**S1 Algorithm. Pseudocode for creating the neural network architecture used in this work.** For the hyperparameter space, see S2 Table.

|  |
| --- |
| // Depth of the first convolution layer (tuned)  base\_depth := 16  // Rate of depth growth with every stride 2 layer (fixed)  depth\_growth := 1.25  // Num stride 2 layers (fixed)  stride\_2\_layers := 4  // Num stride 1 layers per stride 2 layer (tuned)  stride\_1\_layers := 1  // Size of convolution kernel (fixed)  kernel\_size := 3  features = Conv2D(images, base\_depth, kernel\_size, stride=1)  **for** i := 1 to stride\_2\_layers **do**  [depth](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=189&gs=kythe%253A%252F%252Fgoogle3%253Flang%253Dpython%253Fpath%253Dmedical%252Fpathology%252Ftensorflow%252Fcomponents%252Fnetwork%252Fmobilenet.py%2523module.get_mobilenet_conv_defs.depth&gsn=depth&ct=xref_usages) = int([base\_depth](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=159&ct=xref_jump_to_def&gsn=base_depth&rcl=300225872) \* [depth\_growth](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=160&ct=xref_jump_to_def&gsn=depth_growth&rcl=300225872) \*\* [i](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=188&ct=xref_jump_to_def&gsn=i&rcl=300225872))  // [DepthwiseSeparableConv](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=32&ct=xref_jump_to_def&gsn=DepthSepConvDef&rcl=300225872)2D is available as tf.keras.layers.SeparableConv2D  features = [DepthwiseSeparableConv](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=32&ct=xref_jump_to_def&gsn=DepthSepConvDef&rcl=300225872)2D(features, depth, kernel\_size, stride=2)  **for**j := 1 to [stride\_1\_layers](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=162&ct=xref_jump_to_def&gsn=num_stride_1_layers&rcl=300225872) **do**  features = [DepthwiseSeparableConv](https://cs.corp.google.com/piper///depot/google3/medical/pathology/tensorflow/components/network/mobilenet.py?l=32&ct=xref_jump_to_def&gsn=DepthSepConvDef&rcl=300225872)2D(features, depth, kernel\_size, stride=1)  features =AveragePooling2D(features) |