Cancer Image Analysis and Detection Tutorial

Step 1: Importing Required Libraries

The first step is importing the necessary Python libraries. Here's what each library does:

```
import cv2                                                    # For image processing
import numpy as np                                            # For numerical computations
from tensorflow.keras.models import Sequential                # For building the CNN model
from tensorflow.keras.layers import (Conv2D, MaxPooling2D, Flatten, Dense)  # CNN layers
import matplotlib.pyplot as plt                               # For plotting and visualization
```

Explanation:
1. OpenCV (cv2): Used to handle image input, preprocessing, and visualizing results.
2. NumPy (np): Essential for handling arrays and numerical computations.
3. Keras Sequential Model: Used to define the Convolutional Neural Network (CNN) model architecture.
4. Matplotlib: For visualizing the input image, results, and bounding boxes on the detected regions.

Step 2: Downloading Pretrained Model

The pretrained model weights (model.h5) are downloaded using the following code:

```
!gdown --id 1L5TMRMn78eTn7Z1joS2vfCCtadCKG4Mu
```

Explanation:
- gdown: A Python package to download files directly from Google Drive using the file ID.
- The file ID is a unique identifier in the URL of the Google Drive file.

```
Downloading pretrained model:
/usr/local/lib/python3.10/dist-packages/gdown/__main__.py:140: FutureWarning: Option `--id` was deprecated in version 4.3.1 and will be removed in 5.0. You don't need to pass it anymor
  warnings.warn(
Downloading...
From: https://drive.google.com/uc?id=1-yatFvHQokK7fHaaaAMO2TkvlgkUnXhw
To: /content/model.h5
100% 9.59M/9.59M [00:00<00:00, 48.6MB/s]
Done!
```

Step 3: Creating and Compiling the CNN Model

A simple CNN architecture is created and compiled.

```
model = Sequential([
   Conv2D(32, (3, 3), activation='relu', input_shape=(500, 500, 3)),
   MaxPooling2D((2, 2)),
   Conv2D(64, (3, 3), activation='relu'),
   MaxPooling2D((2, 2)),
   Flatten(),
   Dense(128, activation='relu'),
   Dense(1, activation='sigmoid')  # Output for binary classification
])

model.compile(optimizer='rmsprop', loss='binary_crossentropy', metrics=['accuracy'])
```

Explanation:
1. Input Layer: Accepts RGB images of size 500x500x3.
2. Convolutional Layers: Extract features from the input image.
   - Conv2D(32, (3, 3)): 32 filters of size 3x3 are used to extract features.
3. Pooling Layers: Reduces dimensionality while retaining important features.
4. Flatten Layer: Converts the output into a 1D vector.
5. Dense Layers: Fully connected layers for binary classification.
6. Output Layer: Uses sigmoid activation for binary output (e.g., tumor or no tumor).
7. Compilation:
   - Optimizer: rmsprop optimizes the model during training.
   - Loss Function: binary_crossentropy is used since this is a binary classification problem.

Step 4: Loading Pretrained Weights

The trained weights are loaded into the model:

```
model.load_weights('model.h5')
```

Explanation:
The model.h5 file contains the trained model's weights, enabling inference without retraining the model.

Step 5: Reading and Preprocessing the Image

An input image is read, resized, and preprocessed for both bounding box detection and classification.

```
image = cv2.imread('image.png')                                    # Read the image
image = cv2.resize(image, (500, 500))                              # Resize to the required dimensions
gray = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)                     # Convert to grayscale
blur = cv2.GaussianBlur(gray, (5, 5), 0)                           # Smooth the image
_, thresh = cv2.threshold(blur, 0, 255, cv2.THRESH_BINARY + cv2.THRESH_OTSU)  # Thresholding
```

Explanation:

1. Grayscale Conversion: Simplifies the image for thresholding.
2. Gaussian Blur: Reduces noise and smooths the image.
3. Otsu's Thresholding: Automatically determines the optimal threshold value for segmentation.

Step 6: Detecting Tumor Regions

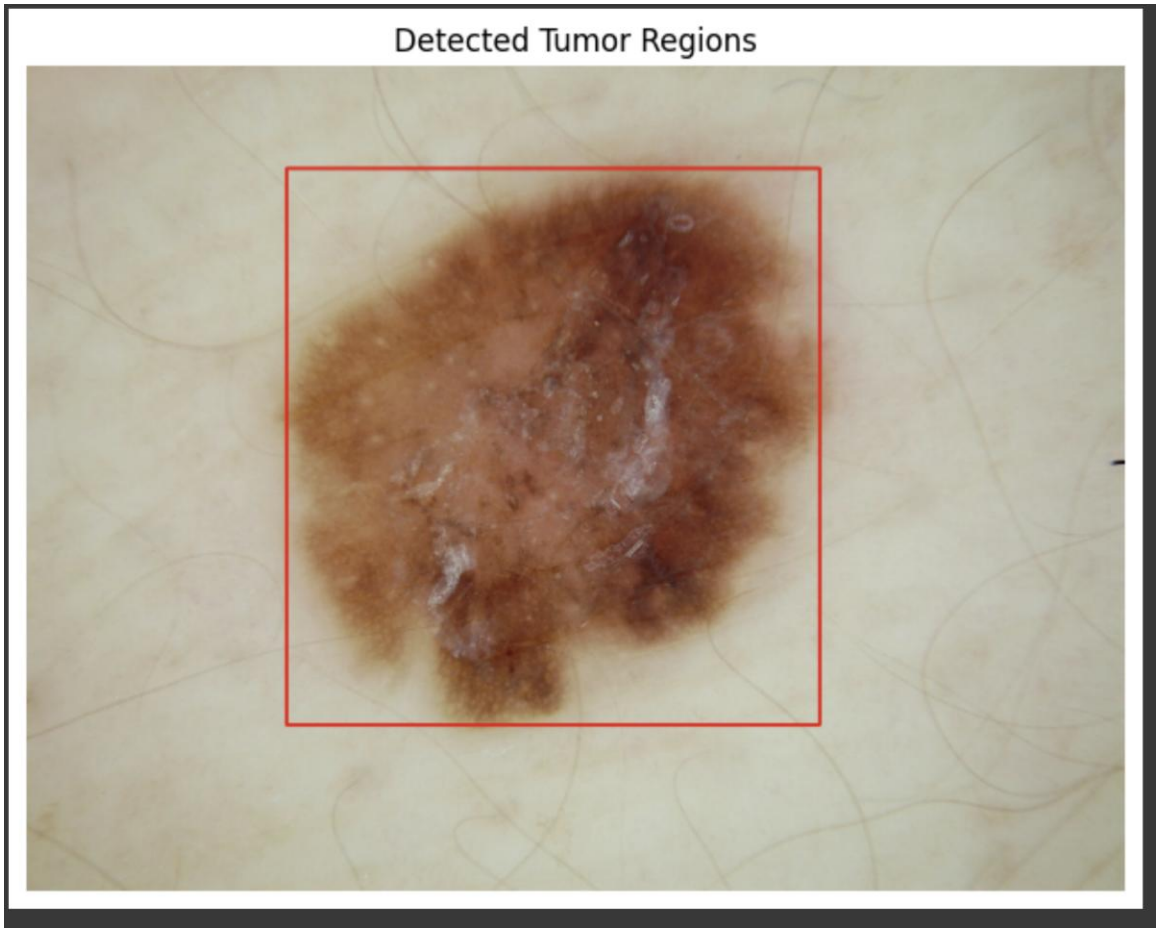
Contours are detected from the binary image (thresholded result) to identify tumor regions.

```
contours, _ = cv2.findContours(thresh, cv2.RETR_EXTERNAL, cv2.CHAIN_APPROX_SIMPLE)
for contour in contours:
    x, y, w, h = cv2.boundingRect(contour)                         # Get bounding box coordinates
    cv2.rectangle(image, (x, y), (x + w, y + h), (0, 255, 0), 2)   # Draw rectangles
```

Explanation:

1. Contours: Extracts boundaries of segmented regions.

2. Bounding Rectangles: For each contour, a bounding box is drawn on the original image to highlight the detected regions.



Step 7: Image Class Prediction

The preprocessed image is reshaped to match the input dimensions required by the model (1, 500, 500, 3) and fed into the model to get predictions. The output class is determined based on the highest predicted probability.

```
[ ]  new_array = np.reshape(new_array, (1, 500, 500, 3,))
     prediction = model.predict([new_array])
     print(classes[np.argmax(prediction)])

     1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 85ms/step
     benign
```

Steps 8-10: Steps 5-7 are repeated for different class image.