## **Introduction**

The following document outlines the design and architecture of a skin cancer classification model using a Sequential model in Keras. The model is designed to classify skin cancer images into one of seven different classes. The architecture of the model consists of convolutional layers, pooling layers, and fully connected layers.

## **Model Architecture**

The skin cancer classification model is built using a Sequential model from the Keras library. The model architecture is as follows:

1. Input Layer: The input layer of the model expects images of size 28x28 pixels with 3 color channels (RGB).
2. Convolutional Layers: The model starts with a convolutional layer with 16 filters, a kernel size of (3, 3), and 'relu' activation function. The layer uses 'same' padding to preserve the spatial dimensions of the input. This is followed by another convolutional layer with 32 filters and the same kernel size and activation function. Both these layers help extract relevant features from the input images.
3. Pooling Layer: After the second convolutional layer, a MaxPooling2D layer with a pool size of (2, 2) is added. This layer performs down-sampling by taking the maximum value within each 2x2 region. It reduces the spatial dimensions of the features maps while retaining important information.
4. Convolutional Layers (with Padding): The model continues with a convolutional layer with 32 filters, a kernel size of (3, 3), 'relu' activation function, and 'same' padding. This is followed by another convolutional layer with 64 filters, the same kernel size and activation function. Both layers utilize padding to ensure the output feature maps have the same spatial dimensions as the input.
5. Pooling Layer (with Padding): Following the second set of convolutional layers, a MaxPooling2D layer with a pool size of (2, 2) and 'same' padding is added. This layer reduces the spatial dimensions further while retaining important information.
6. Flatten Layer: After the pooling layers, a Flatten layer is introduced to flatten the 3D feature maps into a 1D vector. This prepares the data for the fully connected layers.
7. Fully Connected Layers: Two fully connected (Dense) layers are added after the Flatten layer. The first dense layer has 64 units with 'relu' activation function, and the second dense layer has 32 units with 'relu' activation function. These layers help to learn non-linear patterns in the data and extract higher-level features.
8. Output Layer: The final layer of the model is a Dense layer with 7 units, representing the 7 classes of skin cancer. It uses the 'softmax' activation function to produce probabilities for each class, indicating the likelihood of an input image belonging to each class.

## **Model Architecture Justification**

1. Convolutional Layers: Convolutional layers are well-suited for image classification tasks due to their ability to capture local patterns and spatial relationships within the images. By applying multiple convolutional layers, the model can learn hierarchical representations of the input images, starting from low-level features (e.g., edges, textures) to higher-level features (e.g., shapes, structures).
2. Pooling Layers: Pooling layers serve two main purposes in the model architecture. Firstly, they down-sample the feature maps, reducing the spatial dimensions and computational complexity of the subsequent layers. Secondly, they help to extract the most salient features from the feature maps by selecting the maximum value within each pooling region. This aids in retaining important information while discarding irrelevant details, leading to more robust and efficient representations.
3. Flatten Layer: The Flatten layer is introduced after the pooling layers to convert the 3D feature maps into a 1D vector. This flattening process allows the data to be fed into the subsequent fully connected layers. By transforming the spatial information into a linear format, the model can effectively capture the global relationships and dependencies between the features.
4. Fully Connected Layers: Fully connected layers are responsible for learning non-linear patterns in the data and extracting higher-level representations. By connecting every neuron from the previous layer to every neuron in the current layer, these layers can capture complex relationships and make more sophisticated predictions. The use of multiple dense layers allows for the extraction of increasingly abstract features, ultimately leading to better discrimination between the different skin cancer classes.
5. Output Layer: The output layer is a Dense layer with 7 units, representing the 7 classes of skin cancer. The 'softmax' activation function is chosen to produce probabilities for each class. Softmax ensures that the predicted probabilities sum up to 1, allowing for interpretation as class probabilities. This activation function is suitable for multi-class classification problems like skin cancer classification.

## **Summary**

The chosen model architecture, consisting of convolutional layers, pooling layers, and fully connected layers, provides a solid framework for effective skin cancer classification. The convolutional layers extract relevant local features, the pooling layers down-sample the feature maps and retain important information, and the fully connected layers capture higher-level representations. Overall, this architecture strikes a balance between complexity and interpretability, enabling the model to learn discriminative features and make accurate predictions for the given problem statement.