

# Master's Capstone Midterm Report

*Aadi Kalloo*

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# 1 Introduction

The diagnosis of cancers in modern medicine typically involves a biopsy of the tissue in question followed by visual microscopic examination by a licensed pathologist, after biopsy specimens have been sectioned and placed onto glass slides (McKenney, 2017). Pathologists often use both permanent and diagnostic slides to aid in their analysis of the biopsied tissue. The diagnostic slides are obtained by slicing fresh tissue from the sample on a microtome. The pathologist will then confirm with the surgeon about the cancer diagnosis, often when the patient is still in surgery. The biopsied tissue undergoes a different procedure for the making of permanent slides: the tissue is fixed in formalin, water is removed by a machine and replaced with paraffin wax, and the tissue is then cut into thin slices using a microtome and places on slides (Culling, Allison, & Barr, 2014). To visualize the tissue under a microscope, the sections are stained with one or possibly multiple pigments. The aim of staining is to reveal cellular components, while counterstains are used to provide contrast (Gurcan et al., 2009).

Given that human pathologists can reach conclusions based on the physical features of the tissue sample (i.e. cell morphology, presence of artifacts), it follows that computer models can be trained to detect features in a similar manner. The visual nature of this method gives way to improvements in efficiency through automation, particularly through the use of computer vision algorithms. One recent example of this ideology put into practice is the development of a Convolutional Neural Network (CNN) that can produce dermatologist-level accuracy in the classification of skin cancer images (Esteva et al., 2017). That project built upon previous technological developments in neural network architecture by utilizing a network structure developed by Google Inc. named Inception v3 (Szegedy et al., 2016). By taking advantage of this architecture with weights pre-trained from the ImageNet data set, significant developments in multi-class recognition of dermatological lesions was achieved.

While there has been much progress recently in computer-aided diagnosis in areas of medicine including radiology and dermatology, there have been fewer efforts in the development of algorithms that can effectively classify histopathology slides. Technologically focused works in the area of histology have focused primarily on a single cancer type (Cireşan et al., 2013; Xu et al., 2016); it is likely that

work in this arena has been limited by the availability of high quality data sets. To date, no published works have yet been released documenting large-scale multi-class classification efforts in the classification of histopathology disease states based on cellular-level images. The project proposed here overcomes this barrier by using data from the Cancer Digital Slide Archive – a high quality collection of curated histopathology image slides representing 27 disease classes (Gutman et al., 2013).

Developments in computer-aided diagnosis can bring improvements to medicine and patient care through enhancements in efficiency and reduction of costs. One study showed that it can take an average of 5 minutes of analysis by a licensed pathologist per slide, with an average per-slide cost around \$60 (including report preparation) (Wong et al., 2015). While approximately 1 million biopsies are performed in the United States every year, the total number of slides prepared exceeds tens of millions due to non-human research (Madabhushi, 2009). For large institutions that have millions of slides analyzed every year, sums can surpass 125, 000 person-hours of work and financial burden of approximately \$90 million per annum (May, 2010; Wong et al., 2015). Based on these findings, it is clear that even small enhancements in efficiency that can be effected through automation can bring large savings in both financial and time costs.

## 1.1 Artificial Neural Networks

Artificial Neural Networks (ANN) are machine learning algorithms that have been designed to mimic the function of biological neurons of the nervous system (Demuth et al., 2014). An individual neuron can be described by a mathematical model, as shown in **Figure 1**. In this model, the dot product of the input ( $x_i$ ) and a matrix of weights ( $w_i$ ) is taken (Demuth et al., 2014). These models can learn another parameter, known as the bias (b) (Demuth et al., 2014). The bias is directly added to the product of the previous element-wise matrix multiplication. The mathematical model of the neuron will output a signal ( $x_i w_i$ ) based on an activation function (f), which introduces a non-linearity to the equation (Demuth et al., 2014). Taking into account that a single node can receive multiple signals as inputs, a mathematical model can be formed and expressed as shown in **Figure 1**.

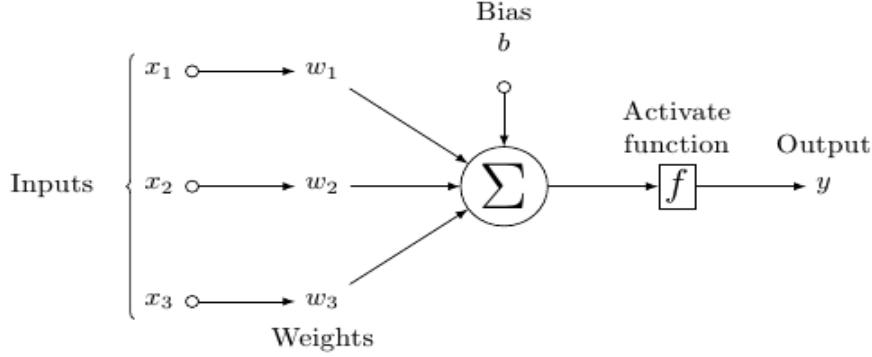


Figure 1: Mathematical model for a single neural network node

The most commonly used activation functions for forming neural network architectures include the sigmoid function ( $\sigma(x) = 1/(1 + e^x)$ ) and the ReLU (Rectified Linear Unit) function ( $f(x) = \max(0, x)$ ), which has a threshold at zero (Specht, 1990; Xu, B et al., 2015). The ReLU activation function is used exclusively in this project.

A fully formed ANN may contain any number of neurons, ranging from dozens to millions (Demuth et al., 2014). Neurons in these networks are classified into three main layers: (i) the input layer (nodes that receive input) (ii) hidden layers, of which there can be any number and can each contain any number of nodes, and (iii) the output layer, which are connected to the hidden layers and produce a final value/result (Demuth et al., 2014). The most common organization involves nodes that are “fully-connected”, where each neuron is connected to each neuron in the next layer (Demuth et al., 2014).

## 1.2 Convolutional Neural Networks

Convolutional Neural Networks (CNN) are based heavily on the structure and function of Artificial Neural Networks (LeCun et al., 1995). CNNs work similarly to regular ANNs: each node receives one or more inputs, elementwise multiplication (dot product) between inputs and associated weights is computed, and a non-linear activation function is applied. The general CNN architecture consists of the following layers: (i) an input layer, containing the raw pixel values from the input image; (ii)

Convolutional layers, which computes a moving dot product for small sections of the input image; (iii) Activation layers; (iv) Pooling layers that downsample the data received; and (v) Fully Connected layers, which compute and output the final probabilities or labels (LeCun et al., 1995).

A CNN is made of multiple combinations of the aforementioned layers, with fully-connected layers being added last (LeCun et al., 1995). It should be noted that only the fully-connected layers contain what are formally regarded as “neurons” or “nodes”.

### 1.3 Optimization algorithms

Optimization algorithms work toward minimizing a Loss (Error) function  $E(x)$  – a mathematical function that depends on the model’s learnable parameters (Masters, 1995). These parameters are used to calculate the predicted values ( $Y$ ) from the set of inputs/predictors ( $X$ ) fed into the model.

The inner parameters contained in a model have an important role in efficient and effective training. The use of various optimization algorithms to update and compute the appropriate values for model parameters greatly influence the training process and the production of accurate results (Masters, 1995).

#### 1.3.1 Stochastic Gradient Descent

While Stochastic Gradient Descent (SGD) has been a very popular choice historically due to its relatively quick ability to update parameters for each training example (Bottou, 2010; Hardt et al., 2015). These frequent updates allow for high variance and thus better likelihood of finding the global minimum (Bottou, 2010). However due to drawbacks with the method – including difficulty choosing an appropriate learning rate, and the inability to tweak the learning rate based on class or parameter (Ruder, 2016) – SGD was not used in these experiments. In recent years, algorithms have been developed that address the shortcomings of SGD (Duchi et al., 2011; Zeiler, 2012). Two of these algorithms, Adadelta and Adagrad, were chosen here for model architecture.

### 1.3.2 Adagrad

Adagrad is commonly seen as an improvement over SGD as it has the ability to change or adapt the learning rate based on the parameters of the data (Duchi et al., 2011). This algorithm can make large updates for less prevalent classes/parameters and smaller updates for more prevalent classes/parameters (Duchi et al., 2011). As such, it is often the algorithm of choice when handling sparse data (Duchi et al., 2011). Adagrad, unlike SGD, is capable of using a different learning rate for each parameter  $\theta$  (Duchi et al., 2011). The main weakness in this algorithm is that its learning rate is always decreasing. This problem of decaying learning rate is addressed in the AdaDelta algorithm.

### 1.3.3 Adadelta

Adadelta is effectively an extension of AdaGrad. It “dynamically adapts over time using only first order information and has minimal computational overhead beyond vanilla stochastic gradient descent” (Zeiler, 2012). The adadelta algorithm uses the magnitude of recent gradients and steps to produce an adaptive step rate (Zeiler, 2012). An exponential moving average over the gradients and steps is kept and a scale of the learning rate is then obtained by their proportion (Zeiler, 2012).

## 2 Data

### 2.1 Acquisition

Data was obtained primarily from the Cancer Digital Slide Archive (CDSA). This archive houses histopathology slides for biopsied cancerous tissue, originating from 31 cancer types (a full list can be found in **Appendix A**). Collected data was comprised of mainly images, and would include some basic accompanying metadata (i.e. disease class). The data is stratified by disease class, patient, and slide type. Slide formats include Diagnostic (DX), and Permanent (PM).

## 2.2 Types

Images for this project will exist in two types, termed here as “Slide Level” and “Tile Level”. Images on CDSA are high-resolution mosaics, which makes the acquisition of multi-resolution tiles possible. For this project, tiles at a level of 15x zoom were chosen as this was deemed to appropriately show detail at the cellular level. An example of these image types is outlined in **Figure 2**.

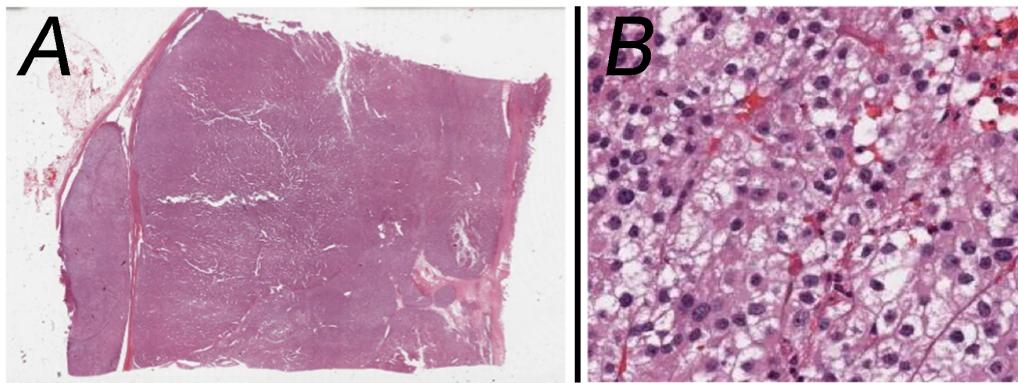


Figure 2: (A) “Slide Level”: Diagnostic section of Adrenocortical Carcinoma (ACC) tissue; (B) “Tile Level”: 15x zoom tile taken from the tissue in Fig 2A

## 2.3 Organization

### 2.3.1 Tile Level Data

Tile Level classification was performed using the following data: the training set consisted of approximately four million tile-level images, with the validation set and test set containing two million and six hundred ten thousand images, respectively. Images for all three sets were randomly selected from a pool of 20 million tile-level images. Random selection allowed classes to have an equivalent distribution between training and test sets. A diagram of this distribution and comparison to per-class cancer incidence, as a percentage of all new cancer cases per year, is shown below:

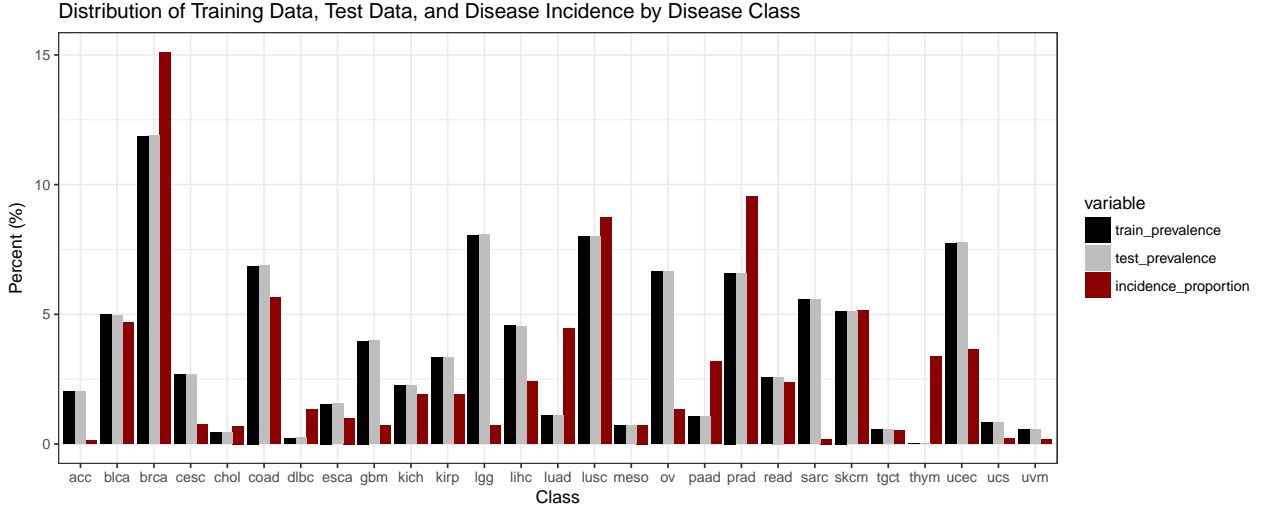


Figure 3: Equivalent distribution between training and test data sets. Incidence proportion is calculated as the percentage of cancer class of all cancers diagnosed per year

### 2.3.2 Slide Level Data

Slide Level classification was performed using “Slide Level” images and data. The training set consisted of approximately 18 thousand slide-level images, while the validation set and test set contained one thousand and five thousand images, respectively. Images for all three sets were randomly selected from a pool of 25 thousand slide-level images. Random selection allowed classes to have an equivalent distribution between training and test sets.

## 2.4 Data Transformation

### 2.4.1 Tile Level data

During the acquisition process, tiles were requested in 256x256 pixel jpeg images. These images were then scaled down to 150x150 in order to be compatible with the VGG19 and Google Inception v3 networks provided through Keras.

#### **2.4.2 Slide Level data**

Slide Level images obtained were originally in very different sizes based on the size of the tissue biopsied. As such, these images were transformed into uniform dimensions, through stretching, to achieve dimensions of 150x150 pixels.

### **3 Aims**

The terminal aim of this project is the development of a computer vision algorithm that can correctly classify a given histology image into one of 27 given classes. Focuses of this project include:

Using both Slide Level and Tile Level images:

- 1) Comparison of de novo neural network architectures, naïve Google Inception v3 architecture, and pre-trained Google Inception v3; the latter will involve reimplementations of the output layer of the network

Using only Slide Level images:

- 2) Accurate Classification of DX and PM sections for a given tumor type
- 3) Differentiation between DX and PM sections for tumor types other than the ones used for training (generalizability)

Using both Slide Level and Tile Level images:

- 4) Differentiation between tumor types that are known to look similar to humans. For example:
  - a. Lung Adenocarcinoma vs. Lung Squamous Cell Carcinoma
  - b. Kidney renal clear cell carcinoma vs. Kidney renal papillary cell carcinoma
  - c. Glioblastoma multiforme vs. Brain Lower Grade Glioma

## 4 Methods

### 4.1 Tile Level Classification

Python was used for machine-learning tasks, in conjunction with the Keras framework. Several model architectures were investigated: **Model A** used an ad-hoc de novo CNN architecture consisting of 10 convolutional layers and 3 fully connected layers; **Model B** used the VGG19 architecture with 10000 fully connected nodes and a 27 node Softmax output layer; **Model C** used a Google Inception v3 architecture with 1024 fully connected nodes and a 27 node Softmax output layer; **Model D** used a Google Inception v3 architecture with 10000 fully connected nodes and a 27 node Softmax output layer; **Model E** used a Google Inception v3 architecture with 100000 fully connected nodes and a 27 node Softmax output layer. All models were run using the adadelta optimization algorithm. **Model E** showed the most promise given the training history based on validation accuracy reached and training stability, and was chosen to run an additional 200 epochs using the adagrad optimization algorithm, producing **Model F**. **Model A** was run for a total of 100 epochs, while **Models B – E** were run for 200 epochs; **Model F** was run for a combined 400 epochs. All models trained on RGB color images with dimensions 150 x 150 x 3. A summary of models built is shown in **Table 1**:

Table 1: Training and architecture parameters for models used

Model.Name	Conv.layers	Total.FCN	Optimizer	Total.Epochs
Model A	10	411	Adadelta	200
Model B	16	10027	Adadelta	200
Model C	42	1051	Adadelta	200
Model D	42	10027	Adadelta	200
Model E	42	100027	Adadelta	200
Model F	42	100027	Adadelta + Adagrad	400

CUDA libraries, developed by NVIDIA, for Python 3.5 were used in addition to Keras as to allow parallel computing and were required to take advantage of processing by Graphics Processing Units (GPUs). One NVidia GeForce GTX TITAN X GPU was used to train and evaluate the models described.

#### **4.1.1 Class Weighting and Imbalance Resolution**

As disease states were not completely balanced in the data, the following method of “Inverse Class Weighting” was used to help ameliorate distribution-related issues during training :

$$p_i = 1 - \frac{n_i}{N}$$

### **4.2 Slide Level Classification**

Experiments in slide level classification fell into two categories: ‘generalizability’ experiments and ‘multi-class classification’ experiments.

#### **4.2.1 Generalizability**

These experiments focused on training a classifier to differentiate diagnostic (DX) slides from permanent (PM) slides. In the first of these experiments, the classifier was trained on approximately 4000 DX and PM slides from BRCA, and was then used to classify 27000 slides into the same categories.

#### **4.2.2 Multi-class Classification**

The format of these experiments mimicked the tile-level classification experiments. A classifier was designed to differentiate between 27 disease states using slide-level images.

## 5 Results

### 5.1 Tile Level Classification

It was found that the Inception v3 models, reaching a peak training accuracy of 83% and a peak test set accuracy of 73%, performed better than both the VGG19 and *de novo* architectures. A history of model training and performance on the validation images is shown in **Figure 3**.

#### 5.1.1 Training and Model Selection

During the process of training and model design, it was found that wider networks – with fewer layers and more neurons per layer – performed better than both shallower networks and deeper networks. Based on training history, the best performing model (**Model E**), based on stability and accuracy achieved, was chosen for further training (**Model F**).

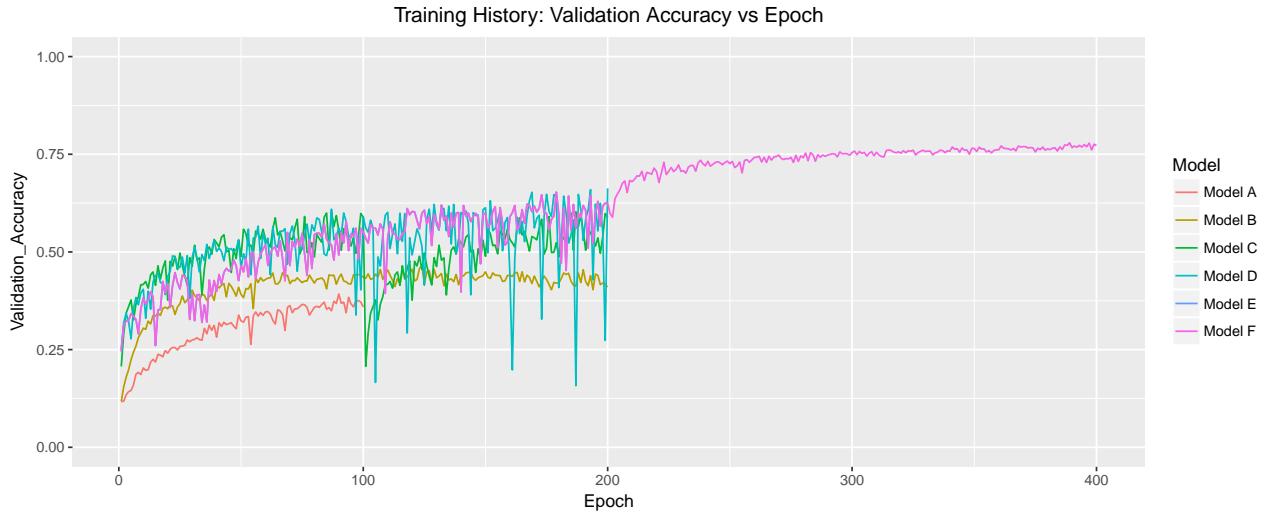


Figure 4: Training history for all multi-class classification models designed

#### 5.1.2 Model Performance on Test Dataset

The test dataset consisted of 610,000 images. In general, it can be seen that later models performed better than earlier models as shown in **Table 2**.

Table 2: Model performance with comparison statistics

model_name	accuracy	Recall_macro	Precision_macro	Kappa	Weighted_Kappa
Model F	0.685	0.610	0.653	0.664	0.640
Model D	0.585	0.496	0.520	0.557	0.512
Model E	0.578	0.466	0.528	0.550	0.515
Model C	0.532	0.412	0.489	0.500	0.456
Model B	0.115	0.078	0.068	0.056	0.025
Model A	0.095	0.078	0.066	0.031	0.029

### 5.1.2.1 Confusion Matrix for Best Performing Model

A confusion matrix was generated for the best-performing model (**Model F**), illustrating how well the classifier performed on each disease state, as shown in **Figure 4**. A confusion matrix for each model developed can be found in **Appendix B**.

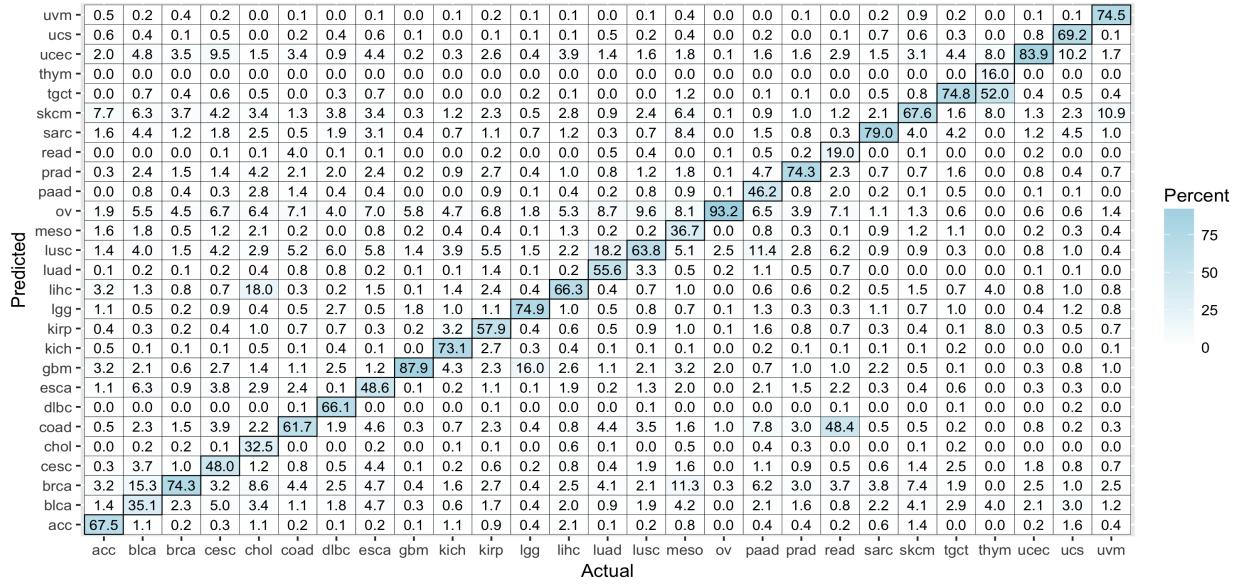


Figure 5: Per-class performance of class predictions compared to true class label. Darker color indicates better performance. Some very similar tissues (i.e. colon and rectal) were easily confused and can be seen outside of the diagonal.

## 5.2 Slide Level Classification

### 5.2.1 Generalizability

#### 5.2.1.1 Training

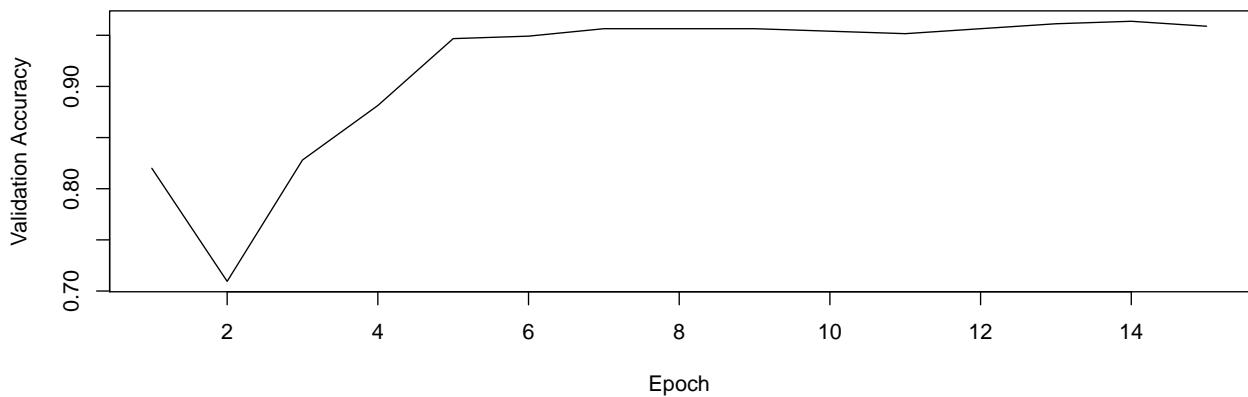


Figure 6: Training history for generalizability model. Model was trained only on BRCA DX/PM slides and applied to all DX/PM slides

### 5.2.1.2 Model Performance

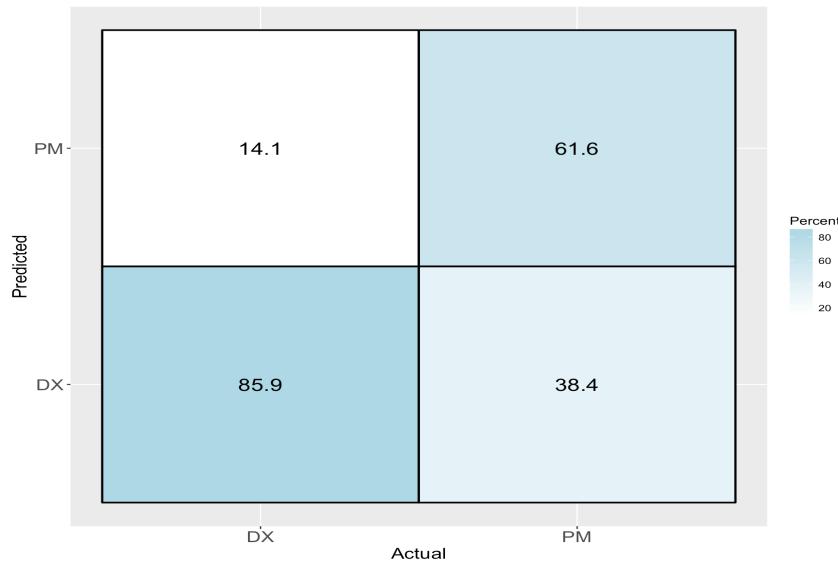


Figure 7: Confusion Matrix for Slide Level Classification Generalizability Experiment. Higher false positive proportion indicates higher variability between DX and PM slides outside of BRCA slides.

DataSubset	n	Accuracy	Sensitivity	Specificity
All Data	27138	0.7051367	0.8594207	0.6164026
BRCA Only	1860	0.9747312	0.9377432	0.9888559

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DataSubset	n	Accuracy	Sensitivity	Specificity
BRCA Excluded	25278	0.6852995	0.8551357	0.5848391

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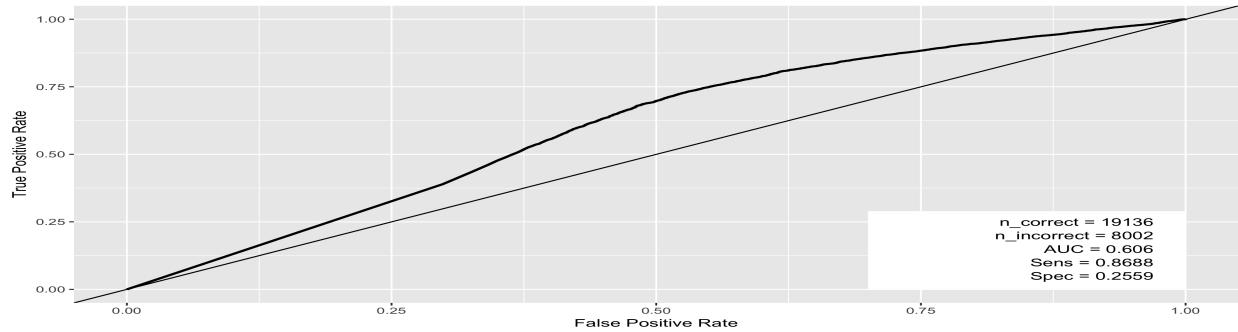


Figure 8: ROC Curve for Generalizability Classifier

## 5.2.2 Multi-class Classification

### 5.2.2.1 Training

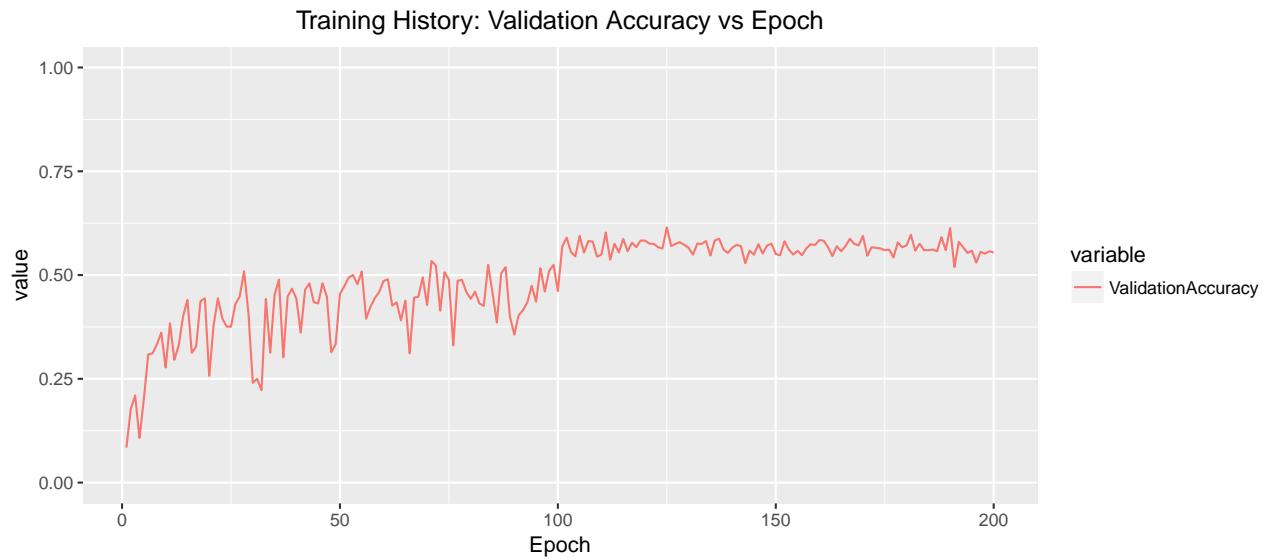


Figure 9: Training history for multi-class classifier. While validation accuracy did not reach significant levels during training, accuracy on test data surpassed 0.8

### 5.2.2.2 Model Performance

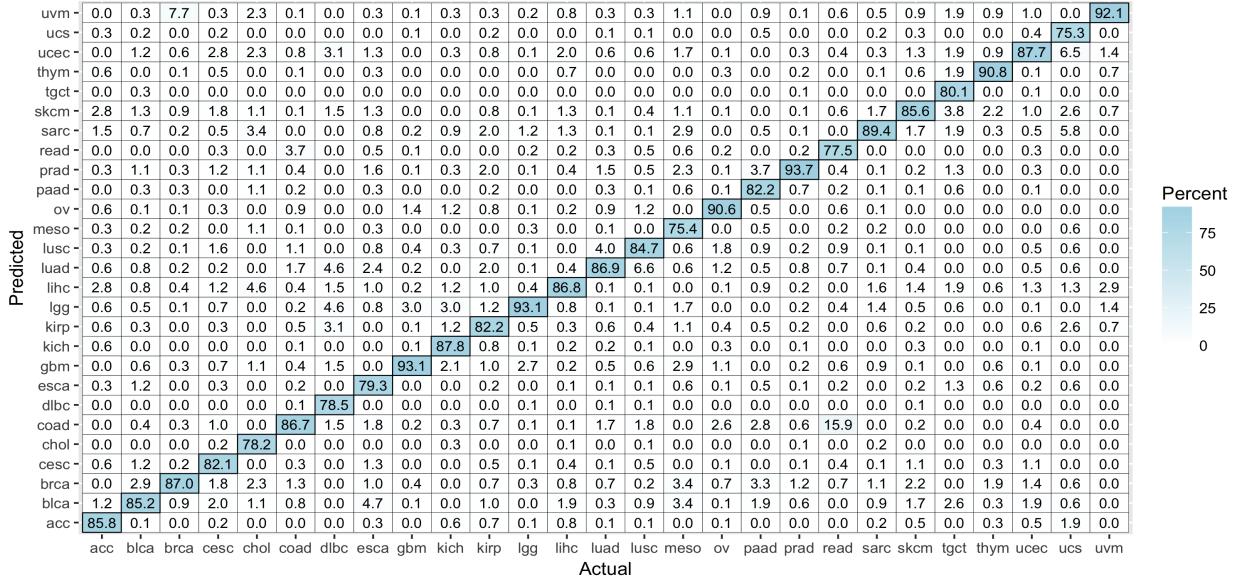


Figure 10: Confusion matrix showing classification performance for multi-class algorithm trained to classify disease states based on overt structures (i.e. using slide-level images)

## 6 Discussion

Classification of cancer subtypes falls largely into the responsibility of pathologists. Pathologists rely on biopsies, imaging techniques such as CT, MRI, and X-ray, and specific tissue staining, to correctly classify the exact cancer subtype for a patient diagnosis. Often, this responsibility is shared among a team of pathologists working closely with surgeons, researchers, and other specialists, and the inter-eater reliability among pathologists can vary. Furthermore, research costs to use pathology services can often be upwards of \$60 per slide, with thousands of slides used for diagnostic and research purposes at large institutions and hospitals (Wong et al., 2015). There is also the use of genomic sequencing to determine if a patient has a specific mutation on the gene, RNA, or protein level, that may give an indication to the cancer subtype and how the tumor will progress. Such genetic testing is currently used in hospitals such as Memorial Sloan Kettering Cancer Center (MSK-IMPACT), however the process is costly and time consuming, since current analysis of mutations (such as insertions, deletions, and

single nucleotide variants) on the genomic level for patients, requires manual review by a team of pathologists, clinicians, and scientists (Cheng et al. 2015). Given the variation among pathologists and cost of services in research and patient care, trained and automated classifiers can help to reduce cost and allow for quicker and more reliable ways to diagnose specific cancer subtypes.

In this study, 27 different cancer types were chosen for classification, among which three were kidney cancer subtypes, two different brain cancer subtypes, two lung cancer subtypes, colon and rectal (both cancers of the large intestine), and various endocrine related cancers were chosen such as thymoma (thymus cancer) and thyroid cancer (visual examples can be found in **Appendix C**). The aims of the classifier were not only to successfully differentiate between different cancers of the body, but also between cancers that share numerous similarities in tissue and structure. A further aim was to correctly classify different cancer subtypes between their permanent pathology slides and diagnostic slides.

Beginning with selecting models and training, **Figure 4** shows the validation accuracy versus epochs for **Models (A-F)**. Accuracy increases with the number of epochs because it gets more exposure to the data and trains more and is better able to find and search for the global minimum. As previously stated, Model E had the best performance (based on stability and accuracy) and was selected for additional training **Model F-H**. **Model A** used an ad-hoc de novo CNN architecture, and had the lowest validation accuracy across 200 epochs. Consequently, this was recognized as the poorest performing model. **Model D** had less stable training most likely due to the fact that it had fewer neurons for training. **Model D** had less stable validation accuracy across 200 epochs. Given that the VGG19 and Inception V3 models show very different training histories despite otherwise using similar parameters, **Figure 4** shows that advanced in model architecture over time has led to improved classification abilities by computer vision algorithms.

Furthermore, a perfect classifier would show 100% across the diagonal in the confusion matrix, and as shown in **Figure 5**, the heat map would present the darkest, and therefore, the most accurate responses, in the darkest blue color. It can be seen in **Figure 5** that classification for many disease

states approach 100%, however, there were a few classes that would, at first appearance, seem to be classified poorly. Very similar tissue types (colon and rectal; different forms of brain cancer; liver and bile duct) resulted in misclassification, but largely between the homologous cancers. Each row represents the instances of predicted cancer types and each column represents the instances of actual cancer types. It is important to note that different cancer subtypes were included to analyze classification between very similar tissues, particular between various kidney cancers, lung, brain, and colon versus rectal cancers. Ovarian serous cystadenocarcinoma (OV - ovarian cancer, 94.3%), glioblastoma multiforme (GBM - brain cancer, 89.7%), and Uterine Corpus Endometrial Carcinoma (UCEC - Cancer of the uterus, 85%) had the three highest per-class accuracies, respectively. Conversely, the three lowest per-class accuracies were Mesothelioma (MESO, 34.7%), Rectum adenocarcinoma (READ, 31.8%), and Thymoma (THYM, 24%). Interestingly, thymoma, a type of thymus cancer frequently associated with myasthenia gravis, a neuromuscular disorder [insert citation here], was classified correctly 24% of the time, yet misclassified as Testicular Germ Cell Tumor (TGCT), 40% of the time. Additionally, rectum adenocarcinoma was classified correctly 31.8% of the time, yet misclassified as Colon adenocarcinoma (COAD) 39.8% of the time. Rectal and colon cancers both arise from the large intestine and subsequently share very similar pathologies and cell structures [insert citation] Mesothelioma (MESO) was classified correctly 34.7% of the time, however, it was misclassified for a variety of other cancer types, such as Breast invasive carcinoma (BRCA, breast cancer) 11.7% of the time, ovarian serous cystadenocarcinoma (OV) 8.2% of the time, and sarcoma (SARC - bone cancer) 6.9% of the time.

**Figure 6** shows the training history for slide level classification. Google Inception V3 using imangenet weights was used to train on BRCA (breast cancer) diagnostic (DX) and permanent (PM) slides. The training was run for 15 epochs, and reached a validation accuracy of 94.6% after 5 epochs. The permanent slides are fixed slices of tissue in formalin and paraffin wax, while the diagnostic slides are images of the fresh biopsied tissue slide (Culling, Allison, & Barr, 2014).

Additionally, **Figure 7** is a confusion matrix for slide level classification using Google Inception V3 trained on BRCA slides only and tested on the other 26 cancer types. The results showed that the test predicted diagnostic slides 85.9% and 14.1% permanent slides. Moreover, the test showed that

actual values for diagnostic slides was 38.4% and 61.6% for permanent slides. Accuracy of classifying BRCA permanent and diagnostic slides alone was 97.47%, however, when tested on all cancer types, the accuracy of classifying between permanent and diagnostic slides was 70.51%. Excluding BRCA, the accuracy of classifying DX and PM was 68.53%. This suggests that there is a high variability between permanent and diagnostic slides.

Moreover, **Figure 8** shows an ROC curve for slide level classification. A possible limitation to this data is that Google Inception V3 was used to train on one (BRCA) out of 27 total cancer types, and was therefore not as accurate. The true positive rate, or sensitivity, was equivalent to 86.88%, while the false positive rate was equivalent to  $1 - specificity$  or 74.41%. Furthermore, the performance quality of the classifier can be measured by the AUC, which was 0.606, while a perfect classifier would have an AUC of 1. Further training on several other cancer types can be tested to see if the classifier performs better between accurately sorting PM and DX slides.

**Figure 9** shows the training history of validation accuracy versus epochs for the Google Inception V3 using imagenet weights. The validation accuracy was higher than 0.5 starting from 100-200 epochs for correctly classifying cancer subtypes using the permanent and diagnostic slide images. Furthermore, in **Figure 1**, the confusion matrix shows an improvement in cancer classification and distinction from similar cancer subtypes using PM and DX slides (tile level classification) in comparison to **Figure 5**, which used slide level classification. Interestingly, Mesothelioma (MESO, 75.4%) and Rectum adenocarcinoma (READ, 77.5%) were still among the lowest per-class accuracies for tile level classification versus in **Figure 5** for slide level classification, however there was an improvement in per-class accuracies across all cancer types. Rectal adenocarcinoma (READ) was also misclassified as colon adenocarcinoma (COAD) 15.9% of the time, in comparison to misclassifying READ as COAD 48.4% of the time in **Figure 5**. Brain Lower Grade Glioma (LGG - brain cancer, 93.1%), glioblastoma multiforme (GBM - brain cancer, 93.1%), and Prostate adenocarcinoma (PRAD - prostate cancer, 93.7%) had the three highest per-class accuracies, respectively. LGG was misclassified as GBM 2.7% of the time, and conversely, GBM was misclassified as LGG 3% of the time. However, the classifier reached high levels of accurate sorting between the two brain cancer types. Further, uveal melanoma (skin cancer

of the eye - UVM) had high per class accuracies in both the tile (74.5%) and slide level classifications (92.1%) (Figs. 5 and 10). However, in the tile level classification **Figure 5**, uveal melanoma was misclassified as Skin Cutaneous Melanoma (skin cancer -SKCM) 10.9% of the time, and misclassified as SKCM 0.7% of the time in the slide level classification **Figure 10**. Therefore, there were notable improvements in per-class accuracy for slide level classification versus tile level classification.

These results show that there is potential for automation of pathology services for diagnosis and classification of cancer subtypes. As previously stated, given the high cost for slide services in research and for diagnostic purposes, and how there are typically teams of pathologists devoted to the diagnosis of cancer subtypes at large institutions such as Memorial Sloan Kettering (Gutman, D. Personal Communication, 2017), this classification system is promising and has potential for use to decrease both the amount of time and cost of research and clinical diagnosis. This is especially in regards to its potential for classifying between similar cancer tissue types, such as glioblastoma (GBM) and brain lower grade glioma (LGG) using both slide and tile level classification. The classifier can also be a strong diagnostic tool in addition to the classification reports based on lead pathologists and other diagnostic tools currently used in hospitals and research centers.

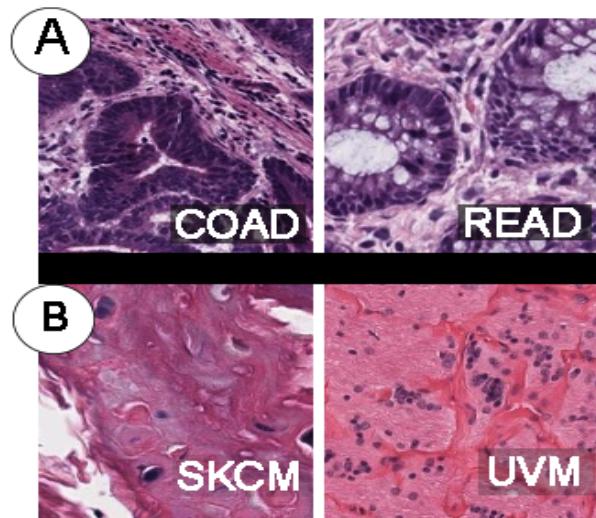


Figure 11: Frequently misclassified disease states. (A) shows adenocarcinoma biopsy tissue taken from colon (left) and rectum (right); (B) shows melanoma biopsy tissue taken from skin (left) and eye (right)

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## 8 Appendix A – Disease Classes on Cancer Digital Slide Archive

Abbreviation	Name	Anatomic Origin
ACC	Adrenocortical carcinoma	Adrenal Gland
BLCA	Bladder Urothelial Carcinoma	Bladder
BRCA	Breast invasive carcinoma	Breast
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma	Uterus/cervix
CHOL	Cholangiocarcinoma	Bile duct
COAD	Colon adenocarcinoma	Colon
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma	Lymph Nodes
ESCA	Esophageal carcinoma	Esophagus
GBM	Glioblastoma multiforme	Brain
KICH	Kidney Chromophobe	Kidney
KIRC	Kidney renal clear cell carcinoma	Kidney
KIRP	Kidney renal papillary cell carcinoma	Kidney
LGG	Brain Lower Grade Glioma	Brain
LIHC	Liver hepatocellular carcinoma	Liver
LUAD	Lung adenocarcinoma	Lung
LUSC	Lung squamous cell carcinoma	Lung
MESO	Mesothelioma	Abdominal Organs
OV	Ovarian serous cystadenocarcinoma	Ovaries
PAAD	Pancreatic adenocarcinoma	Pancreas
PCPG	Pheochromocytoma and Paraganglioma	Adrenal Gland
PRAD	Prostate adenocarcinoma	Prostate
READ	Rectum adenocarcinoma	Rectum
SARC	Sarcoma	Bones
SKCM	Skin Cutaneous Melanoma	Skin

Abbreviation	Name	Anatomic.Origin
STAD	Stomach adenocarcinoma	Stomach
TGCT	Testicular Germ Cell Tumors	Testicles
THCA	Thyroid carcinoma	Thyroid
THYM	Thymoma	Thymus
UCEC	Uterine Corpus Endometrial Carcinoma	Uterus
UCS	Uterine Carcinosarcoma	Uterus
UVM	Uveal Melanoma	Eyes

## 9 Appendix B – Confusion Matrices for All Models

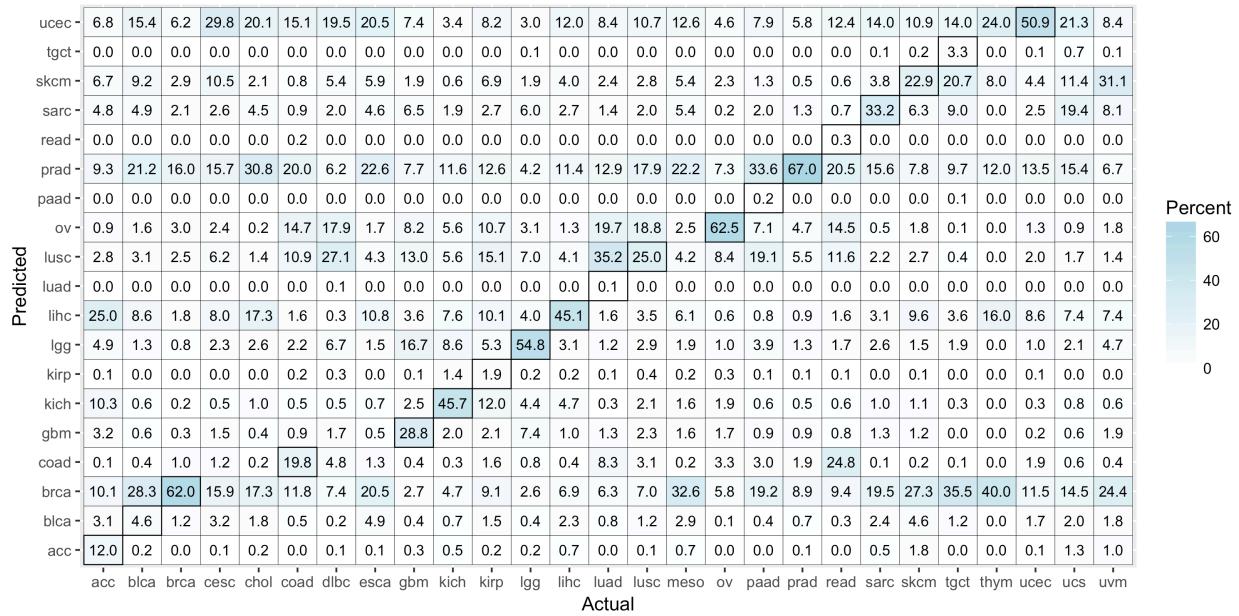


Figure 12: Model A

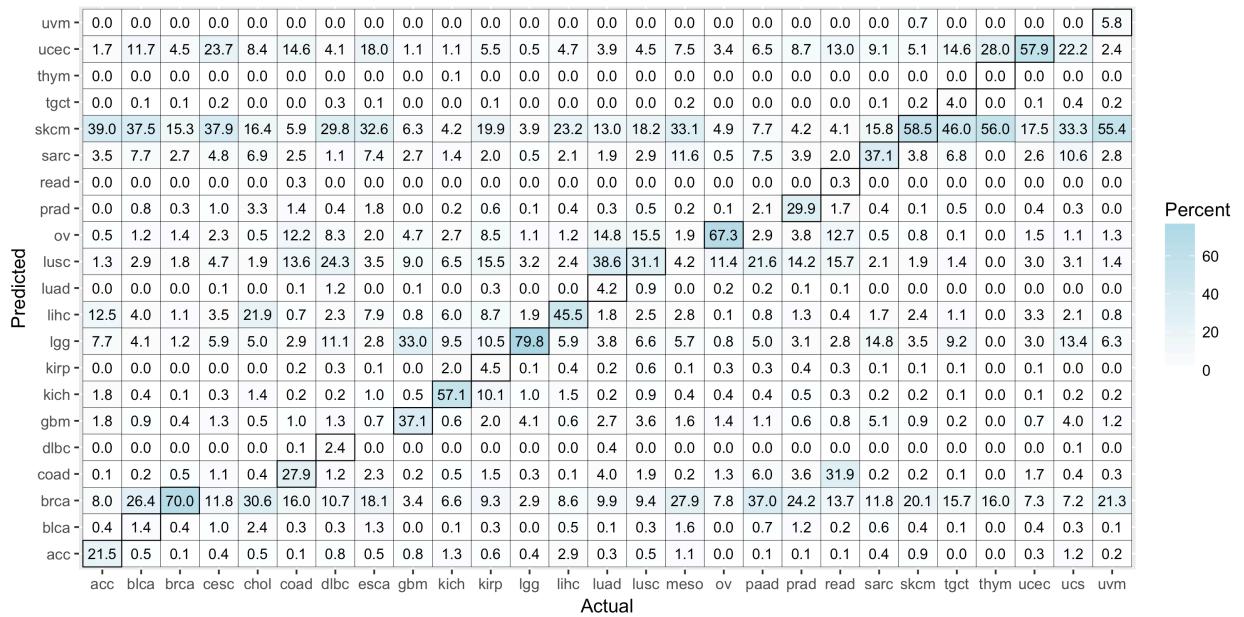
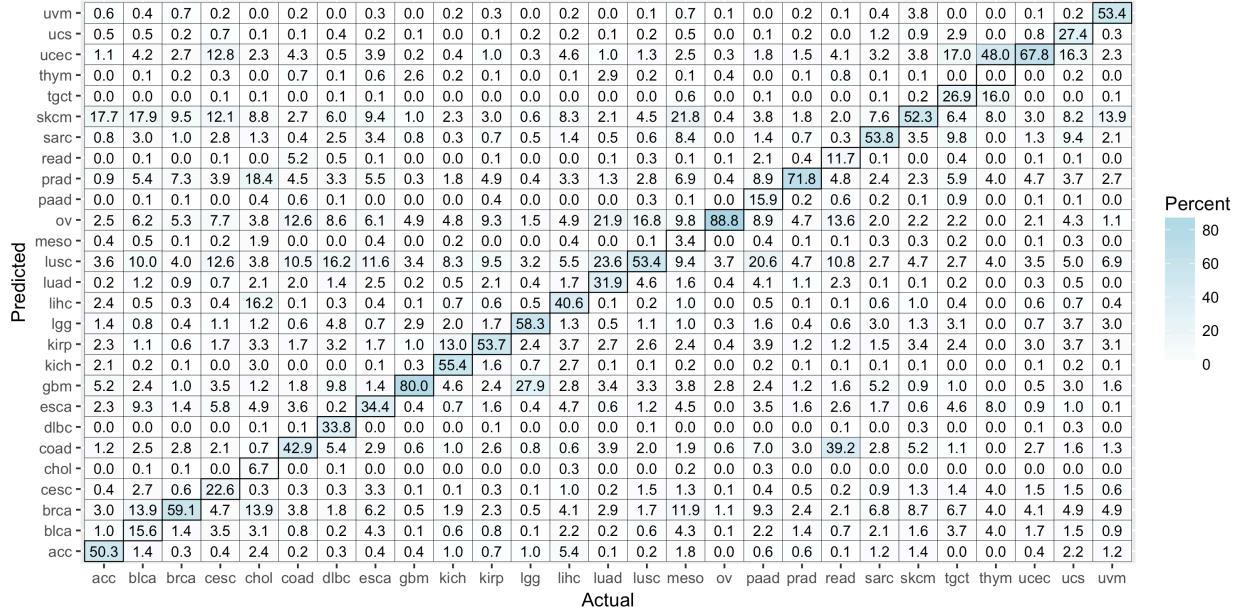


Figure 13: Model B



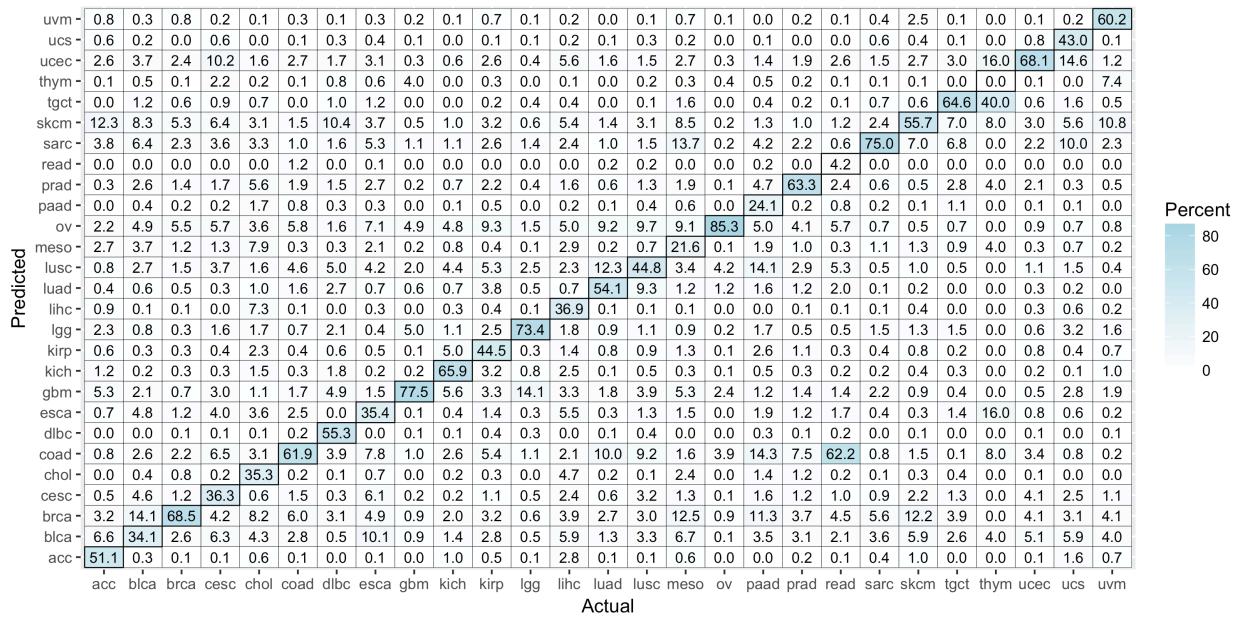
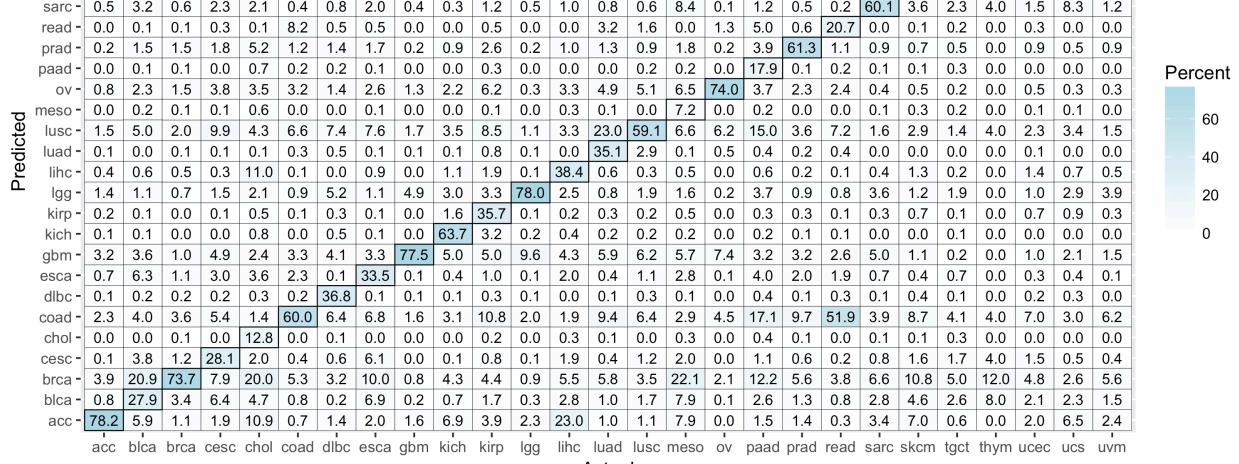


Figure 15: Model D



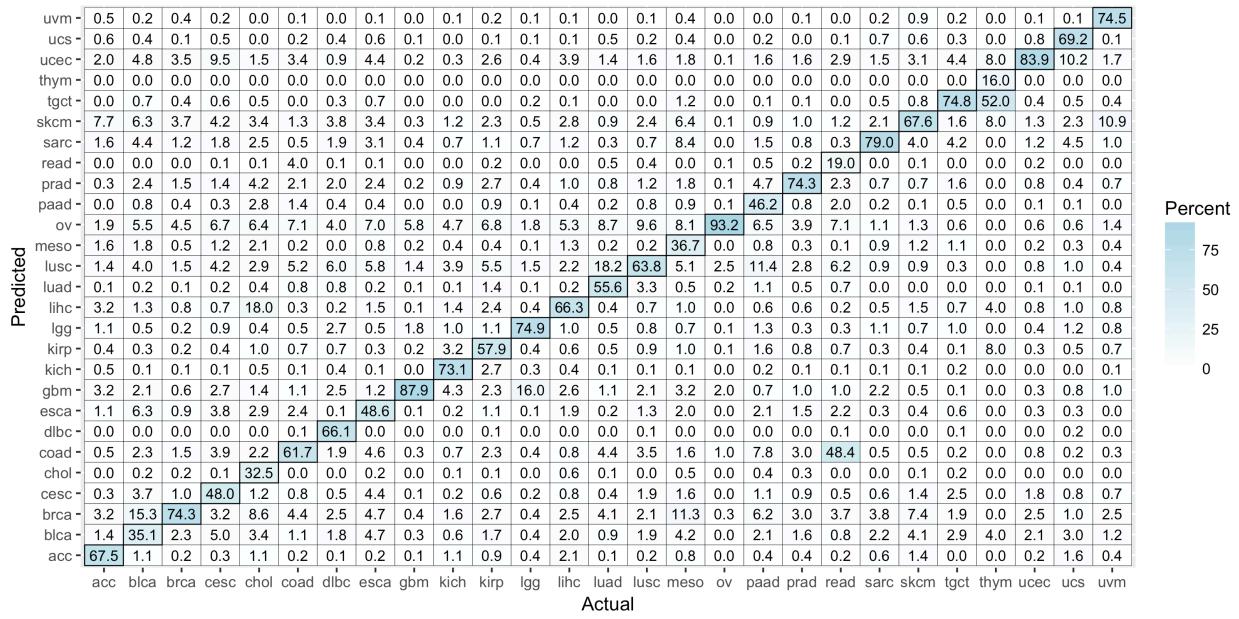


Figure 17: Model F

## 10 Appendix C – Visualization of Cancer Classes

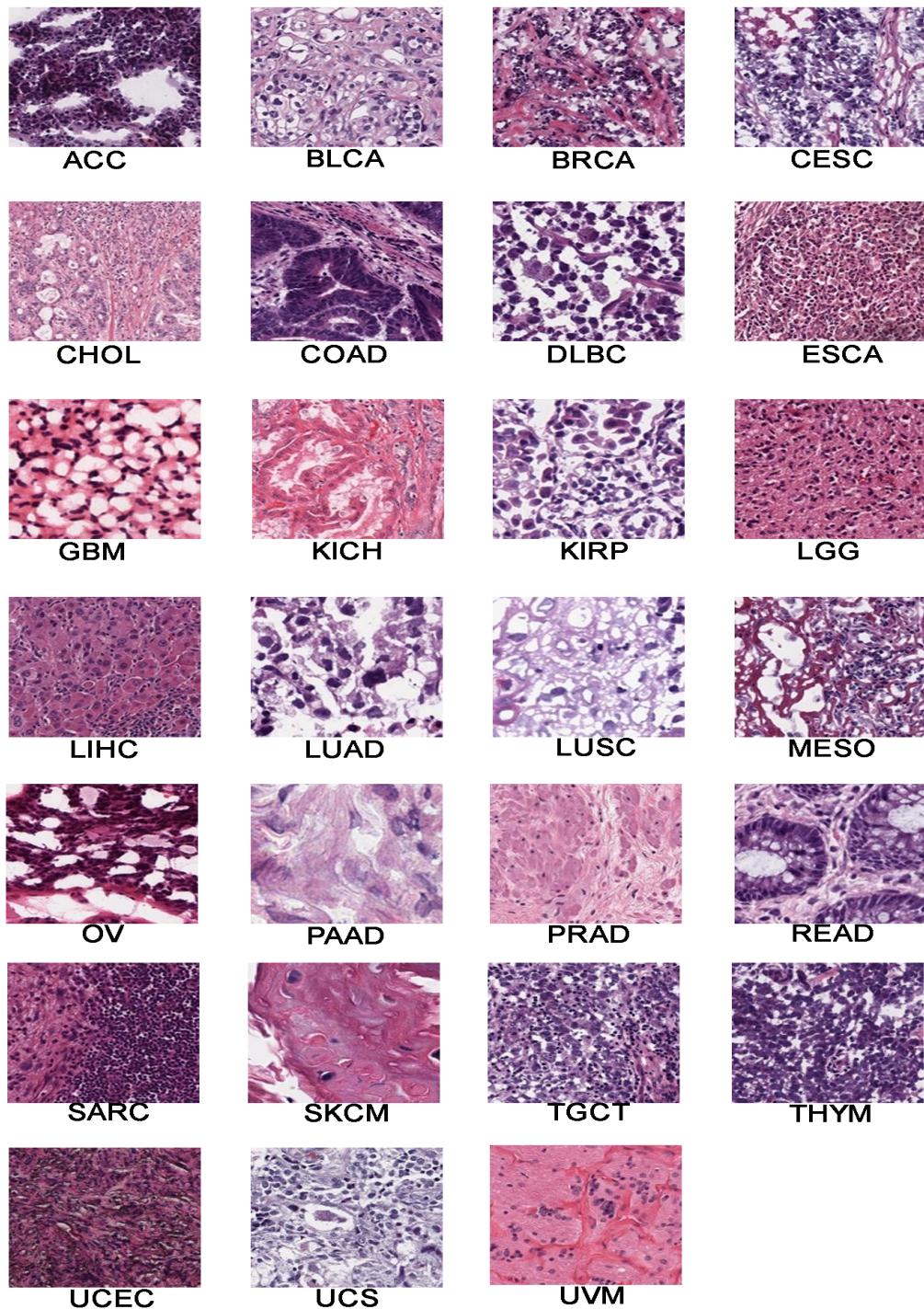


Figure 18: An example of each disease state