Skin Cancer lesion classification using the HAM10000 dataset.

Dataset link: https://www.kaggle.com/datasets/kmader/skin-cancer-mnist-ham10000

The 7 classes of skin Cancer lesions included in this dataset are: akiec, bcc, bkl, df, nv, mel, vasc

```
import os
import glob
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import random
from PIL import Image
from PIL import Image
import cv2
```

```
# Mount your Google Drive
from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).
```

```
!apt-get update -qq && apt-get install -y -qq unrar
```

```
W: Skipping acquire of configured file 'main/source/Sources' as repository 'https://r2u.stat.illinois.edu/ubuntu jammy InRelease
```

```
!mkdir -p /content/HAM10000
!unrar x "/content/drive/MyDrive/HAM10000.rar" /content/HAM10000/
```

```
Streaming output truncated to the last 5000 lines.
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029323.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029324.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029325.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029326.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029327.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029328.jpg  OK
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Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029330.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029331.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029332.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029333.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029334.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029335.jpg  OK
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Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029337.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029338.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029339.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029340.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029341.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029342.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029343.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029344.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029345.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029346.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029347.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029348.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029349.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029350.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029351.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029352.jpg  OK
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Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029357.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029358.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029359.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029360.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029361.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029362.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029363.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029364.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029365.jpg  OK
```

```
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029366.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029367.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029368.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029369.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029370.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029371.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029372.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029373.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029374.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029375.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029376.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029377.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029378.jpg  OK
Extracting  /content/HAM10000/archive (2)/HAM10000_images_part_2/ISIC_0029379.jpg  OK
```

```
!ls -lah /content/HAM10000
!find /content/HAM10000 -maxdepth 2 -type d -print
```

```
total 12K
drwxr-xr-x 3 root root 4.0K Jan  8 19:09  .
drwxr-xr-x 1 root root 4.0K Jan  8 19:09  ..
drwxr-xr-x 4 root root 4.0K Sep 18 12:03 'archive (2)'
/content/HAM10000
/content/HAM10000/archive (2)
/content/HAM10000/archive (2)/HAM10000_images_part_1
/content/HAM10000/archive (2)/HAM10000_images_part_2
```

```
from pathlib import Path

DATA_DIR = Path("/content/HAM10000/archive (2)")  # adjust if needed
p1 = DATA_DIR / "HAM10000_images_part_1"
p2 = DATA_DIR / "HAM10000_images_part_2"

n1 = len(list(p1.glob("*.jpg")))
n2 = len(list(p2.glob("*.jpg")))
print("part_1 jpgs:", n1, " | part_2 jpgs:", n2, " | total:", n1+n2)  # expect 10015
```

```
part_1 jpgs: 5000  | part_2 jpgs: 5015  | total: 10015
```

```
import pandas as pd

metadata_path = os.path.join(DATA_DIR, "HAM10000_metadata.csv")
metadata = pd.read_csv(metadata_path)
metadata.head()
```

	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

```
metadata.shape
```

```
(10015, 7)
```

Load the images paths: Create 2 paths from drive. The images are separeted in these paths, so if they do not exist in path 1 they probably exist in path 2. Scanning all the rows using the "dx" and the "image_id" columns we can add the image path in a separete column in the dataframe.

```
import os, glob
import pandas as pd

# 0) Confirm your metadata DF exists
print("metadata shape:", metadata.shape)

# 1) Set correct base dirs (NO class subfolders)
DATA_DIR  = "/content/HAM10000/archive (2)"
```

```
BASE1_DIR = os.path.join(DATA_DIR, "HAM10000_images_part_1")
BASE2_DIR = os.path.join(DATA_DIR, "HAM10000_images_part_2")

print("BASE1 exists?", os.path.isdir(BASE1_DIR), "->", BASE1_DIR)
print("BASE2 exists?", os.path.isdir(BASE2_DIR), "->", BASE2_DIR)

# 2) Index all image files from both parts
jpgs = glob.glob(os.path.join(BASE1_DIR, "*.jpg")) + glob.glob(os.path.join(BASE2_DIR, "*.jpg"))
print("Total jpgs found:", len(jpgs))
assert len(jpgs) > 0, "No .jpg files found. Check that your dataset is extracted under /content/HAM10000/archive (2)."

# 3) Build id -> fullpath dict (e.g., 'ISIC_0024306' -> '/content/.../ISIC_0024306.jpg')
id2path = {os.path.splitext(os.path.basename(p))[0]: p for p in jpgs}
print("Unique ids indexed:", len(id2path))

# 4) Map into the DF (length will ALWAYS match)
metadata["image_path"] = metadata["image_id"].map(id2path.get)

# 5) Report any misses
missing = metadata["image_path"].isna().sum()
print("Missing paths:", missing)
if missing:
    print("Example missing IDs:", metadata.loc[metadata["image_path"].isna(), "image_id"].head().tolist())

# 6) Peek
metadata.head()
```

```
metadata shape: (10015, 7)
BASE1 exists? True -> /content/HAM10000/archive (2)/HAM10000_images_part_1
BASE2 exists? True -> /content/HAM10000/archive (2)/HAM10000_images_part_2
Total jpgs found: 10015
Unique ids indexed: 10015
Missing paths: 0
```

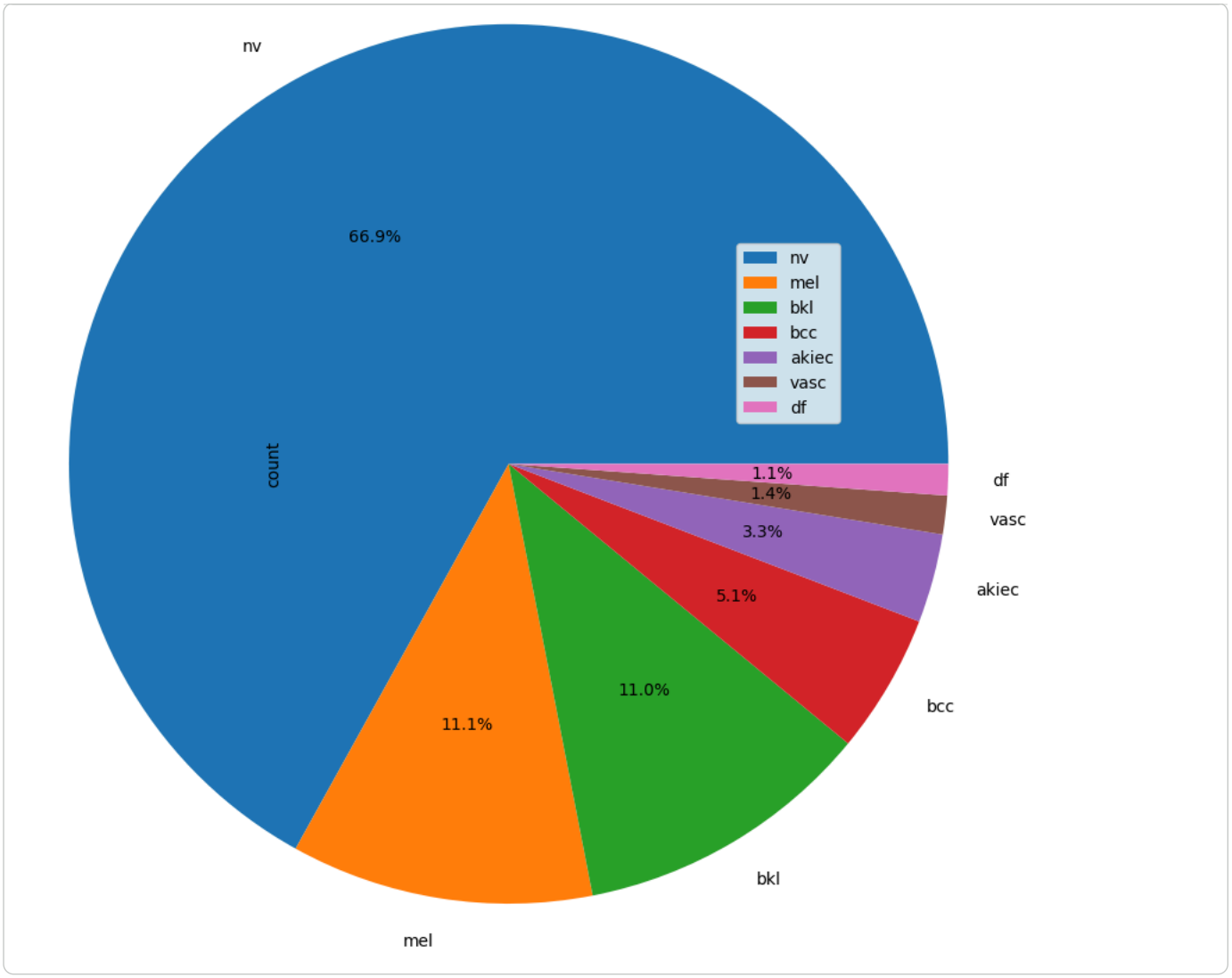
	lesion_id	image_id	dx	dx_type	age	sex	localization	image_path
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp	/content/HAM10000/archive (2)/HAM10000_images_...
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp	/content/HAM10000/archive (2)/HAM10000_images_...
2	HAM_0002730	ISIC_0026769	bkl	histo	80.0	male	scalp	/content/HAM10000/archive (2)/HAM10000_images_...
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp	/content/HAM10000/archive (2)/HAM10000_images_...
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear	/content/HAM10000/archive (2)/HAM10000_images_...

Check the distribution of the class

```
import os

DATA_DIR = "/content/HAM10000/archive (2)"
print("✅ DATA_DIR:", DATA_DIR)
print(os.listdir(DATA_DIR))
print("metadata shape:", metadata.shape)             # should be (10015, ?)
print("unique image_id:", metadata["image_id"].nunique())  # 10015
print("dx distribution:\n", metadata["dx"].value_counts().sort_index())
```

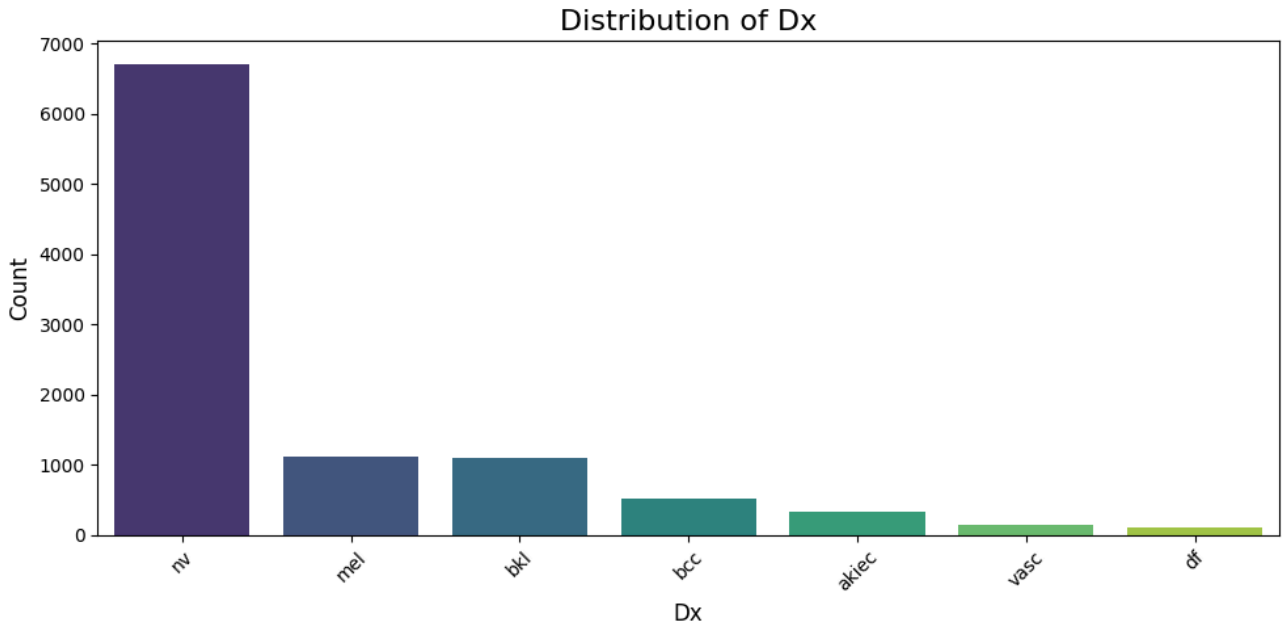
```
✅ DATA_DIR: /content/HAM10000/archive (2)
['HAM10000_images_part_1', 'HAM10000_metadata.csv', 'HAM10000_images_part_2']
metadata shape: (10015, 8)
unique image_id: 10015
dx distribution:
 dx
akiec     327
bcc       514
bkl      1099
df        115
mel      1113
nv       6705
vasc      142
Name: count, dtype: int64
```

```
count = metadata['dx'].value_counts()
ax = count.plot(kind="pie", autopct='%1.1f%%', legend=True,radius=2.5)
ax.legend(bbox_to_anchor=(1, 1.02), loc='upper left')
plt.show()
```

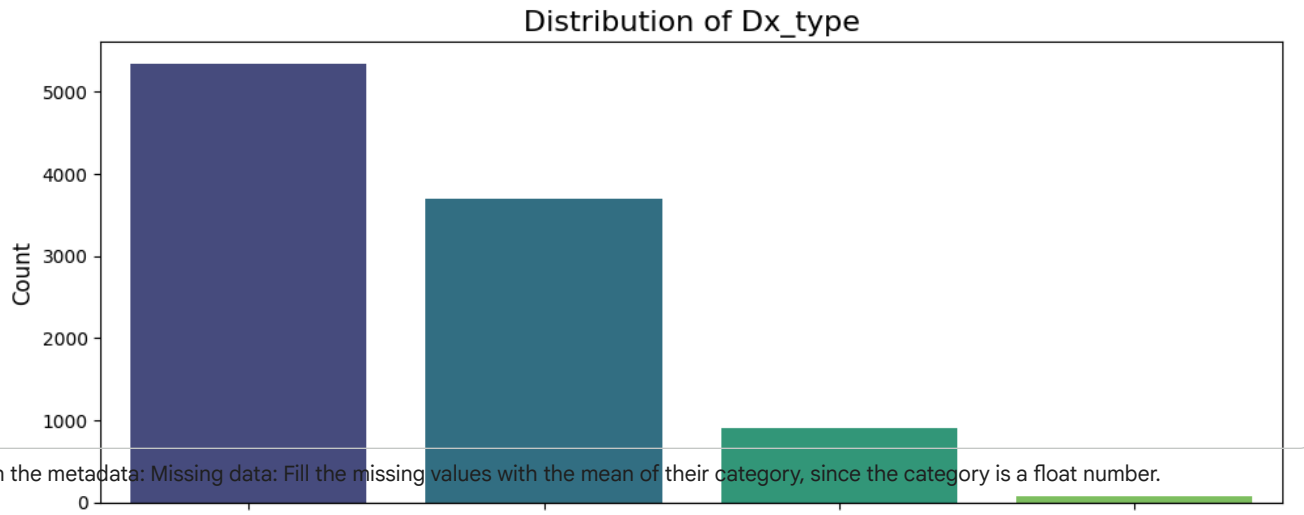



```
import matplotlib.pyplot as plt
import seaborn as sns

columns_exp = ['dx','dx_type', 'sex', 'localization']

for column in columns_exp:
    plt.figure(figsize=(10,5))

    sns.countplot(
        data=metadata,
        x=column,
        order=metadata[column].value_counts().index,
        palette="viridis"
    )

    plt.title(f"Distribution of {column.capitalize()}", fontsize=16)
    plt.xlabel(column.capitalize(), fontsize=12)
    plt.ylabel("Count", fontsize=12)
    plt.xticks(rotation=45)
    plt.tight_layout()
    plt.show()

# AGE as histogram (correct method)
plt.figure(figsize=(10,5))
sns.histplot(metadata["age"].dropna(), bins=30, kde=True, color="teal")
plt.title("Age Distribution", fontsize=16)
plt.xlabel("Age", fontsize=12)
plt.ylabel("Frequency", fontsize=12)
plt.show()
```

```
/tmp/ipython-input-1737115017.py:9: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and se

  sns.countplot(
```




```
/tmp/ipython-input-1737115017.py:9: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and se

  sns.countplot(
```

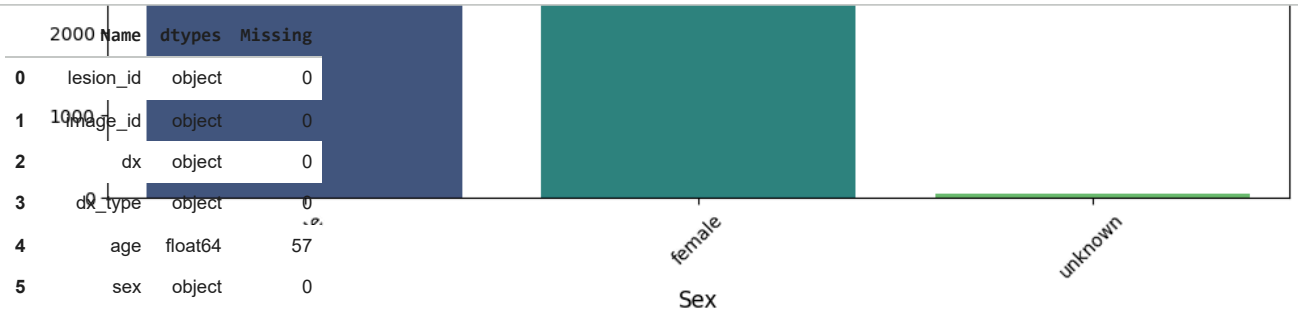


Clean the metadata: Missing data: Fill the missing values with the mean of their category, since the category is a float number.

```
def check_for_missing_data(df):
    summary = pd.DataFrame(df.dtypes,columns=['dtypes'])
    summary = summary.reset_index()
    summary['Name'] = summary['index']
    summary = summary[['Name','dtypes']]
    summary['Missing'] = df.isnull().sum().values
    return summary
```

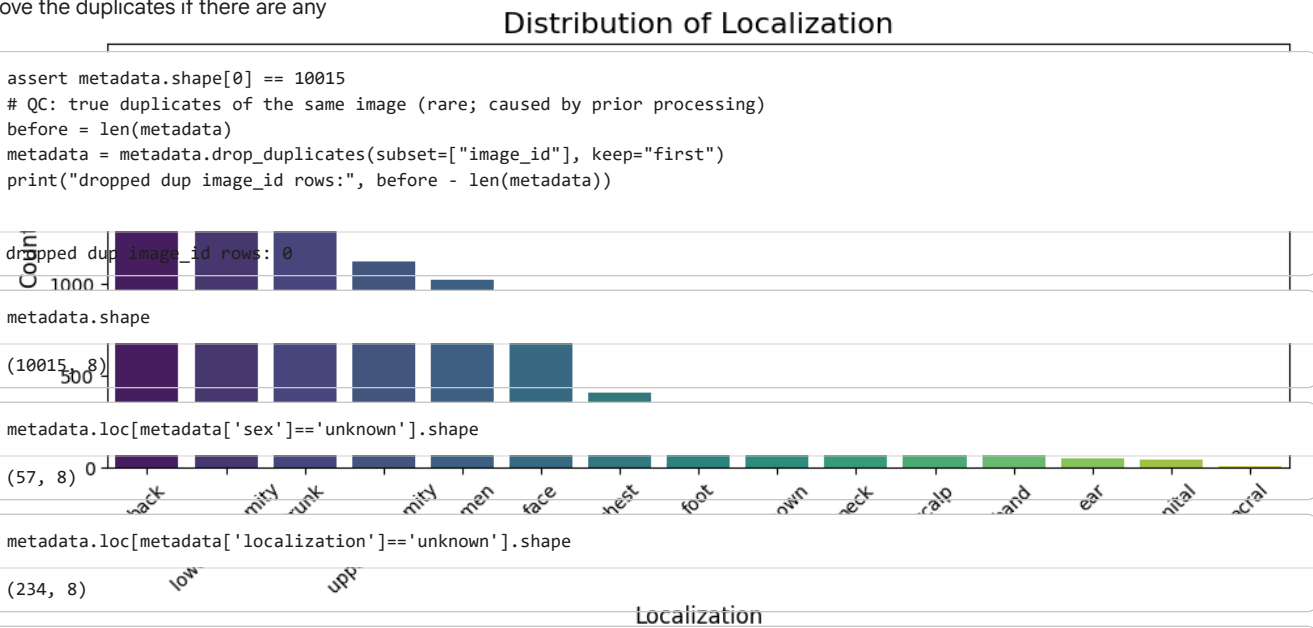
```
check_for_missing_data(metadata)
```

	Name	dtypes	Missing
0	lesion_id	object	0
1	image_id	object	0
2	dx	object	0
3	dx_type	object	0
4	age	float64	57
5	sex	object	0
6	localization	object	0
7	image_path	object	0




```
y:9: FutureWarning:
Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and se
  sns.countplot(
```

Remove the duplicates if there are any




```
assert metadata.shape[0] == 10015
# QC: true duplicates of the same image (rare; caused by prior processing)
before = len(metadata)
metadata = metadata.drop_duplicates(subset=["image_id"], keep="first")
print("dropped dup image_id rows:", before - len(metadata))
```

```
dropped dup image_id rows: 0
```

```
metadata.shape
```

```
(10015, 8)
```

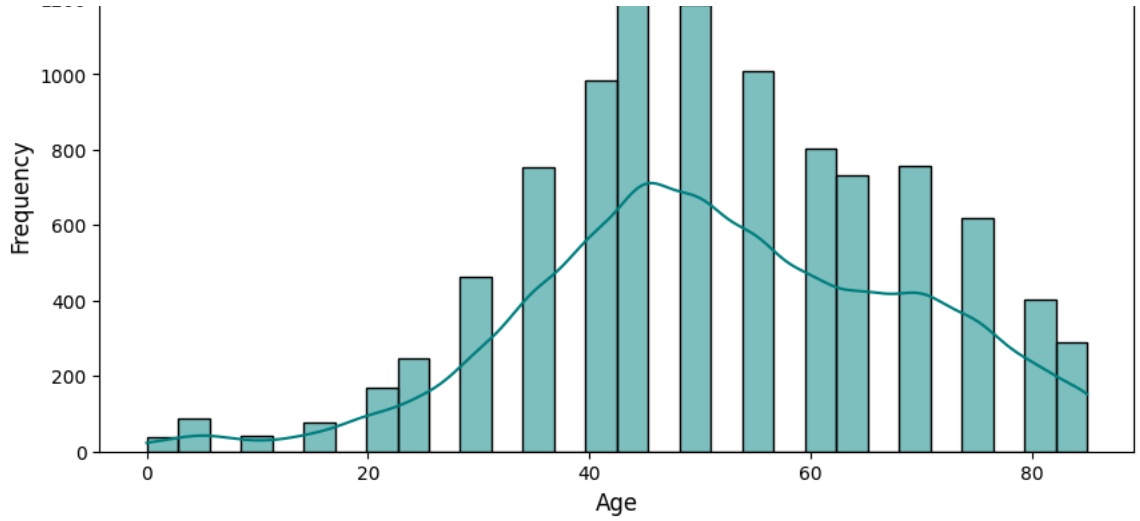
```
metadata.loc[metadata['sex']=='unknown'].shape
```

```
(57, 8)
```

```
metadata.loc[metadata['localization']=='unknown'].shape
```

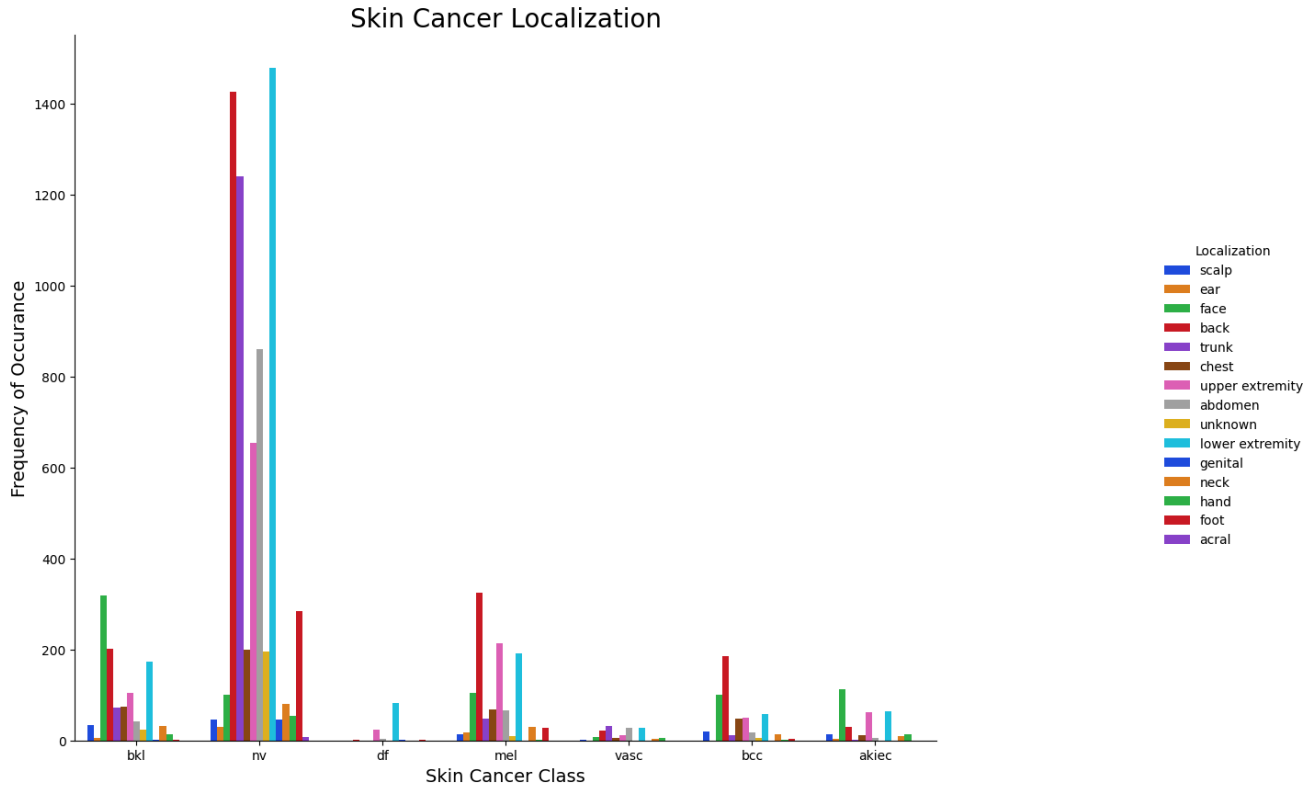
```
(234, 8)
```

```
plt.figure(figsize=(12,6))
sns.violinplot(data=metadata, x="dx", y="age", palette="Set3")
plt.title("Age Distribution per Lesion Type", fontsize=16)
plt.show()
```



```
/tmp/ipython-input-3830741751.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set

  sns.violinplot(data=metadata, x="dx", y="age", palette="Set3")
```


```
g = sns.catplot(x="dx", kind="count", hue="localization", palette='bright', data=metadata)
g.fig.set_size_inches(16, 9)

g.ax.set_title('Skin Cancer Localization', fontsize=20)
g.set_xlabels('Skin Cancer Class', fontsize=14)
g.set_ylabels('Frequency of Occurance', fontsize=14)
g._legend.set_title('Localization')
```

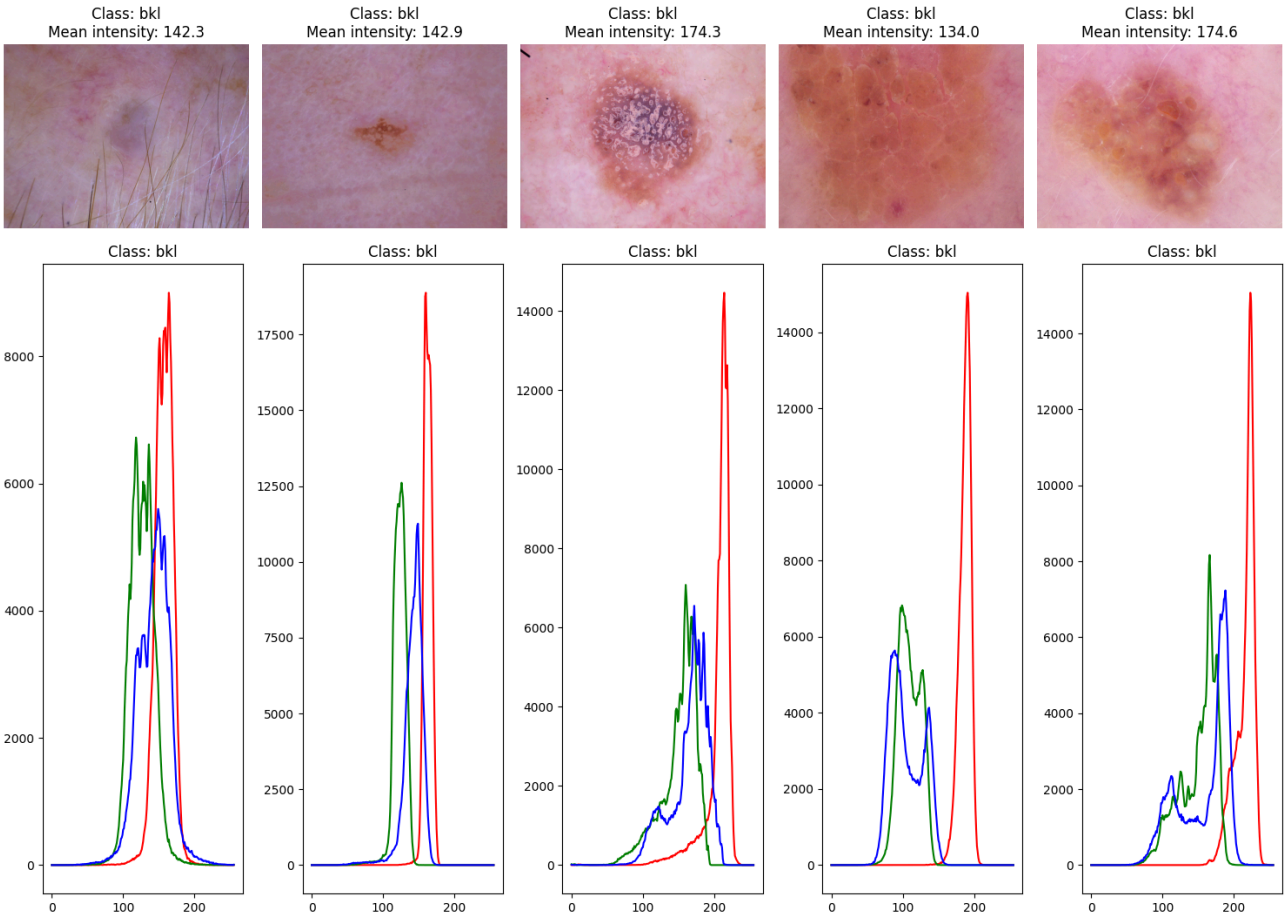


Plot images from each class and their color distributions

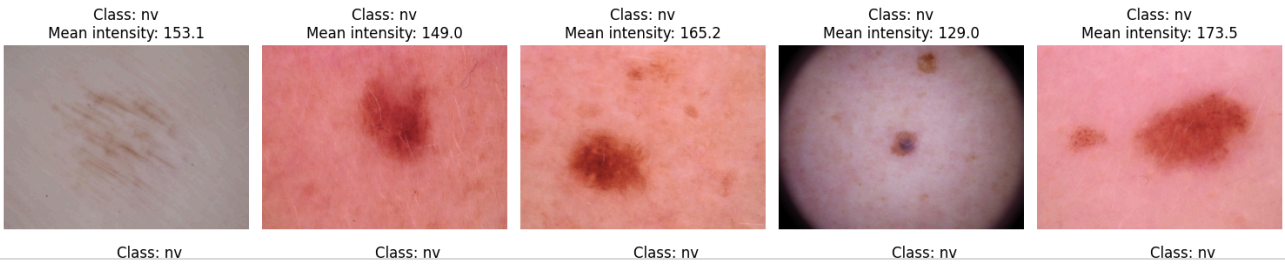
```
def pltImg(images, labels, row_num, col_num):
    fig, axes = plt.subplots(row_num, col_num, figsize=(15, 8))
    axes = axes.ravel()  # Flatten axes array

    for i, image in enumerate(images):
        axes[i].imshow(image)
        axes[i].axis('off')
        axes[i].set_title(f"Class: {labels[i]}\nMean intensity: {np.mean(image):.1f}")

    plt.tight_layout()
    plt.show()


def pltHist(images, labels, row_num, col_num):
    fig, axes = plt.subplots(row_num, col_num, figsize=(15, 8))
    axes = axes.ravel()  # Flatten axes array
    colors = ["red", "green", "blue"]

    for i, image in enumerate(images):
        image_array = np.array(image)

        # Plotting all channels with colors
        for channel in range(3):
            hist, bin_edges = np.histogram(image_array[:, :, channel], bins=256, range=(0, 256))
            axes[i].plot(bin_edges[:-1], hist, color=colors[channel])
```

```
            axes[i].set_title(f"Class: {labels[i]}")

        plt.tight_layout()
        plt.show()
    def randImg(df, label, seed, sample_size):
        # Filter dataframe for specific label/class
        df_class = df[df['dx'] == label]

        # Randomly sample images from this class
        random.seed(seed)
        sample_df = df_class.sample(n=sample_size)

        images = []
        labels = []
        for index, row in sample_df.iterrows():
            image_path = row['image_path']
            if os.path.exists(image_path):
                image = Image.open(image_path).convert("RGB")
                images.append(image)
                labels.append(label)
            else:
                print(f"Image not found: {image_path}")

        return images, labels


    class_labels = ['bkl', 'nv', 'df', 'mel', 'vasc', 'bcc', 'akiec']

    for class_label in class_labels:
        print(f"\n--- Showcasing examples for class: {class_label} ---\n")
        images, labels = randImg(df=metadata, label=class_label, seed=42, sample_size=5)

        # For displaying images
        pltImg(images, labels, 1, 5)
        # pltImgEq(images, labels, 1, 5)
        # For displaying histograms
        pltHist(images, labels, 1, 5)
```

```
--- Showcasing examples for class: bkl ---
```




```
--- Showcasing examples for class: nv ---
```




```
from pathlib import Path
import pandas as pd

DATA_DIR = Path("/content/HAM10000/archive (2)")
p1 = DATA_DIR / "HAM10000_images_part_1"
p2 = DATA_DIR / "HAM10000_images_part_2"

# Build a fresh id -> path dictionary
id2path = {}
for folder in [p1, p2]:
    for f in folder.glob("*.jpg"):
        id2path[f.stem] = str(f.resolve())

# Attach/refresh image_path on the *metadata* DF
metadata["image_path"] = metadata["image_id"].map(id2path)

missing = metadata["image_path"].isna().sum()
print("Rows missing image files in metadata:", missing)
```

```
Rows missing image files in metadata: 0
```

```
MAL = {'mel','bcc','akiec'}           # 1 = malignant
BEN = {'nv','bkl','df','vasc'}        # 0 = benign

df = metadata[metadata["dx"].isin(MAL | BEN)].copy()
df["label"] = df["dx"].apply(lambda x: 1 if x in MAL else 0)

# sanity
print("Columns in df:", list(df.columns)[:10])
assert "image_path" in df.columns
```

```
Columns in df: ['lesion_id', 'image_id', 'dx', 'dx_type', 'age', 'sex', 'localization', 'image_path', 'label']
```