Deep Learning in Medicine: Classifying Melanoma

Part 1: Training a Model

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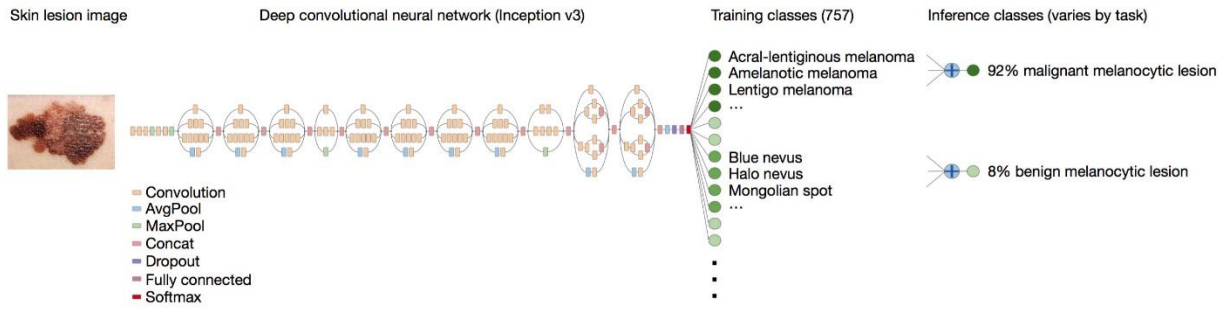
Deep learning offers the opportunity to improve clinical outcomes in medicine, enabling healthcare providers to serve growing patient populations with scarce clinical resources, and providing care givers with the tools they need to focus on patients with critical conditions.

The applications for the use of deep learning image classification extend across all areas where visual diagnosis is used in patient care. This includes radiology (arteriography, mammography, radiomics), dermatology, and oncology, as well as clinical and biotech R&D.

In this series, we will explore applications of deep learning in medicine, including the staging of data, training of deep learning models, evaluating models, the use of distributed compute, and the operationalization of our models.

In this article, we will take a look using deep learning to classify Melanoma. Specifically, we will use images of skin, to classify whether the patient associated with the image, has a malignant tumor. The diagram below shows a classification model based on Stanford Medicines classification of skin disease using the Inception v3 CNN architecture (reprinted from https://research.googleblog.com/2016/03/train-your-own-image-classifier-with.html, and https://cs.stanford.edu/people/esteva/nature/)

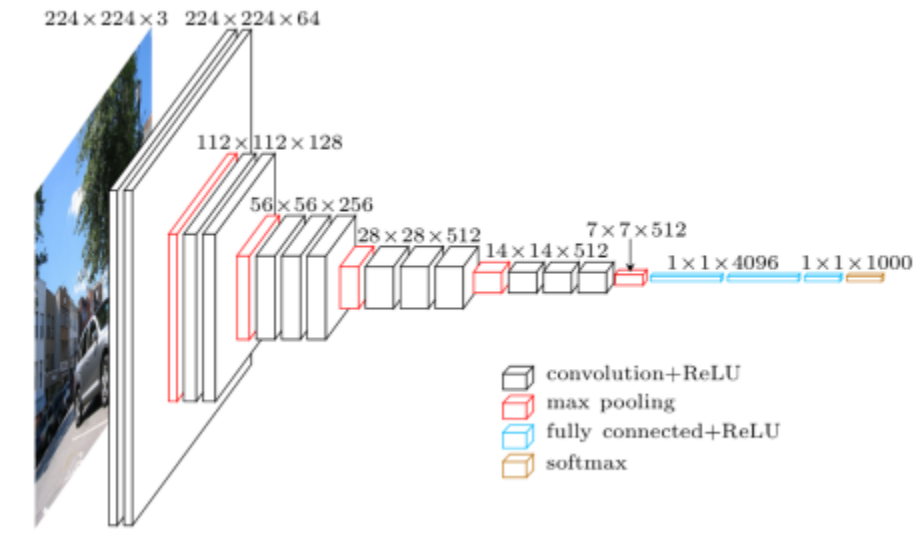


We will explore the use of a pre-trained CNN based on the VGG16 CNN architecture, trained on the ImageNet data set, and we will retrain that CNN to classify melanoma, using transfer learning.

Numerous CNN architectures are available today, specifically designed for image classification. These include, ResNet, Inception, and Xception, as well as VGG16. While training these CNN's from scratch requires significant computational resources, and significant datasets, pre-trained weights are available for each as a part of open source libraries, allowing us to build performant classifiers, with significantly reduced input data sets. This means that as clinicians, health care providers, and biotechnology researchers, it is possible to achieve results even with smaller data sets.

In our example we will explore building a classifier with a limited data set of several thousand images.

The VGG16 architecture we will be using is shown in the diagram below.



In a pretrained VGG16 model, the convolutional layers towards the visible layer of the network, have already learned numerous tasks necessary for image recognition, such as edge detection, shape detection, spatial relationships, etc.

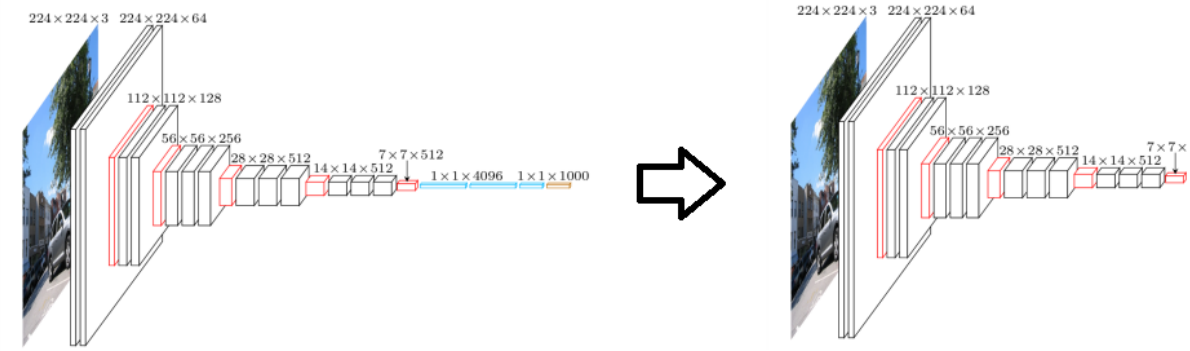
The top 5 layers of the network, have learned much higher levels of abstraction, and at the top of the network, are performing the classification of our images.

Pretrained VGG16 networks available in open source deep learning libraries such as Keras are typically pretrained on the ImageNet dataset. That dataset comprises of 14 million images open sourced images, none of which include skin samples. The broad classifications for these images are included below.

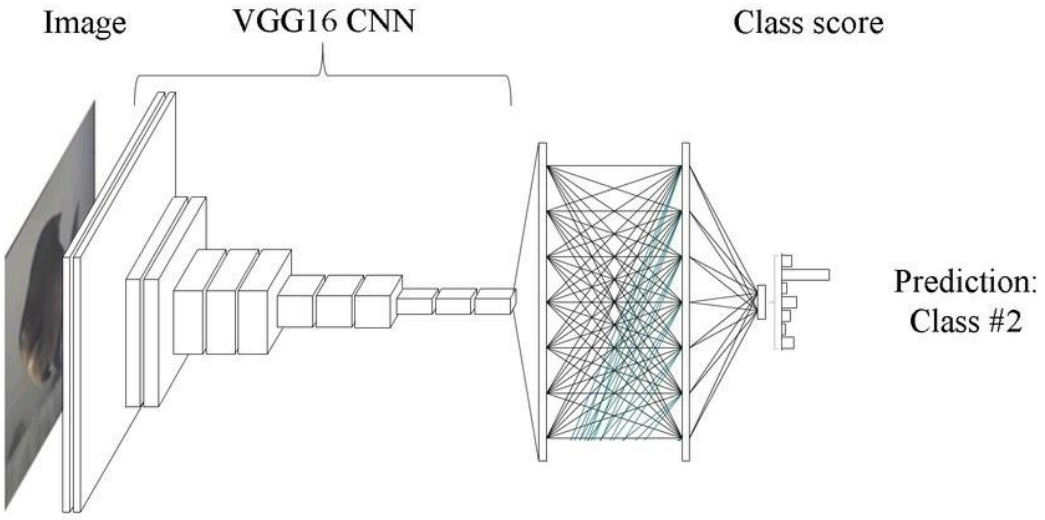
High level category	# synset (subcategories)	Avg # images per synset	Total # images
amphibian	94	591	56K
animal	3822	732	2799K
appliance	51	1164	59K
bird	856	949	812K
covering	946	819	774K
device	2385	675	1610K
fabric	262	690	181K
fish	566	494	280K
flower	462	735	339K
food	1495	670	1001K
fruit	309	607	188K
fungus	303	453	137K
furniture	187	1043	195K
geological formation	151	838	127K
invertebrate	728	573	417K
mammal	1138	821	934K
musical instrument	157	891	140K
plant	1666	600	999K
reptile	268	707	190K
sport	166	1207	200K
structure	1239	763	946K
tool	316	551	174K
tree	993	568	564K
utensil	86	912	78K
vegetable	176	764	135K
vehicle	481	778	374K
person	2035	468	952K

In order for us to build a model suited for a specific task such as classifying melanoma, we will need to retrain VGG16, to perform this more specific classification.

The first thing we will do is remove the top 5 layers of the pre-trained VGG16 model, and keep only the convolutional layers. Remember, the top layers have been trained to recognize features of classes such as animals, plants, people, and objects. These will not be needed in classifying melanoma.



Next we will want to replace the top layers we removed with layers that are more adapted to classify melanoma. To do this we will first feed forward our skin images through our "truncated" VGG16 network – i.e. the convolutional layers. We will then use the output (features) to train a fully connected classifier.



After this we will reconnect the fully connected classifier onto our truncated VGG16 network, and we will then retrain the whole model.