - accuracy: 0.9998
Epoch 32: ReduceLROnPlateau reducing learning rate to 1.000000082740371e-08.
470/470 [==============================] - 4s 8ms/step - loss: 0.0020 - accuracy: 0.9998
- val_loss: 0.0770 - val_accuracy: 0.9796 - lr: 1.0000e-07
```

```
Epoch 33/50
470/470 [==============================] - 4s 8ms/step - loss: 0.0021 - accuracy: 0.9999
- val_loss: 0.0758 - val_accuracy: 0.9800 - lr: 1.0000e-08
Epoch 33: early stopping
```

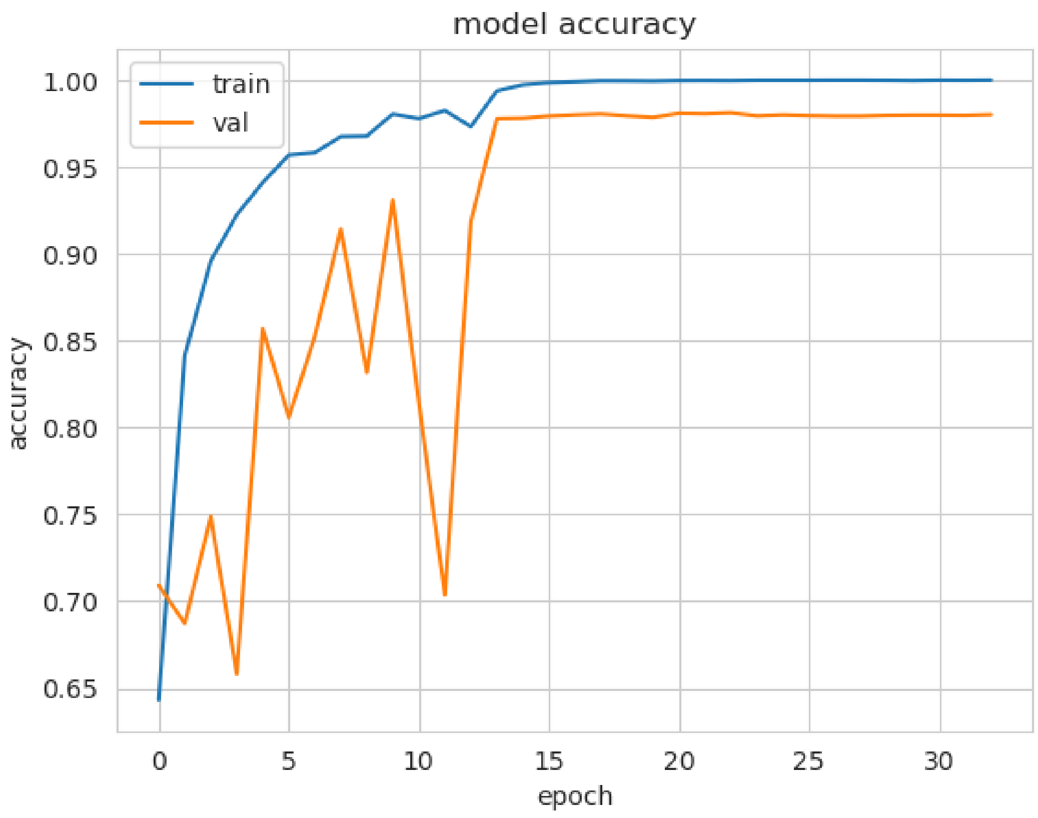
In [59]:

```
results = model_CNN.evaluate(X_test , Y_test, verbose=0)

print("CNN Model Test Results")
print("        Test Loss: {:.5f}".format(results[0]))
print("    Test Accuracy: {:.2f}%".format(results[1] * 100))
```

```
CNN Model Test Results
        Test Loss: 0.07440
    Test Accuracy: 98.08%
```

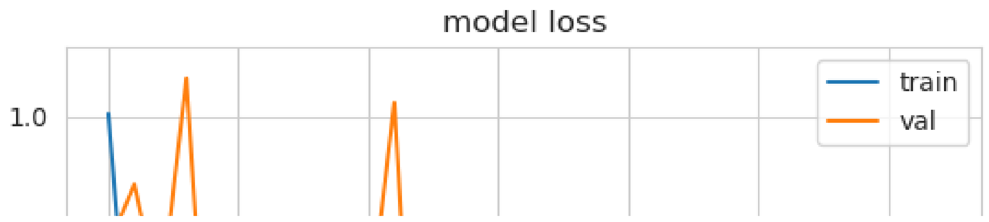
In [60]:

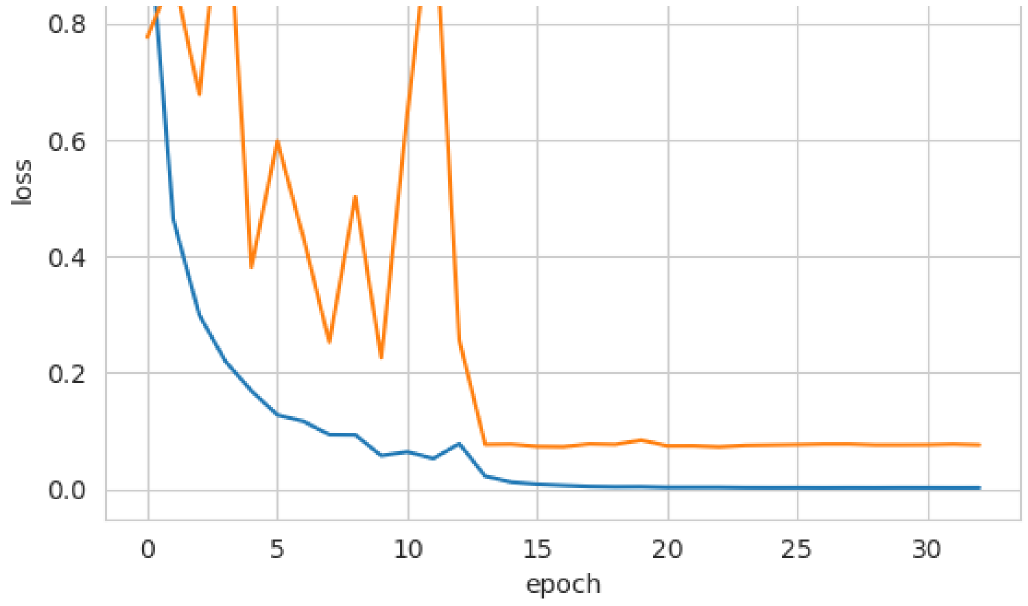
```
plt.plot(history.history['accuracy'])
plt.plot(history.history['val_accuracy'])
plt.title('model accuracy')
plt.ylabel('accuracy')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
```



In [61]:

```
plt.plot(history.history['loss'])
plt.plot(history.history['val_loss'])
plt.title('model loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper right')
plt.show()
```





In [62]:

```
from sklearn.metrics import confusion_matrix , classification_report

y_true_CNN = list(Y_test)
y_pred_CNN = model_CNN.predict(X_test)
y_pred_CNN = list(map(lambda x: np.argmax(x), y_pred_CNN))
print("Predicting First Ten Rows:")
print('Y Actual Values :' , y_true_CNN[0:10])
print('Y Predicted Values :' , y_pred_CNN[0:10])
```

```
294/294 [==============================] - 1s 2ms/step
Predicting First Ten Rows:
Y Actual Values : [5, 1, 4, 0, 5, 0, 2, 0, 3, 2]
Y Predicted Values : [5, 1, 4, 0, 5, 0, 2, 0, 3, 2]
```

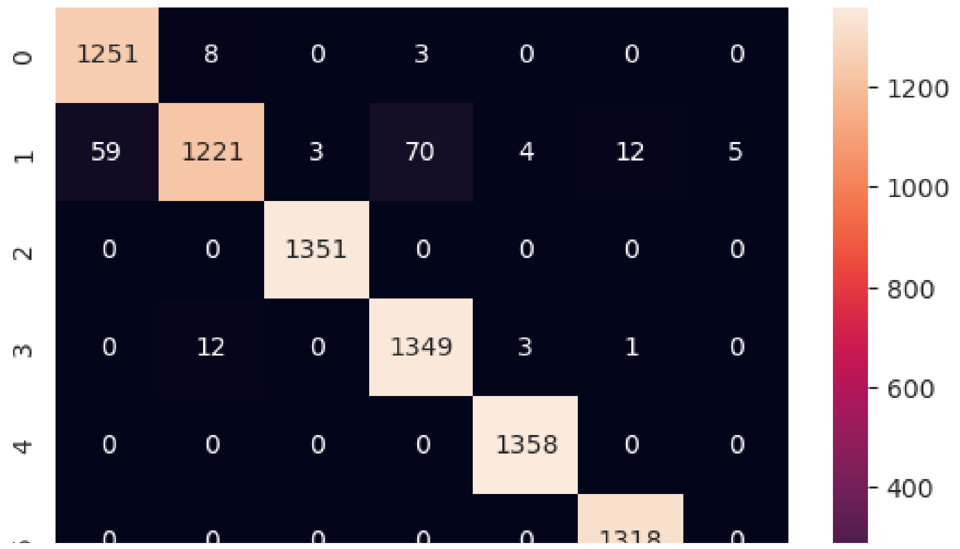
In [63]:

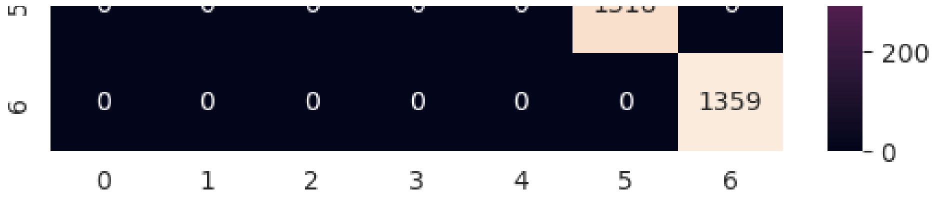
```
cm_CNN = confusion_matrix(y_true_CNN,y_pred_CNN,labels=classes_labels)
print(confusion_matrix(y_true_CNN,y_pred_CNN,labels=classes_labels))
sns.heatmap(cm_CNN, annot = True, fmt='')
```

```
[[1251    8    0    3    0    0    0]
 [  59 1221    3   70    4   12    5]
 [   0    0 1351    0    0    0    0]
 [   0   12    0 1349    3    1    0]
 [   0    0    0    0 1358    0    0]
 [   0    0    0    0    0 1318    0]
 [   0    0    0    0    0    0 1359]]
```

Out[63]:

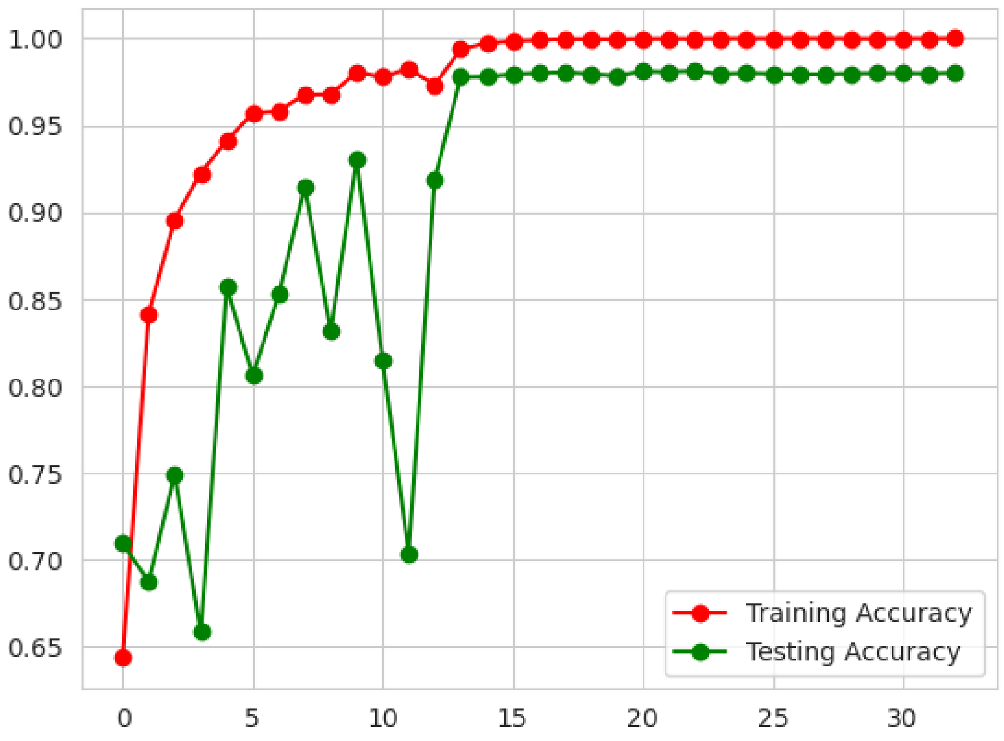
```
<AxesSubplot:>
```





In [64]:

```
#training acc vs testing acc graph
plt.plot(history.history["accuracy"] , 'ro-' , label = "Training Accuracy")
plt.plot(history.history["val_accuracy"] , 'go-' , label = "Testing Accuracy")
plt.legend()
plt.show()
```



In [65]:

```
#predicting
y_pred_CNN  = model_CNN.predict(X_test)
target_names = [f"{classes[i]}" for i in range(7)]
y_pred_CNN = list(map(lambda x: np.argmax(x), y_pred_CNN))
print("CNN Model Prediction Results")
print(classification_report(Y_test , y_pred_CNN,target_names=target_names))
```

```
294/294 [==============================] - 1s 2ms/step
CNN Model Prediction Results
                                                            precision    recall  f1-score   suppor
t

Actinic keratoses and intraepithelial carcinomae       1.00      1.00      1.00      135
9
                                     basal cell carcinoma       0.99      1.00      1.00      131
8
                              benign keratosis-like lesions       0.95      0.99      0.97      126
2
                                           dermatofibroma       1.00      1.00      1.00      135
1
                                         melanocytic nevi       0.98      0.89      0.93      137
4
                        pyogenic granulomas and hemorrhage       0.99      1.00      1.00      135
8
                                                 melanoma       0.95      0.99      0.97      136
5

                                                 accuracy                           0.98      93
87
```

```
                                          macro avg       0.98      0.98      0.98       938
7
                                       weighted avg       0.98      0.98      0.98       938
7
```

In [66]:

```
# Layers definitions
from keras import backend as K
for l in range(len(model_CNN.layers)):
    print(l, model_CNN.layers[l])
```

```
0 <keras.layers.convolutional.conv2d.Conv2D object at 0x7be998003350>
1 <keras.layers.normalization.batch_normalization.BatchNormalization object at 0x7be93865
7e90>
2 <keras.layers.pooling.max_pooling2d.MaxPooling2D object at 0x7be997db88d0>
3 <keras.layers.convolutional.conv2d.Conv2D object at 0x7be938637310>
4 <keras.layers.normalization.batch_normalization.BatchNormalization object at 0x7be93862
3810>
5 <keras.layers.pooling.max_pooling2d.MaxPooling2D object at 0x7be9385cd690>
6 <keras.layers.convolutional.conv2d.Conv2D object at 0x7be9385c6cd0>
7 <keras.layers.normalization.batch_normalization.BatchNormalization object at 0x7be9385d
7e50>
8 <keras.layers.pooling.max_pooling2d.MaxPooling2D object at 0x7be9981c45d0>
9 <keras.layers.reshaping.flatten.Flatten object at 0x7be9385cd3d0>
10 <keras.layers.core.dense.Dense object at 0x7be9385fb310>
11 <keras.layers.normalization.batch_normalization.BatchNormalization object at 0x7be9385
e71d0>
12 <keras.layers.core.dense.Dense object at 0x7be9385987d0>
13 <keras.layers.core.activation.Activation object at 0x7be9385f5f50>
14 <keras.layers.normalization.batch_normalization.BatchNormalization object at 0x7be9385
fb510>
15 <keras.layers.core.dense.Dense object at 0x7be938581090>
16 <keras.layers.core.activation.Activation object at 0x7be9385b7a90>
17 <keras.layers.normalization.batch_normalization.BatchNormalization object at 0x7be9385
98790>
18 <keras.layers.core.dense.Dense object at 0x7be938581050>
19 <keras.layers.core.activation.Activation object at 0x7be938560e90>
```

In [67]:

```
model_CNN.layers[-2]
```

Out[67]:

```
<keras.layers.core.dense.Dense at 0x7be938581050>
```

In [68]:

```
import os
os.environ["KERAS_BACKEND"] = "tensorflow"
kerasBKED = os.environ["KERAS_BACKEND"]
print(kerasBKED)
```

```
tensorflow
```

Separating Features Layers from the CNN Model

In [69]:

```
import tensorflow as tf
# feature_extractor = tf.keras.Model(inputs=model_CNN.input,
#                                     outputs=model_CNN.get_layer(-2).output)
# output_layers_model =tf.keras.Model(inputs=model_CNN.input, outputs=model_CNN.output)
# cnn_layer_output = model_CNN.layers[-2].output
# cnn_model_features = tf.keras.Model(inputs=model_CNN.input, outputs=cnn_layer_output)
cnn_model_features = tf.keras.Model(inputs=model_CNN.input, outputs=model_CNN.layers[-3]
.output)
```

Extracting Features from CNN Model

In [70]:

```
# Extract features from input data using the CNN model
X_train_cnn = cnn_model_features.predict(X_train)
X_test_cnn = cnn_model_features.predict(X_test)
```

```
1174/1174 [==============================] - 3s 2ms/step
294/294 [==============================] - 1s 2ms/step
```

Integrating CNN with SVM Classifier using Grid Search for Best Perameters

In [71]:

```
import numpy as np
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV

clf=SVC(kernel='rbf',C=100,gamma=0.001)
kf=KFold(n_splits=5)
scores_SVM = cross_val_score(clf, X_train_cnn, Y_train, cv=kf)
print(scores_SVM)
print("%0.2f accuracy with a standard deviation of %0.2f" % (scores_SVM.mean(), scores_SV
M.std()))
clf.fit(X_train_cnn, Y_train)
# Evaluate the combined CNN-SVM model on a test dataset
svm_accuracy = clf.score(X_test_cnn, Y_test)
print('SVM Accuracy:', svm_accuracy*100)
y_testSVM = clf.predict(X_test_cnn)
```

```
[1.         0.99986684 1.         1.         0.98122253]
1.00 accuracy with a standard deviation of 0.01
SVM Accuracy: 98.87077873655055
```

In [72]:

```
svm_accuracy = clf.score(X_test_cnn, Y_test)
print('SVM Accuracy:', svm_accuracy*100)
```

```
SVM Accuracy: 98.87077873655055
```

In [73]:

```
from sklearn.metrics import confusion_matrix, classification_report, accuracy_score

print(classification_report(Y_test, y_testSVM,target_names=target_names))
print("Accuracy: {0}".format(accuracy_score(Y_test, y_testSVM)*100))
```

```
                                                   precision    recall  f1-score   suppor
t

Actinic keratoses and intraepithelial carcinomae       1.00      1.00      1.00      135
9
                            basal cell carcinoma       1.00      1.00      1.00      131
8
                   benign keratosis-like lesions       0.98      0.99      0.98      126
2
                                  dermatofibroma       1.00      1.00      1.00      135
1
                                melanocytic nevi       0.98      0.94      0.96      137
4
              pyogenic granulomas and hemorrhage       1.00      1.00      1.00      135
8
                                        melanoma       0.97      0.99      0.98      136
5

                                        accuracy                           0.99      93
```

```
87                                              macro avg       0.99      0.99      0.99       938
7
                                             weighted avg       0.99      0.99      0.99       938
7

Accuracy: 98.87077873655055
```

Integrating CNN with Random Forest Classifier using Grid Search for Best Perameters

In [74]:

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV
rgclf = RandomForestClassifier(max_depth=3,
              max_features=1,
              min_samples_split=3,
              bootstrap=False,
              criterion=  "entropy",
              n_estimators=20)
kf=KFold(n_splits=5)
scores_RF = cross_val_score(rgclf, X_train_cnn, Y_train, cv=kf)
print(scores_RF)
print("%0.2f accuracy with a standard deviation of %0.2f" % (scores_RF.mean(), scores_RF.
std()))
rgclf.fit(X_train_cnn, Y_train)
RFC_accuracy = rgclf.score(X_test_cnn, Y_test)
print('Random Forest Classifier Accuracy:', RFC_accuracy*100)
y_test_RF = rgclf.predict(X_test_cnn)
print("Accuracy: {0}".format(accuracy_score(Y_test, y_test_RF)*100))
```

```
[0.99720373 0.9976032  0.99533955 0.99826874 0.96990278]
0.99 accuracy with a standard deviation of 0.01
Random Forest Classifier Accuracy: 96.65494833280069
Accuracy: 96.65494833280069
```

In [75]:

```
y_test_RF = rgclf.predict(X_test_cnn)
print("Accuracy: {0}".format(accuracy_score(Y_test, y_test_RF)*100))
```

```
Accuracy: 96.65494833280069
```

In [76]:

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import GridSearchCV

# parameters = {"n_neighbors": [1],
#                "weights": ['uniform', 'distance'],
#                "metric": ['minkowski','euclidean','manhattan'],
#                "algorithm": ['auto', 'ball_tree', 'kd_tree', 'brute']}
kgclf = KNeighborsClassifier(n_neighbors=1,
             weights='distance',
             metric='euclidean',
             algorithm= 'auto')
kf=KFold(n_splits=5)
scores_KNN = cross_val_score(kgclf, X_train_cnn, Y_train, cv=kf)
print("%0.2f accuracy with a standard deviation of %0.2f" % (scores_KNN.mean(), scores_KN
N.std()))
kgclf.fit(X_train_cnn, Y_train)
KNN_accuracy = kgclf.score(X_test_cnn, Y_test)
print('KNN Classifier Accuracy:', KNN_accuracy*100)
```

```
1.00 accuracy with a standard deviation of 0.01
KNN Classifier Accuracy: 99.12645147544477
```

In [77]:

```
y_testKNN = kgclf.predict(X_test_cnn)
from sklearn.metrics import confusion_matrix, classification_report, accuracy_score

print(classification_report(Y_test, y_testKNN,target_names=target_names))
print("Accuracy Score: {0}".format(accuracy_score(Y_test, y_testKNN)*100))
```

```
                                                    precision    recall  f1-score   suppor
t

Actinic keratoses and intraepithelial carcinomae         1.00      1.00      1.00      135
9
                            basal cell carcinoma         0.99      1.00      1.00      131
8
                   benign keratosis-like lesions         0.98      1.00      0.99      126
2
                                  dermatofibroma         1.00      1.00      1.00      135
1
                                melanocytic nevi         1.00      0.94      0.97      137
4
              pyogenic granulomas and hemorrhage         1.00      1.00      1.00      135
8
                                        melanoma         0.97      1.00      0.99      136
5

                                        accuracy                             0.99      93
87
                                       macro avg         0.99      0.99      0.99      938
7
                                    weighted avg         0.99      0.99      0.99      938
7

Accuracy Score: 99.12645147544477
```

Integrating CNN with Logistic Regression Classifier using Grid Search for Best Perameters

In [78]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix, classification_report, accuracy_score



# Create a logistic regression object
grid_search_LR = LogisticRegression(C=100,
              penalty='l2')
kf=KFold(n_splits=5)
scores_LR = cross_val_score(grid_search_LR, X_train_cnn, Y_train, cv=kf)
print(scores_LR)
print("%0.2f accuracy with a standard deviation of %0.2f" % (scores_LR.mean(), scores_LR.
std()))
# Perform grid search with 5-fold cross-validation
grid_search_LR.fit(X_train_cnn, Y_train)

# Print the best hyperparameters and the corresponding accuracy score
y_test_LR = grid_search_LR.predict(X_test_cnn)

print(classification_report(Y_test, y_test_LR,target_names=target_names))
print("Accuracy: {0}".format(accuracy_score(Y_test, y_test_LR)*100))
```

```
/opt/conda/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:818: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
```

```
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
/opt/conda/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:818: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
/opt/conda/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:818: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
/opt/conda/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:818: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
```

```
[1.         1.         1.         1.         0.98108936]
1.00 accuracy with a standard deviation of 0.01
                                                    precision    recall  f1-score   suppor
t

Actinic keratoses and intraepithelial carcinomae       1.00      1.00      1.00       135
9
                             basal cell carcinoma       1.00      1.00      1.00       131
8
                    benign keratosis-like lesions       0.97      0.99      0.98       126
2
                                   dermatofibroma       1.00      1.00      1.00       135
1
                                  melanocytic nevi       0.98      0.94      0.96       137
4
               pyogenic granulomas and hemorrhage       1.00      1.00      1.00       135
8
                                         melanoma       0.97      0.99      0.98       136
5

                                         accuracy                          0.99      93
87
                                        macro avg       0.99      0.99      0.99       938
7
                                     weighted avg       0.99      0.99      0.99       938
7

Accuracy: 98.78555449025248
```

```
/opt/conda/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:818: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
```

In [ ]:

In [ ]:

```
```

In [ ]:

```
```