



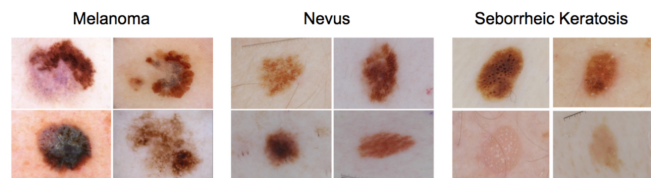
- ✓ 10. Quiz: Random vs Pre-initia...
- ✓ 11. Solution: Random vs Pre-initia...
- ✓ 12. Validating the Training
- ✓ 13. Quiz: Sensitivity and Specificity
- ✓ 14. Solution: Sensitivity and Speci...
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Mini Project: Dermatologist AI

Introduction

In this mini project, you will design an algorithm that can visually diagnose **melanoma**, the deadliest form of skin cancer. In particular, your algorithm will distinguish this malignant skin tumor from two types of benign lesions (**nevi** and **seborrheic keratoses**).

The data and objective are pulled from the [2017 ISIC Challenge on Skin Lesion Analysis Towards Melanoma Detection](#). As part of the challenge, participants were tasked to design an algorithm to diagnose skin lesion images as one of three different skin diseases (melanoma, nevus, or seborrheic keratosis). In this project, you will create a model to generate your own predictions.



Getting Started

1. Clone the [repository](#) and create a **data/** folder to hold the dataset of skin images.



```
com/udacity/dermatologist  
-ai.git  
mkdir data; cd data
```

2. Create folders to hold the training, validation, and test images.

```
mkdir train; mkdir valid;  
mkdir test
```

3. Download and unzip the [training data](#) (5.3 GB).
4. Download and unzip the [validation data](#) (824.5 MB).
5. Download and unzip the [test data](#) (5.1 GB).
6. Place the training, validation, and test images in the [data/](#) folder, at [data/train/](#), [data/valid/](#), and [data/test/](#), respectively. Each folder should contain three sub-folders ([melanoma/](#), [nevus/](#), [seborrheic_keratoses/](#)), each containing representative images from one of the three image classes.

You are free to use any coding environment of your choice to solve this mini project! In order to rank your results, you need only use a pipeline that culminates in a CSV file containing your test predictions.

Create a Model

Use the training and validation data to train a model that can distinguish between the



performance of your model.)

If you would like to read more about some of the algorithms that were successful in this competition, please read [this article](#) that discusses some of the best approaches. A few of the corresponding research papers appear below.

- Matsunaga K, Hamada A, Minagawa A, Koga H. [“Image Classification of Melanoma, Nevus and Seborrheic Keratosis by Deep Neural Network Ensemble”](#). International Skin Imaging Collaboration (ISIC) 2017 Challenge at the International Symposium on Biomedical Imaging (ISBI).
- Daz IG. [“Incorporating the Knowledge of Dermatologists to Convolutional Neural Networks for the Diagnosis of Skin Lesions”](#). International Skin Imaging Collaboration (ISIC) 2017 Challenge at the International Symposium on Biomedical Imaging (ISBI). ([github](#))
- Menegola A, Tavares J, Fornaciali M, Li LT, Avila S, Valle E. [“RECOD Titans at ISIC Challenge 2017”](#). International Skin Imaging Collaboration (ISIC) 2017 Challenge at the International Symposium on Biomedical Imaging (ISBI). ([github](#))

While the original challenge provided additional data (such as the gender and age of the patients), we only provide the image data to you. If you would like to download



All three of the above teams increased the number of images in the training set with additional data sources. If you'd like to expand your training set, you are encouraged to begin with the [ISIC Archive](#).

Evaluation

Inspired by the ISIC challenge, your algorithm will be ranked according to three separate categories.

Category 1: ROC AUC for Melanoma Classification

In the first category, we will gauge the ability of your CNN to distinguish between malignant melanoma and the benign skin lesions (nevus, seborrheic keratosis) by calculating the area under the receiver operating characteristic curve ([ROC AUC](#)) corresponding to this binary classification task.

If you are unfamiliar with ROC (Receiver Operating Characteristic) curves and would like to learn more, you can check out the documentation in [scikit-learn](#) or read [this Wikipedia article](#).

The top scores (from the ISIC competition) in this category can be found in the image below.



Category 2: ROC AUC for Melanocytic Classification

In the second category, we will test the ability of your CNN to distinguish between melanocytic and keratinocytic skin lesions by calculating the area under the receiver operating characteristic curve (**ROC AUC**) corresponding to this binary classification task.

The top scores in this category (from the ISIC competition) can be found in the image below.

Category 3: Mean ROC AUC

<https://classroom.udacity.com/nanodegrees/nd101/parts/b9c4c3c3-b524-427b-8832-9d0748f14a2e/modules/cb574ac4-7144-4b...> 5/9



below.

Rank	User	Title	Organization	Documentation	Date	Score
1	Razibius Matsunaga	ResNet ensemble with normalized image	Castle and Shinshu University joint team	[D]	Wed, 1 Mar 2017, 10:18:03 pm	0.911
2	moncy python	gpru-LSTM	Malware Processing Group - Universidad Carlos III de Madrid	[D]	Wed, 1 Mar 2017, 11:07:56 pm	0.910
3	BECCO Team	resnet50 (SISemi) "skin test"	BECCO Team / UNICAM	[D]	Wed, 1 Mar 2017, 10:42:07 pm	0.908
4	poppley	EffNet (single scale w/o atrous)	UCL-BMT	[D]	Wed, 1 Mar 2017, 7:04:42 pm	0.896
5	Ruler Yang	multi-task deep learning model for skin lesion segmentation and classification	Institute of High-Performance Computing - National Skin Center, Singapore	[D]	Tue, 28 Feb 2017, 5:34:10 pm	0.886
6	Y-D	Leat Minus Submission???	University of Guelph - MLRG	[D]	Wed, 1 Mar 2017, 10:03:59 pm	0.886
7	Cristina Vasconcelos	conv5	Luiff	[D]	Tue, 28 Feb 2017, 12:11:27 pm	0.851
8	Cristina Vasconcelos	all	Luiff	[D]	Tue, 28 Feb 2017, 12:06:44 pm	0.850
9	Eulgon Ahn	DeepNet	UCL-BMT	[D]	Wed, 1 Mar 2017, 9:30:13 am	0.836
10	HJ	ResNet_LSTM_Loss	CHU	[D]	Wed, 1 Mar 2017, 10:17:56 pm	0.829
11	Radouk Harangi	Ensemble of deep convolutional neural networks	University of Debrecen	[D]	Wed, 1 Mar 2017, 7:25:16 pm	0.825
12	INSECTECNIA	Final	INSECTECNIA / TECNIA	[D]	Wed, 1 Mar 2017, 6:05:40 pm	0.823
13	Rafael Souza	Angaria Medical Vision Lab - GoogleNet	Universidade Federal de Mato Grosso	[D]	Wed, 1 Mar 2017, 2:20:22 pm	0.823
14	Dylan Stein	task3_Final_KQ	Computer Vision Institute, Shenzhen University	[D]	Wed, 1 Mar 2017, 8:20:22 pm	0.823
15	Yu-Jen	task3_Final_AJKE	Computer Vision Institute, Shenzhen University	[D]	Wed, 1 Mar 2017, 8:15:10 pm	0.816
16	Mash Muband	Skin Lesion Classification Using Hybrid Deep Neural Networks	IPA	[D]	Wed, 1 Mar 2017, 11:51:43 am	0.811
17	Matt Beresh	Final Classification Submission	NLP/LOGIX / WEBSITE.AI	[D]	Tue, 28 Feb 2017, 5:52:47 am	0.804
18	Dennis Murphy	Transfer Learning from Inception	Dennis Murphy	[D]	Wed, 1 Mar 2017, 10:06:39 pm	0.790
19	Hao Chang	MRNet	Yale	[D]	Wed, 1 Mar 2017, 10:53:05 pm	0.790
20	Wenhao Zhang	resPhase	CSMedical	[D]	Wed, 1 Mar 2017, 6:08:07 pm	0.658
21	Jaakko S.M.	Lesion Classification	DSN/MLG	[D]	Wed, 1 Mar 2017, 8:25:02 pm	0.655
22	Muwei-Ji	Dr Ji PJ Test	Dr Jinwei Institute College of Engineering	[D]	Wed, 1 Mar 2017, 11:46:52 pm	0.497
23	Naresh Singh	Ensemble of people	MIT	[D]	Wed, 1 Mar 2017, 7:00:13 am	0.455

Getting your Results

Once you have trained your model, create a CSV file to store your test predictions. Your file should have exactly 600 rows, each corresponding to a different test image, **plus** a header row. You can find an example submission file ([sample_submission.csv](#)) in the repository.

Your file should have exactly 3 columns:

- **Id** - the file names of the test images (in the **same** order as the sample submission file)
- **task_1** - the model's predicted probability that the image (at the path in **Id**) depicts melanoma
- **task_2** - the model's predicted probability that the image (at the path in **Id**) depicts seborrheic keratosis

Once the CSV file is obtained, you will use the [get_results.py](#) file to score your submission. To set up the environment to run this file, you need to create (and activate) an environment with Python 3.5 and a few pip-installable packages:



```
python=3.5
```

```
source activate derm-ai  
pip install -r requirements.t  
xt
```

Once you have set up the environment, run the following command to see how the sample submission performed:

```
python get_results.py sample_  
predictions.csv
```

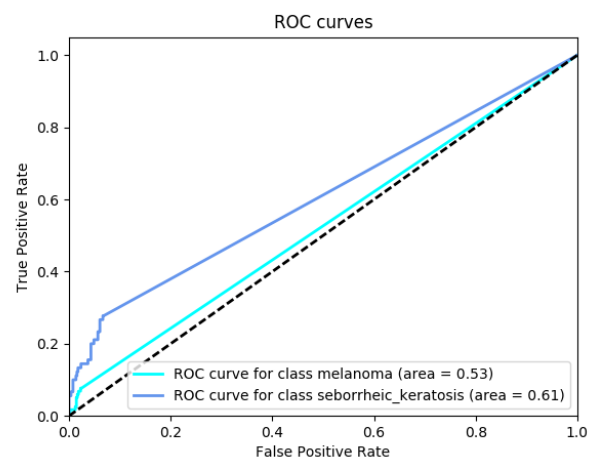
Check the terminal output for the scores obtained in the three categories:

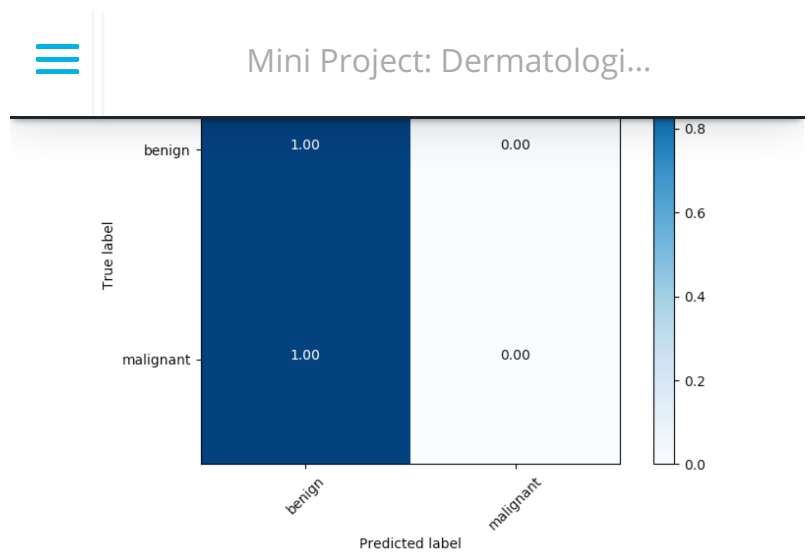
```
Category 1 Score: 0.526
```

```
Category 2 Score: 0.606
```

```
Category 3 Score: 0.566
```

The corresponding **ROC curves** appear in a pop-up window, along with the **confusion matrix** corresponding to melanoma classification.





As you can see from the confusion matrix, the sample submission currently predicts that most of the images in the test dataset correspond to benign lesions. Let's see if your model can improve these results, towards better detecting cancer!

The code for generating the confusion matrix assumes that the threshold for classifying melanoma is set to 0.5. To change this threshold, you need only supply an additional command-line argument when calling the `get_results.py` file. For instance, to set the threshold at 0.4, you need only run:

```
python get_results.py sample_predictions.csv 0.4
```

To test **your own** submission, change the code to instead include the path to **your** CSV file.

[NEXT](#)

