# Melanoma

#### **Tumor Size Prediction**











## Melanoma Facts

- Evolves from melanocytes
- Most dangerous type of skin cancer
- Prevalent among individuals with low melanin level
- Appears in various shapes/sizes/colors

#### **Problem**

- Diagnosis/Prognosis Difficult
- High Prevalence



#### Solution

Size as an early indicator



## Stakeholders



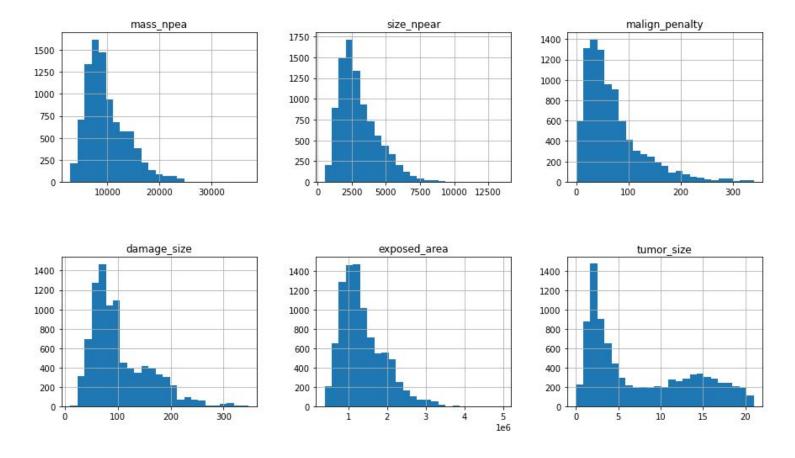


#### **Data Information**

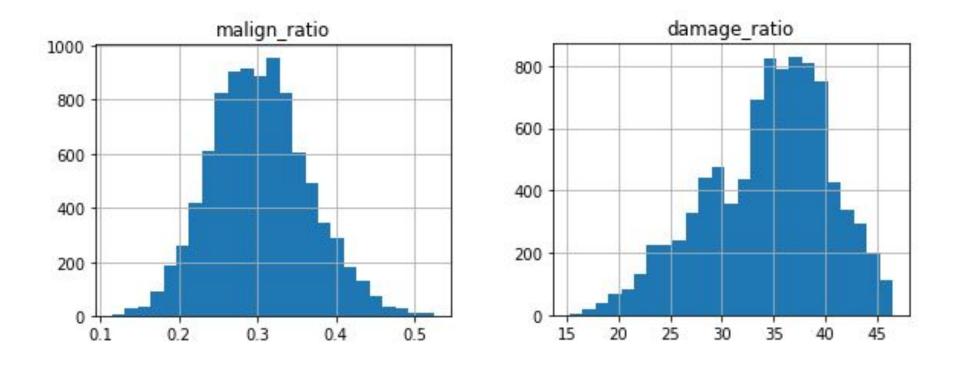
- Source: Machine Hack: Melanoma Tumor Size Prediction
- Training Set + Test Set
- Tumor Size and relevant attributes
- Number of entries: 9,146
- Number of features: 10
- Number of null values: 0

## **Features**

- Mass of the Area
- Size of the Area
- Normal/Malign Surface Ratio
- Damage Size
- Total Area Exposed to the Tumor
- Standard Deviation of Malign Skin Measurements
- Error in Malign Skin Measurements
- Penalty Imposed due to Measurement Error
- Damage/Total Spread Ratio
- Tumor Size



Apparent correlations due to the inherent proportionality between mass/volume



- Mean of **malign\_ratio** (normal/malign) ≈ 0.3 → malignancy prevalent in the dataset
- Left-skewed distribution of damage\_ratio supports this notion

Melanoma Tumor Correlation Heatmap 0.91 0.93 0.97 0.62 -0.9 -0.0047 mass\_npea 0.91 0.79 0.9 0.91 0.57 -0.79 size npear malign ratio 0.029 0.081 -0.069-0.89 0.94 -0.160.93 0.79 0.029 0.93 damage size 0.93 0.9 0.96 0.62 -0.9 -0.0036 exposed area -0.88 0.91 0.96 0.6 0.67 0.97 0.94 std dev malign -0.58 0.0045 0.62 0.57 0.081 0.62 0.6 err malign 0.59 0.68 0.67 -0.65 malign penalty -0.79-0.069 -0.89 -0.88 -0.58-0.65damage ratio -0.0036 -0.03 0.0045 0.012 tumor size damage\_size err\_malign malign\_penalty damage\_ratio

- Notable tumor\_size correlations
  - size\_npear

- 1.00

- 0.75

- 0.50

- 0.25

0.00

-0.25

-0.50

-0.75

- malign\_ratio
- o damage\_size

- Other notable correlations
  - mass\_npea/damage\_ratio
  - size\_npear/malign\_ratio

## Modeling Overview

Supervised Learning

Regression

Machine Learning Tools: Scikit-Learn, Keras

## Modeling Procedure

- I. Data Preprocessing
- 1. Training Validation Split (70%: 30%)
- 2. Feature Standardization
- II. Randomized Search
  - cv = 3
  - n\_iter = 50
  - scoring = "neg\_mean\_squared\_error"

III. Training with Tuned Parameters

IV. Performance Evaluation

- Evaluation Metric: R2, MSE
- Separate Test Dataset

## Techniques/Algorithms Used

#### Hyperparameter Tuning Technique

Randomized Search from Scikit-Learn

#### Regression Algorithms

- 1) Multiple Linear Regression
- 2) Random Forest
- 3) Support Vector Machine
- 4) Multi-Layer Perceptron
- 5) Keras Regression

## Model Comparison

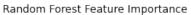
Model	MSE	R2
Multiple Linear Regression	26.43	0.29
Random Forest	16.21	0.57
Support Vector Machine	21.53	0.42
Multi-Layer Perceptron	29.62	0.21
Keras Regression	18.69	-

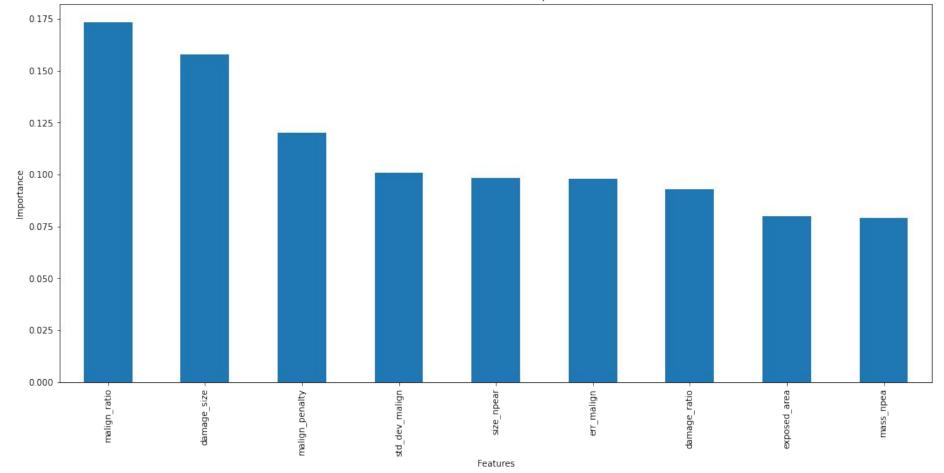
High Performance Models: Random Forest, Keras Regression

## Performance on Test Set

Model	MSE	R2
Random Forest	8.25	0.23
Keras Regression	12.12	-

Best Model: Random Forest





## Assumptions/Limitations

- Primary Assumption
  - All measurements obtained with sufficient accuracy/precision
- Limitations
  - Insufficient number of entries for training set compared to those of test set (mere 9146, while 36584 for test set)
  - Low number of features

## Conclusion

- All features used
- Best model: Random Forest
- Primary features of importance: malign\_ratio, damage\_size, malign\_penalty
- Prospective improvement
  - Larger volume of data for training set
  - Hyperparameter tuning with Grid Search
  - Further experiment with neural network/deep learning models