Histopathologic Cancer Detection on PCam

Stanford CS231n Project Proposal

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- **What is the problem that you will be investigating? Why is it interesting?**

  Pathology identification for medical imaging is a main domain of computer vision. It has the capacity to revolutionize medicine through more efficient and accurate diagnosis. In particular, it is important to analyse tissues to allow early detection and increase the chance of recovery. In this project, we are going to investigate the possibilities to predict cancers from histopathologic images. Our interest lies in using and comparing classical CNN architectures to solve this binary classification problem. Also, we are interested in exploiting the specificities of our type of image (e.g. invariance by symmetry and rotation) to improve our results.

- **What reading will you examine to provide context and background?**

  We will be working on the Histopathologic Cancer Detection problem and related dataset. The original paper [1] released the dataset, PatchCamelyon (PCam), and proposed to use a modified DenseNet to account for rotation/reflection symmetry. DenseNets were introduced in [2] which received CVPR 2017's Best Paper Award. When released, this paper outperformed the existing state-of-the-art models, on several datasets including CIFAR, SVHN and ImageNet. In DenseNet, each layer obtains additional inputs from all preceding layers, and the added connectivity can be beneficial for better propagating error signals and can lead to a more compact network. Finally [3] introduces Ensemble of Deep Learning Networks for the Histopathologic Cancer Dataset using pre trained VGG19, MobileNet, and DenseNet.

- **What data will you use? If you are collecting new data, how will you do it?**

  In this problem, we are going to use PCam dataset introduced in [1]. This dataset contains 327,680 patches extracted from a larger dataset with a size of 96x96 pixels with 10x magnification. The dataset has a 75/12.5/12.5% train/validate/test split.

- **What method or algorithm are you proposing? If there are existing implementations, will you use them and how? How do you plan to improve or modify such implementations? You don't have to have an exact answer at this point, but you should have a general sense of how you will approach the problem you are working on.**

  Our starting point will be a Dense Convolutional Network. Following [3], we will also perform data augmentation and normalization. We will then modify our architecture [1] using Group Equivariant Convolutional Networks [4] for rotation and reflection invariance. Instead of having a pooling layer followed by a sigmoid activation function to classify the images, we may introduce a fully connected neural network. We expect most hyperparameters to be set to the optimal values from the mentionned papers.

- **How will you evaluate your results? Qualitatively, what kind of results do you expect (e.g. plots or figures)? Quantitatively, what kind of analysis will you use to evaluate and/or compare your results (e.g. what performance metrics or statistical tests)?**

  In the dataset set, the Cancer/No Cancer proportion is approximately 40/60. Hence, the *accuracy* is a good metric for this problem. We will also observe precision, recall and F1 score since they are important metrics in medical applications.

References

[1] Bastiaan S Veeling, Jasper Linmans, Jim Winkens, Taco Cohen, and Max Welling. Rotation equivariant CNNs for digital pathology. June 2018.

[2] Gao Huang, Zhuang Liu, and Kilian Q. Weinberger. Densely connected convolutional networks. *CoRR*, abs/1608.06993, 2016.

[3] Michal J. Wesolowski Kevin A. Schneider Ralph Deters Sara Hosseinzadeh Kassani, Peyman Hosseinzadeh Kassani. Classification of histopathological biopsy images using ensemble of deep learning networks. September 2019.

[4] Max Welling Taco S. Cohen. Group equivariant convolutional networks. June 2016.