

In [OSIC Pulmonary Fibrosis Progression competition](#)

on Kaggle, participants are tasked to determine the likelihood of recovery (**prognosis**) of several patients affected by a lung disease. For each patient, the maximum volume of air they can exhale after a maximum inhalation (**FVC**, Forced Vital Capacity) is measured over the weeks, for approximately 1-2 years of time.

In addition, we have the following information about these people:

- A **chest computer scan** obtained at time `Week=0`
- Their **age**
- Their **sex**
- Their **smoking status**: currently smokes, ex-smoker, never smoked

The challenge is to **assess the lung function's health by forecasting the FVC** (I'm not asking myself here, if it's the good or bad way to do that). What I like about this competition, is that there are **many ways to approach it**. Here's a non-exhaustive list:

1. One way could be to **construct a Statistical/Machine Learning (ML) model on the whole dataset**, and study the (conditional) distribution of the FVC, knowing the scan, age, sex, and smoking status. In this first approach we consider that disease evolution can be generalized among categories of patients sharing the same patterns. A [Bayesian](#) ML model could capture the uncertainty around predictions, or we could use a more or less sophisticated [bootstrapping](#) procedure for the same purpose. Or, even, consider that ML model residuals are irregularly spaced time series.

2. Another way, the *quick and dirty* one I'll present here, **considers each patient's case individually**. Age, sex, smoking status and the chest scan are not used, but the measurement week is. If we are only interested in forecasting the **FVC**, the approach will be fine. But if we want to understand how each one of the factors we previously described [influence the FVC](#), either individually or in conjunction, then the first approach is better.

0 – Functions

These are the functions that I use in the analysis. The first one extracts a patient's information from the whole database, based on his/her identifier. The second one fits a [smoothing spline](#) to a patient's data, and forecasts his/her FVC.

get patient data

```
suppressPackageStartupMessages(library(dplyr))

# 0 - 1 get patient data -----
get_patient_data <- function(id, train)
{
  df <- dplyr::select(dplyr::filter(train, Patient == id), c(Weeks,
FVC))
  df$log_Weeks <- log(13 + df$Weeks) # the relative timing of FVC
measurements (varies widely)
  df$log_FVC <- log(df$FVC) # transformed response variable
```

```

df$Patient <- id
return(df)
}

```

fit and forecast FVC

```

# 0 - 2 fit, predict and plot -----
fit_predict <- function(df, plot_=TRUE)
{
  min_week <- 13
  n <- nrow(df)

  test_seq_week <- seq(-12, 133)
  log_test_seq_week <- log(min_week + test_seq_week)

  # Fit a smoothing spline, using Leave-one-out cross-validation for
  regularization
  fit_obj <- stats::smooth.spline(x = df$log_Weeks,
                                y = df$log_FVC,
                                cv = TRUE)

  resids <- residuals(fit_obj)
  mean_resids <- mean(resids)
  conf <- max(exp(sd(resids)), 70) # https://www.kaggle.com/c/osic-pulmonary-fibrosis-progression/overview/evaluation

  preds <- predict(fit_obj, x=log_test_seq_week)

  res <- list(Weeks_pred = test_seq_week, FVC_pred = exp(preds$y))
  conf_sqrt_n <- conf/sqrt(n)
  ubound <- res$FVC_pred + mean_resids + 1.96*conf_sqrt_n # strong
hypothesis
  lbound <- res$FVC_pred + mean_resids - 1.96*conf_sqrt_n

  if (plot_)
  {
    leg.txt <- c("Measured FVC", "Interpolated/Extrapolated FVC", "95%
Confidence interval bound")

    plot(df$Weeks, df$FVC, col="blue", type="l", lwd=3,
         xlim = c(-12, 133),
         ylim = c(min(min(lbound), min(df$FVC)),
                   max(max(ubound), max(df$FVC)) ),
         xlab = "Week", ylab = "FVC",
         main = paste0("Patient: ", df$Patient[1]))
    lines(res$Weeks_pred, res$FVC_pred)
    lines(res$Weeks_pred, ubound, lty=2, col="red")
    lines(res$Weeks_pred, lbound, lty=2, col="red")
    abline(v = max(df$Weeks), lty=2)
    legend("bottomright", legend = leg.txt,

```

```

        lwd=c(3, 1, 1), lty=c(1, 1, 2),
        col = c("blue", "black", "red"))
    }

    return(invisible(list(res = res,
        conf = rep(conf, length(res$FVC_pred)),
        mean = res$FVC_pred,
        ubound = ubound,
        lbound = lbound,
        resids = resids)))
}

```

1 - Import the whole dataset

```

# Training set data
train <- read.csv("~/Documents/Kaggle/OSIC_August2020/train.csv")

# Training set snippet
print(head(train))
print(tail(train))

```

```

# Training set snippet
print(head(train))

```

```

##           Patient Weeks  FVC  Percent Age  Sex SmokingStatus
## 1 ID00007637202177411956430   -4 2315 58.25365 79 Male      Ex-smoker
## 2 ID00007637202177411956430    5 2214 55.71213 79 Male      Ex-smoker
## 3 ID00007637202177411956430    7 2061 51.86210 79 Male      Ex-smoker
## 4 ID00007637202177411956430    9 2144 53.95068 79 Male      Ex-smoker
## 5 ID00007637202177411956430   11 2069 52.06341 79 Male      Ex-smoker
## 6 ID00007637202177411956430   17 2101 52.86865 79 Male      Ex-smoker

```

```
print(tail(train))
```

```

##           Patient Weeks  FVC  Percent Age  Sex SmokingStatus
## 1544 ID00426637202313170790466   11 2976 73.07730 73 Male      Never smoked
## 1545 ID00426637202313170790466   13 2712 66.59464 73 Male      Never smoked
## 1546 ID00426637202313170790466   19 2978 73.12641 73 Male      Never smoked
## 1547 ID00426637202313170790466   31 2908 71.40752 73 Male      Never smoked
## 1548 ID00426637202313170790466   43 2975 73.05275 73 Male      Never smoked
## 1549 ID00426637202313170790466   59 2774 68.11708 73 Male      Never smoked

```

2 - Predict FVC for a few patients (4)

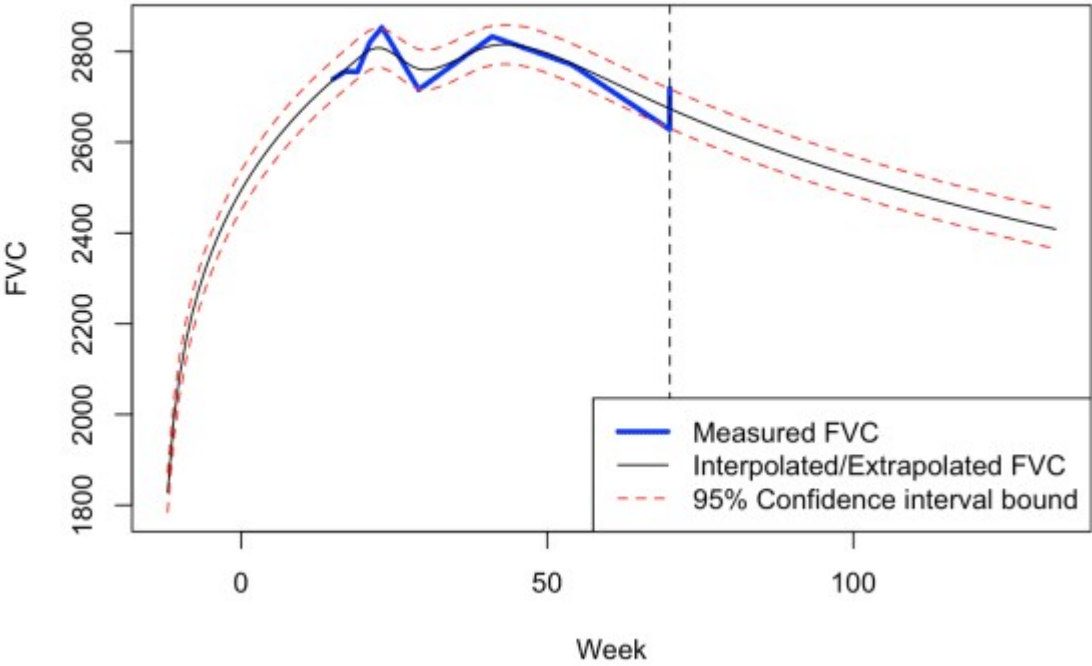
```

# Four patient ids are selected
ids <- c("ID00421637202311550012437", "ID00422637202311677017371",
        "ID00426637202313170790466", "ID00248637202266698862378")

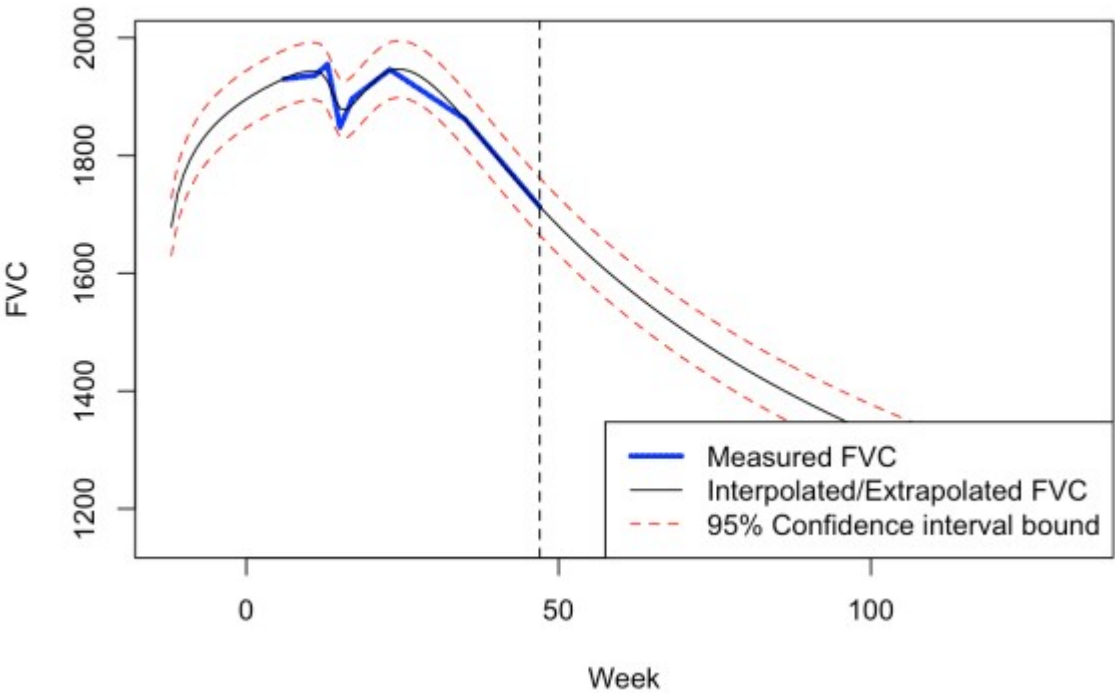
#par(mfrow=c(2, 2))
for(i in 1:length(ids))
{
    # Extract patient's data based on his/her ID
    (df <- get_patient_data(id=ids[i], train))
    # Obtain FVC forecasts, with 95% confidence interval
    # warnings when repeated measures in the same week
    suppressWarnings(fit_predict(df, plot_=TRUE))
}

```

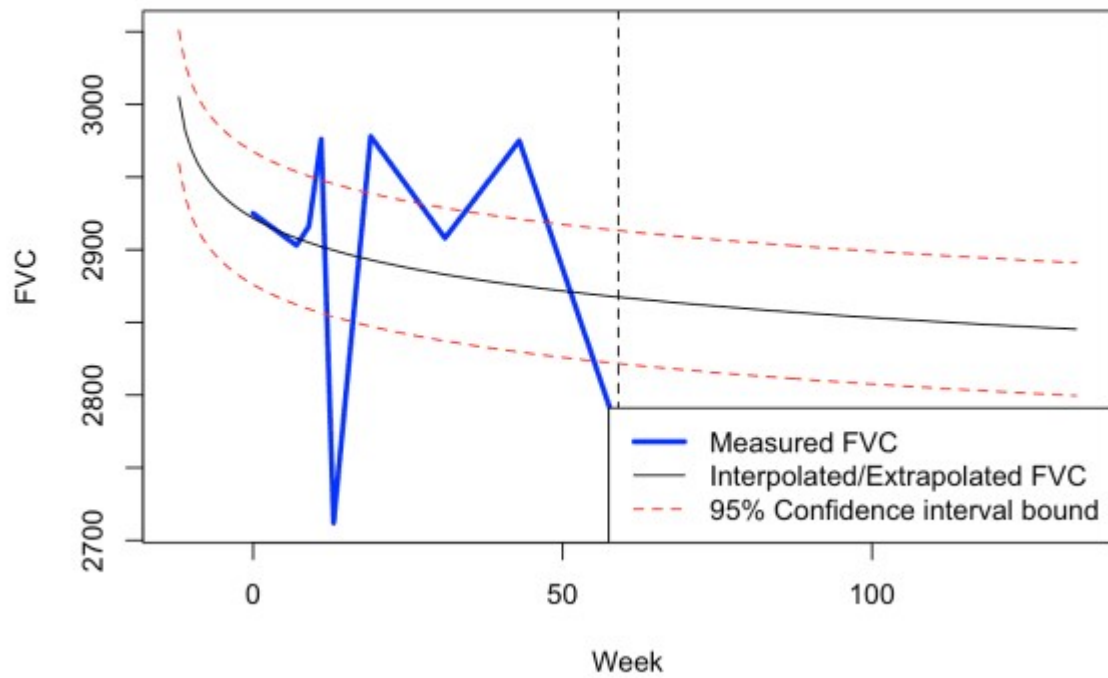
Patient: ID00421637202311550012437



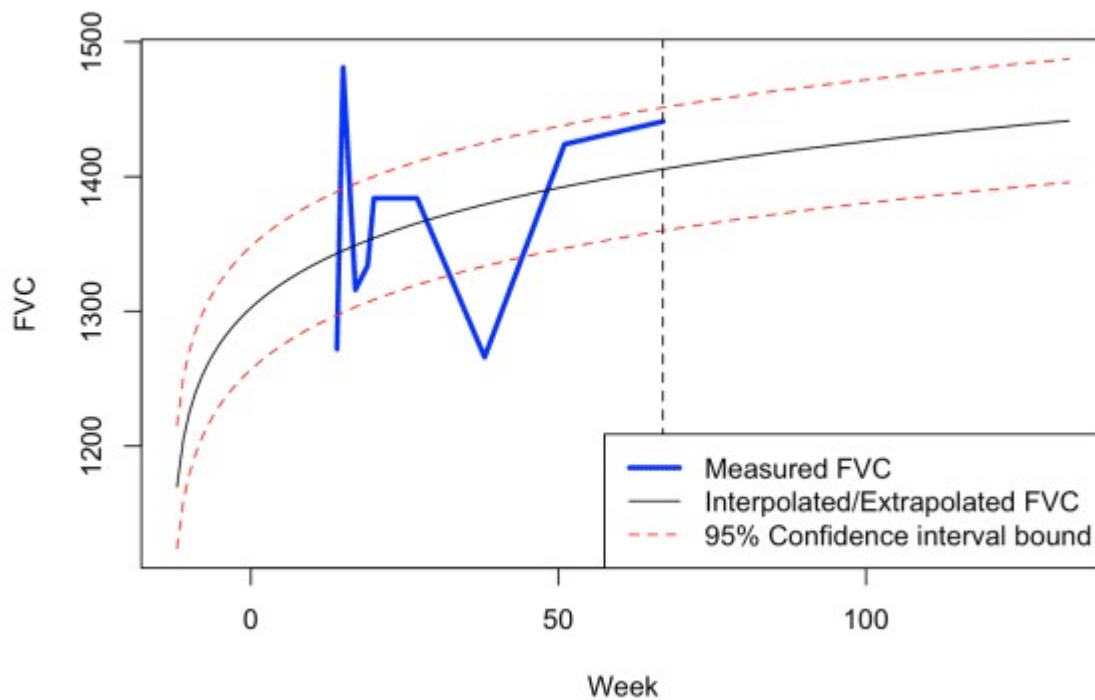
Patient: ID00422637202311677017371



Patient: ID00426637202313170790466



Patient: ID00248637202266698862378



For a *quick and dirty* baseline model, this one seems to produce quite coherent forecasts, which could be used for decision making. Of course, validation data (unseen by the model) could reveal a whole different truth.