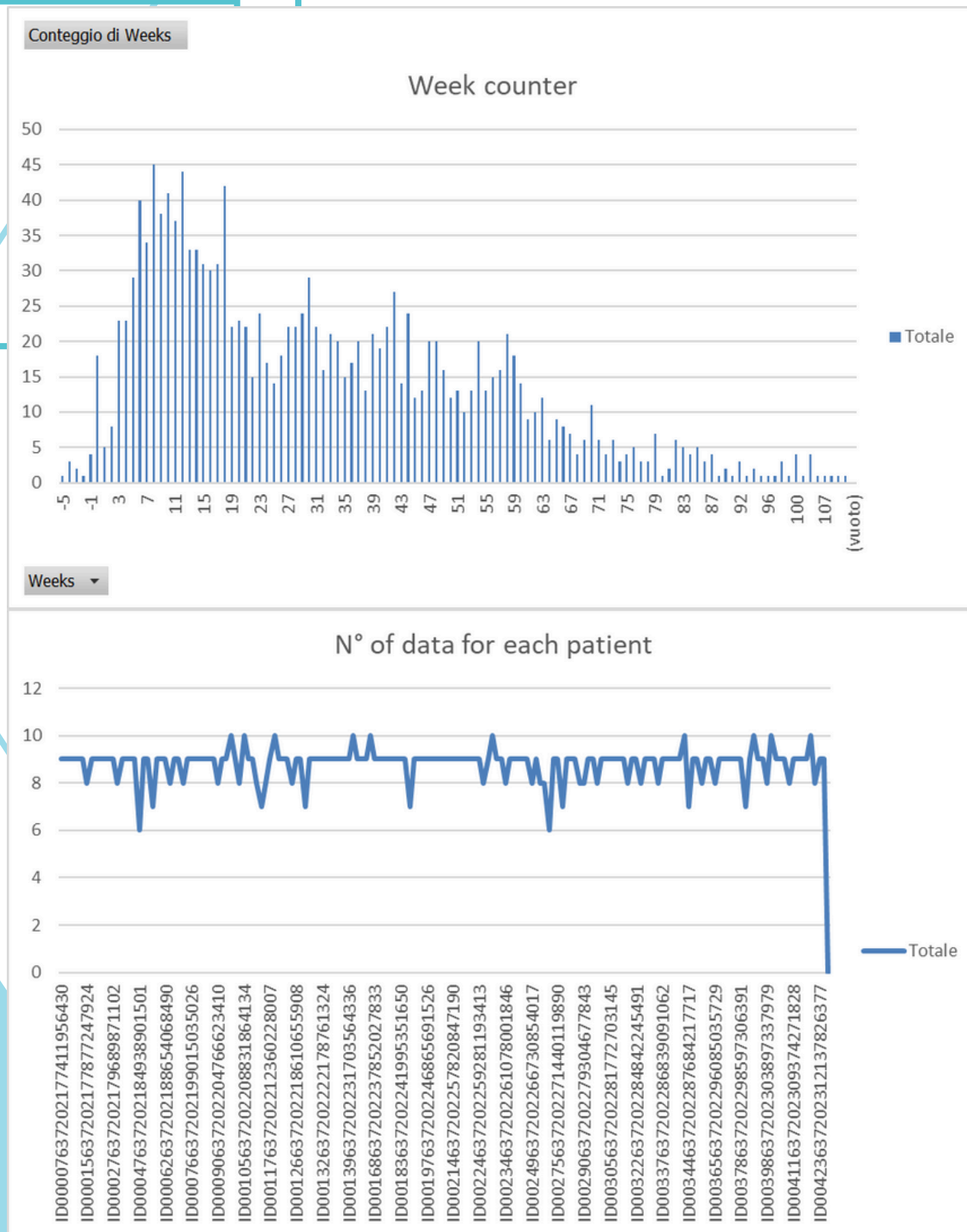




# **PROGRESS PREDICTION**

## **3°WEEK**

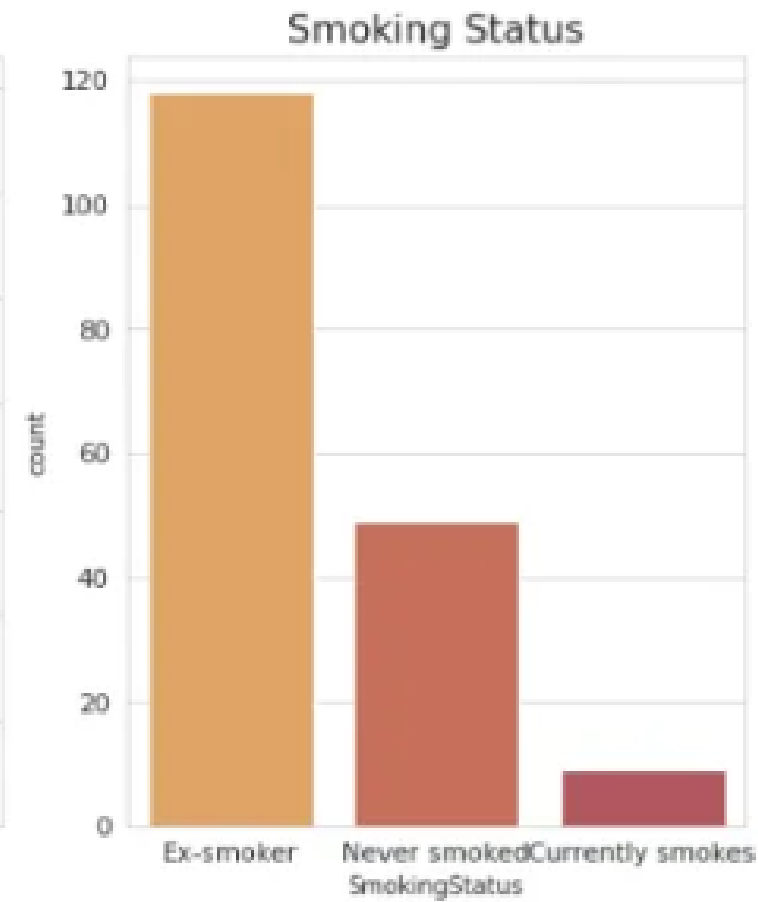
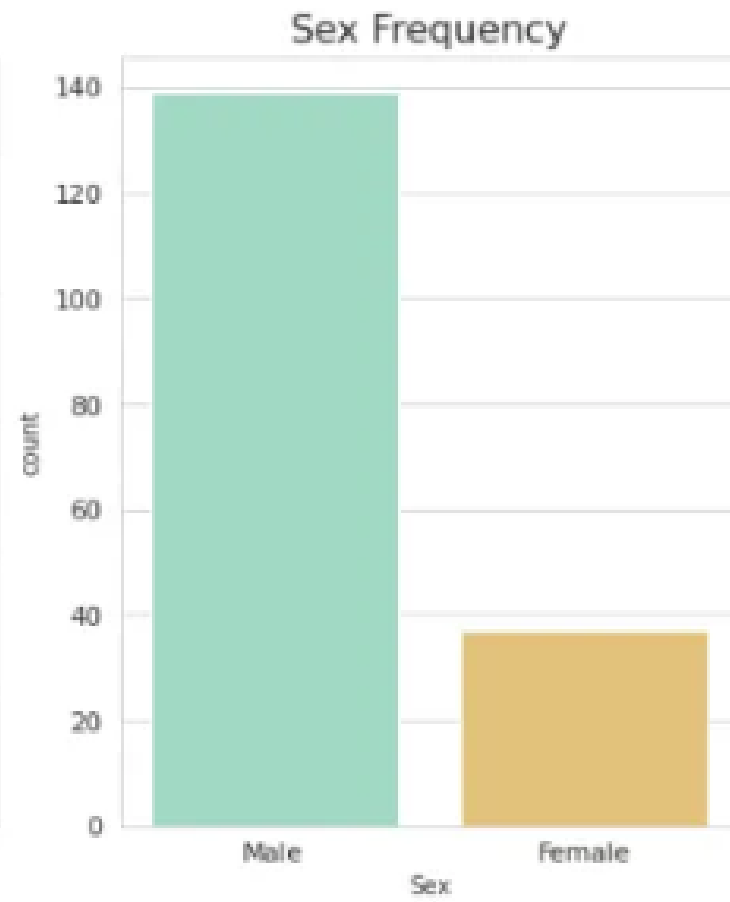
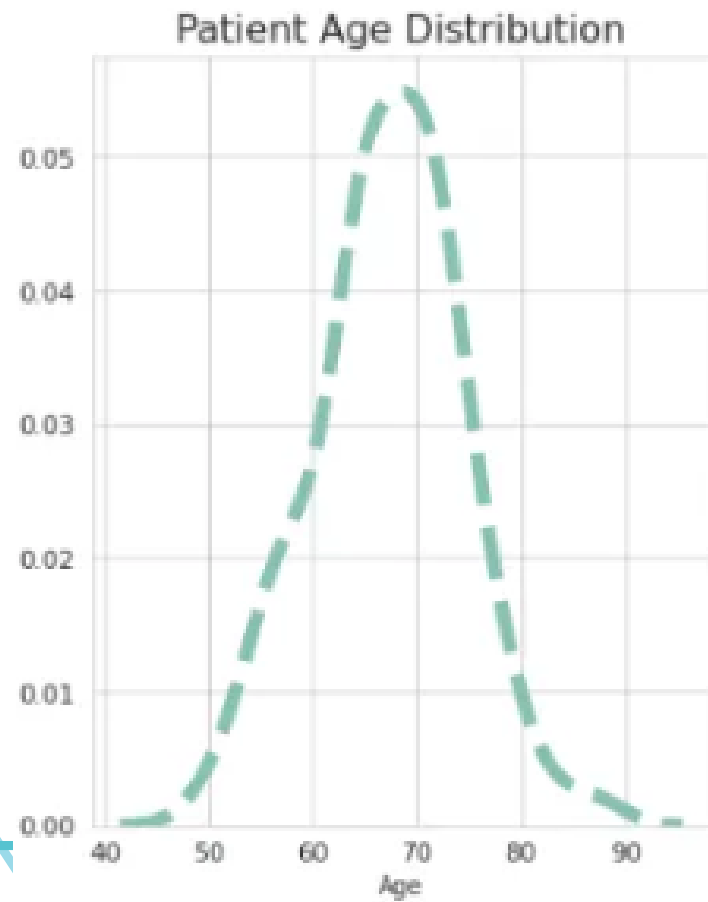
# Data analysis



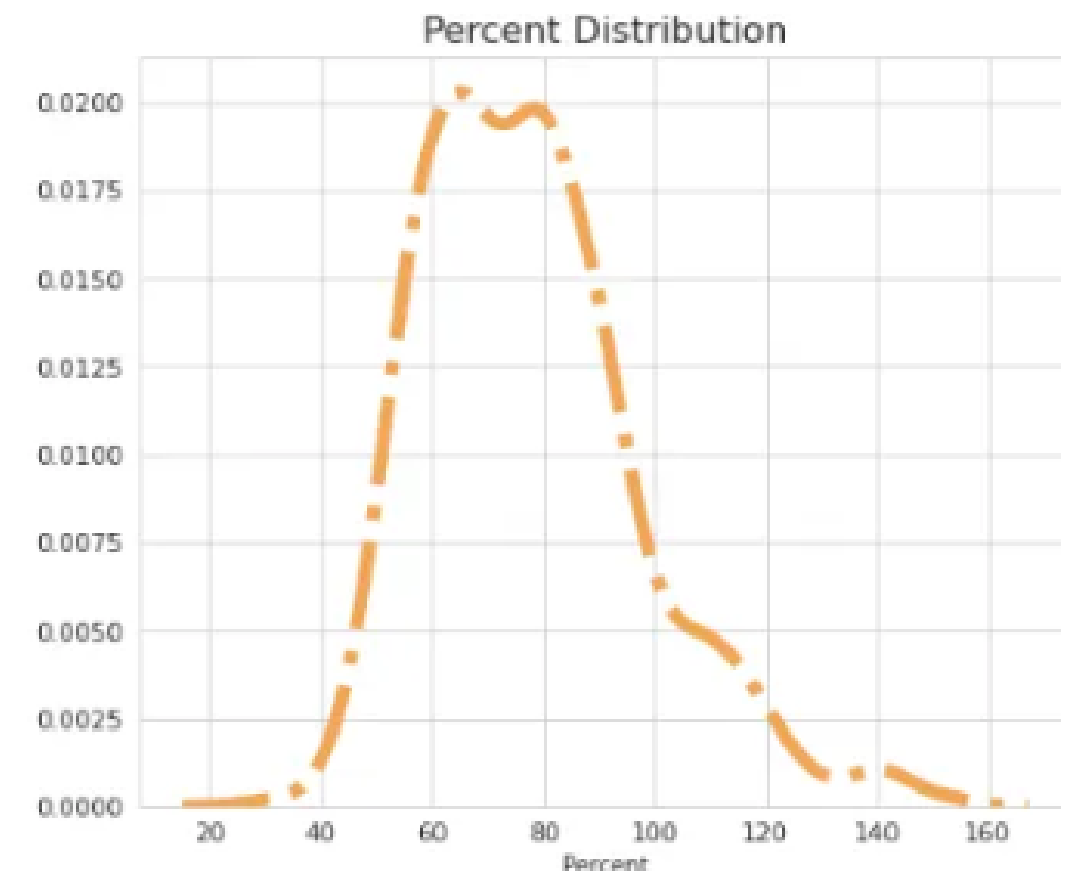
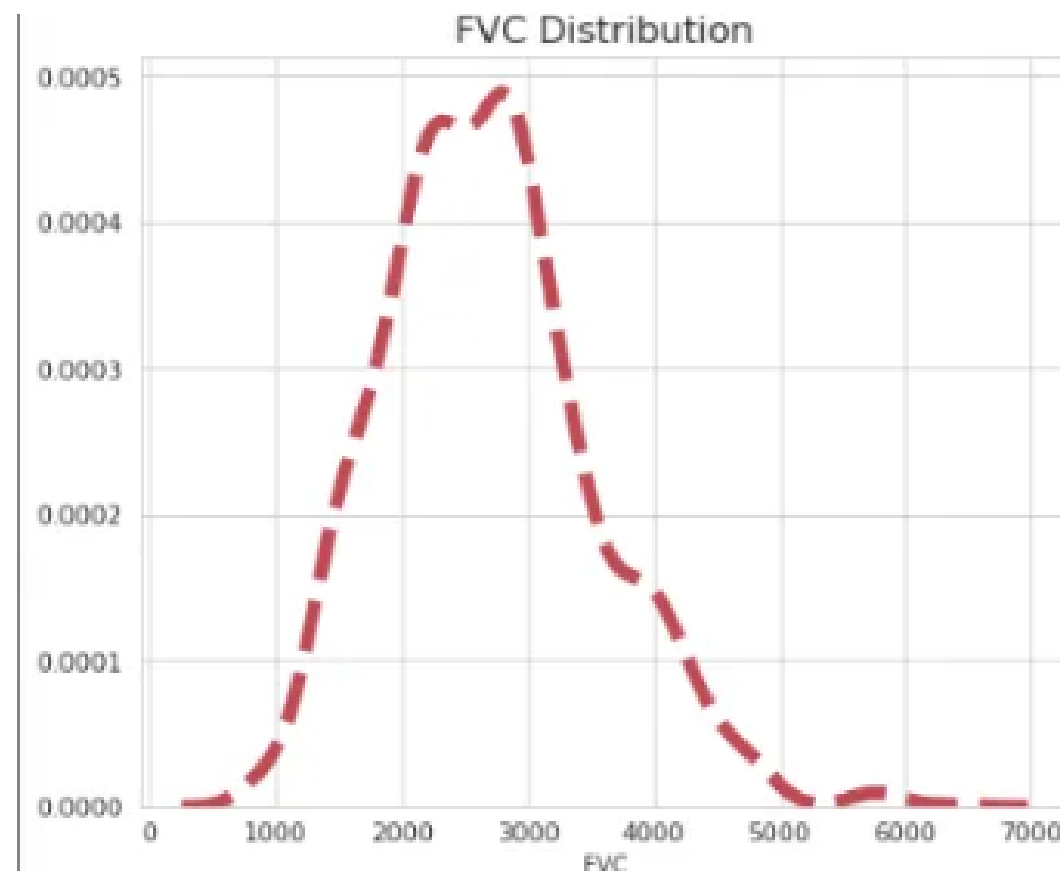
## Week analysis:

- 18 patients have data at time 0
- Week 8 is the most present with 45 pairs
- Most patients have more or less same amount of data (176 distinct patients)

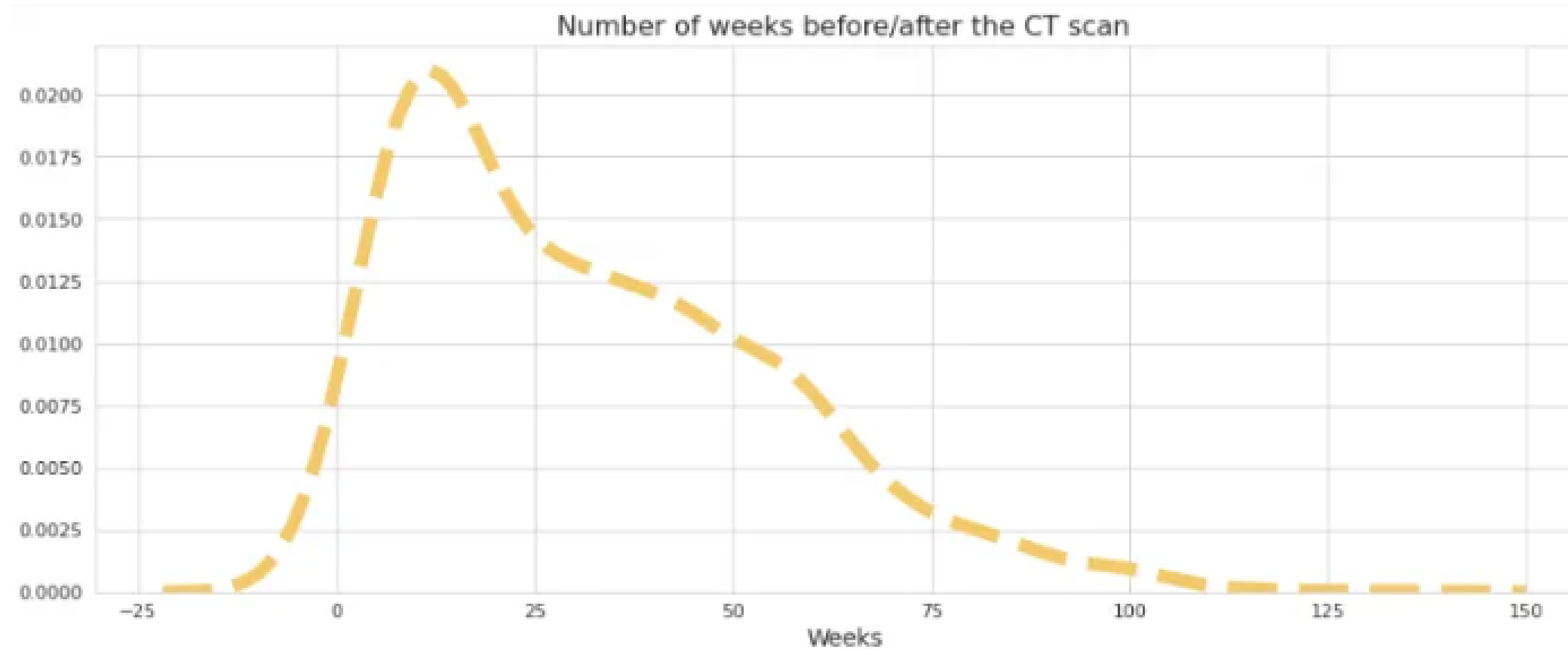
# Data analysis



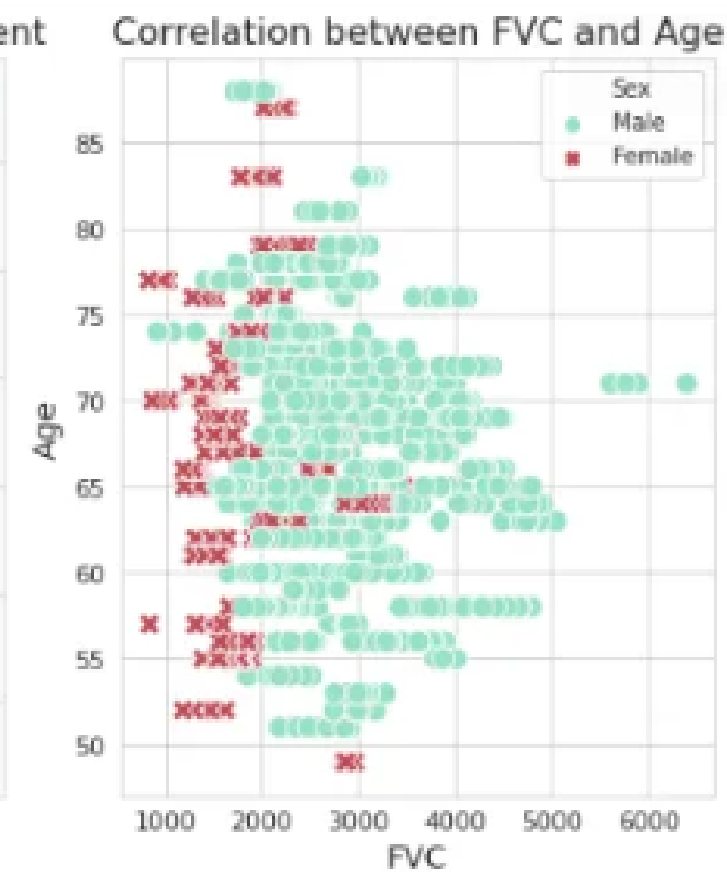
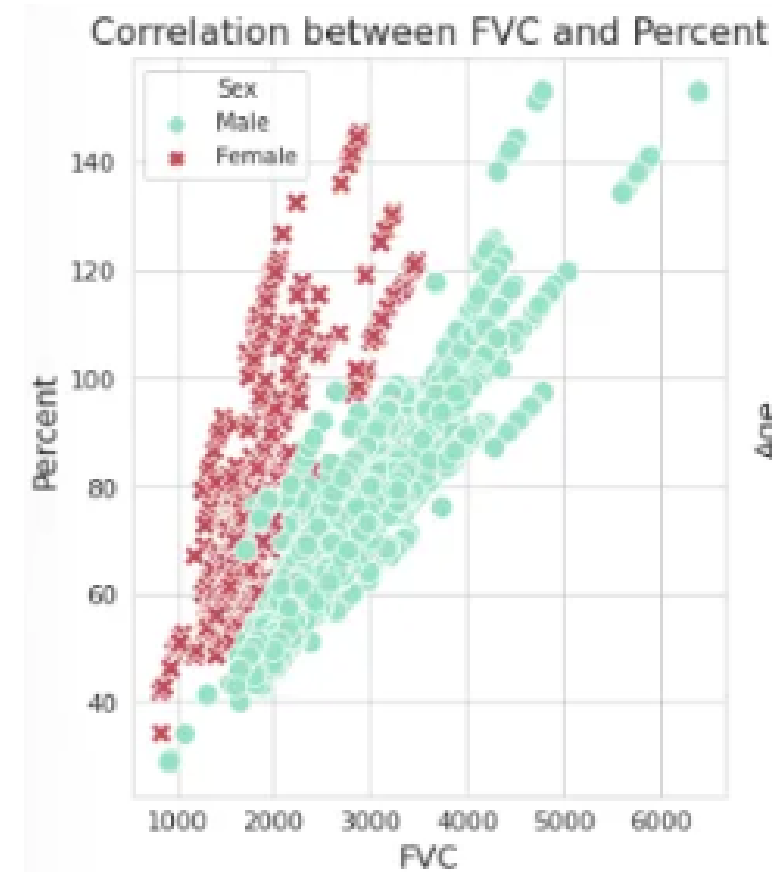
- Patient age mean → 67 years
- Male most prevalent
- Ex- smoker most prevalent

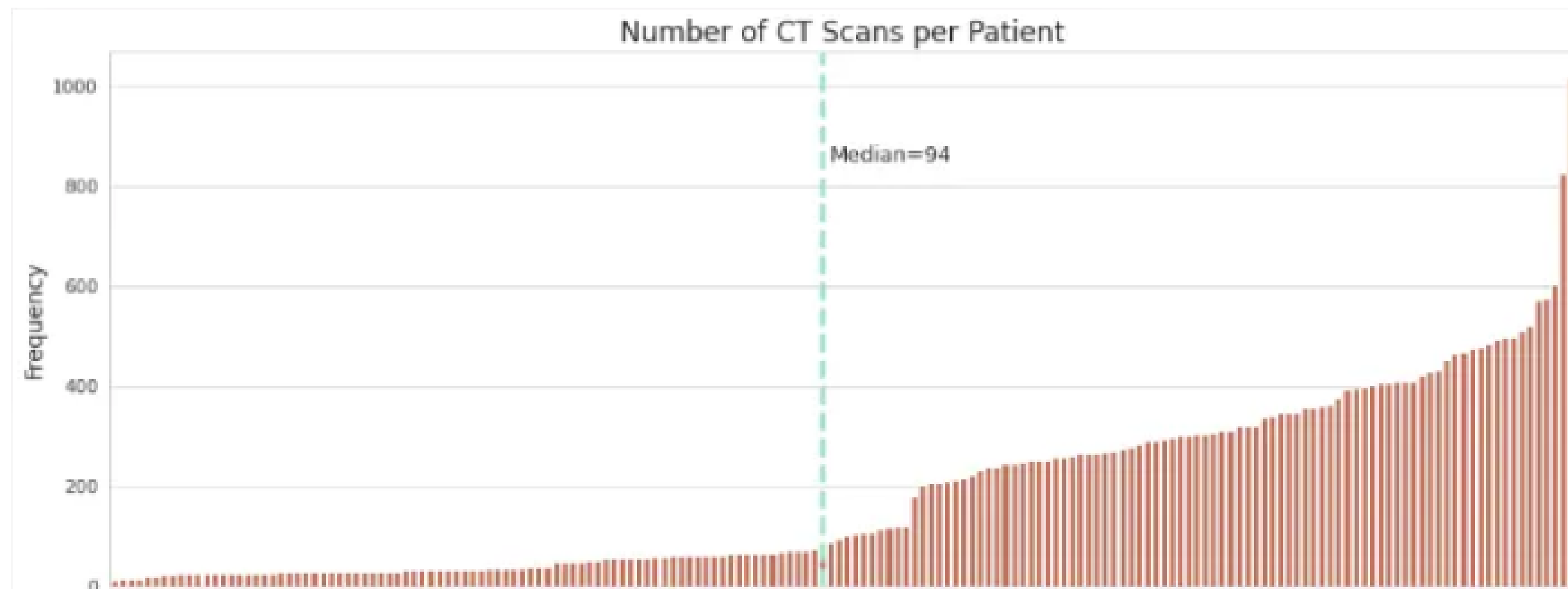
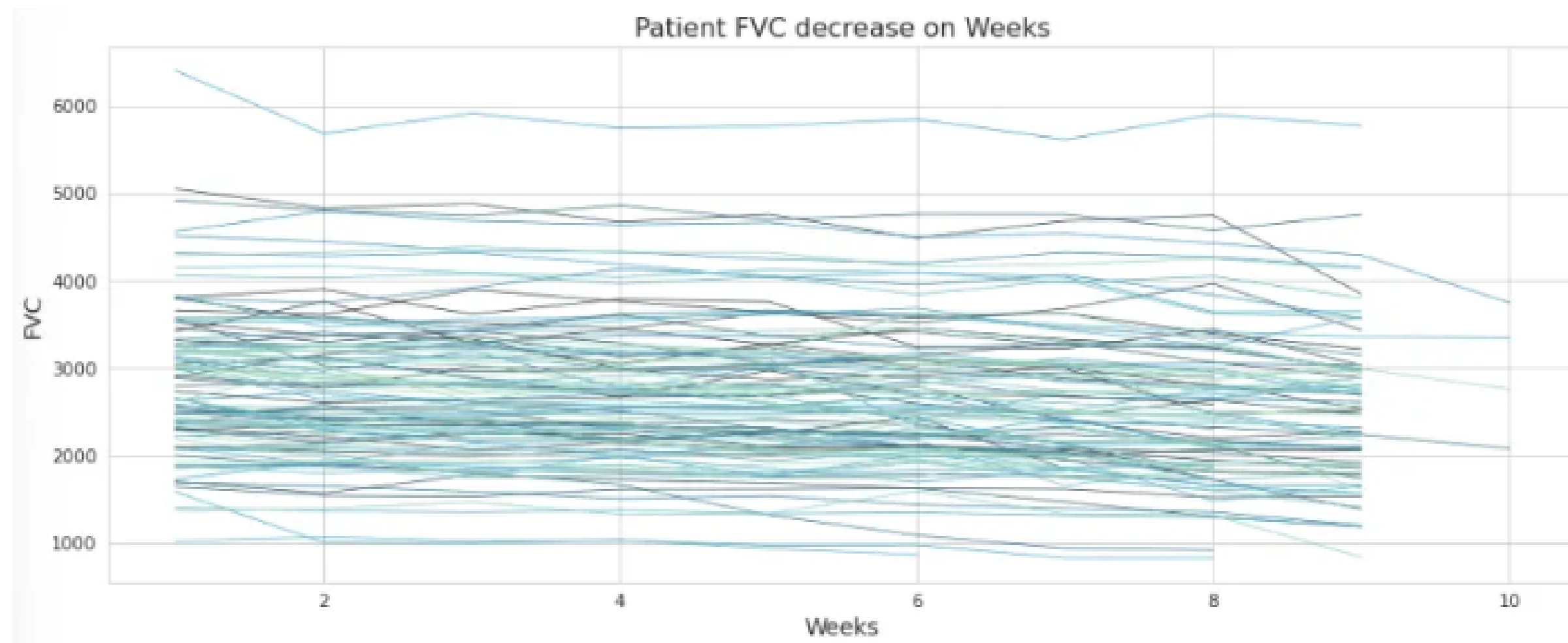


# Data analysis



- **PEARSON CORR FVC X PERCENT: 0.672**
- **PEARSON CORR FVC X AGE: -0.09**
- **PEARSON CORR PERCENT X AGE: 0.096**





# KAGGLE SOLUTION



**11 images from the middle 30-60 percentile for each CT scan.**

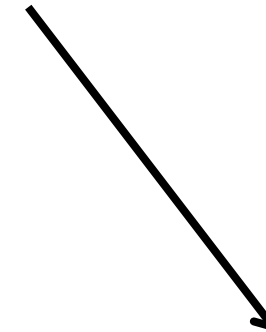
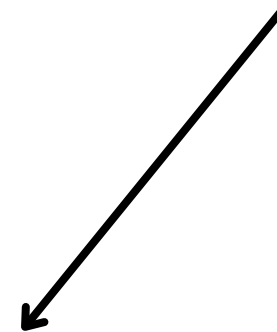
**Using this the following features were extracted:**

- **Lung volume**
- **Average of number of tissue pixels present across all selected images for a patient**
- **Average tissue area**
- **Average tissue volume**
- **Average of (number of tissue pixels)/(Total pixels on image)**
- **Average of (tissue area)/(lung area)**

**Then merge image and metadata, clean outliers and normalize data.**

# KAGGLE BEST SOLUTION

**Model ensemble**



**Linear Regression  
CNN**

**+**

**Quantile Regression**



# KAGGLE BEST SOLUTION



## 1<sup>st</sup> model

- **Linear Regression** → **Take as input (Weeks,FVC) and determine a slope “a”**
- **Slope “a”** → **Indicates the progression through the weeks**

**The slope is then used as a target for the pair (CT scans, data)**

- **CNN (EfficientNet)** → **Take as input CT scan and data**



# **1<sup>st</sup> model**

- **K-fold cross-validation : 5 folds**

**Quantiles pre-defined for each fold as [0.8, 0.5, 0.1, 0.1, 0.1]**

**For each fold:**

**The model makes predictions for each patient, 20 CT slices are selected, for each slice a slope is determined and the quantile is used to aggregate the per-slice predictions.**

**The FVC at each week is predicted using the formula:**

$$\text{FVC} = \alpha * w + B$$

**(B is the intercept calculated based on the known FVC at week 0.**

## **2<sup>nd</sup> model**

- **MLP**

**Takes as input only the available data + metadata.**

**Doesn't take in consideration features extracted from the CT scan.**

## **Model ensemble**

**The two predictions are combined giving more importance to the 2<sup>nd</sup> model (0.6).**

- **1<sup>st</sup> model : Gains complex information and patterns from the CT scans**
- **2<sup>nd</sup> model: Stabilize the predictions**

**Final Output :**

**PatientID - Week - FVC - Confidence**