T.C.

ÜSKÜDAR ÜNİVERSİTESİ

MÜHENDİSLİK VE DOĞA BİLİMLERİ FAKÜLTESİ

ADLİ BİLİMLER BÖLÜMÜ

ABL440

Adli Bilimlerde Büyük Veri

FİNAL ÖDEVİ

Hazırlayan

Aysu İĞDİ

200207016

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İÇİNDEKİLER

Takibi Yapılan Kitabın Künyesi

Kitap Adı : R and Data Mining -- Examples and Case Studies

Yazar : Yanchang Zhao

Yayınevi : Academic Press, Elsevier

Yayım Tarihi : Aralık 2012

ISBN : 978-0-123-96963-7

Uygulama

GitHub : [igdiaysu/big-data-in-fs]

Konsoldan çalışma alanı ayarlandı.

```
> setwd("D:/GitRepository/big-data-in-fs/final")
```

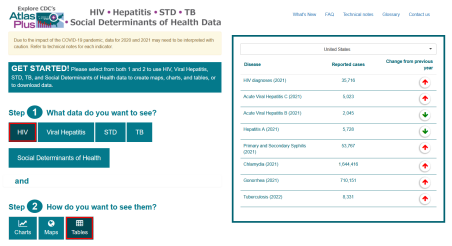
—

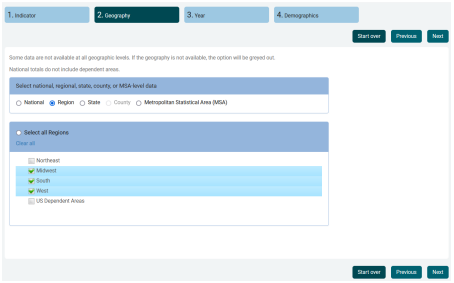
İlk bulunan dataset: [AIDS Deaths by State]

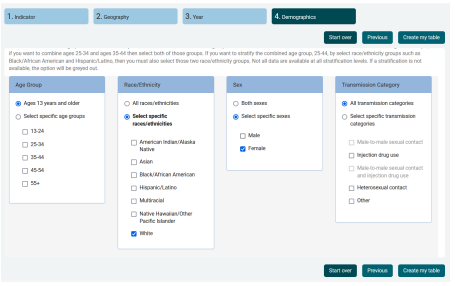
Source: [NCHHSTP AtlasPlus Portal]

Ayarlanan datasetin özellikleri:

- Gösterge (indicator) : HIV ölümleri
- Coğrafya : Bölge (region)
    - Midwest
    - West
    - South
- Yıl : 2008-2019
    - Veriler 2008-2021 arası olsa da sitede pandemi sebepli verilerle ilgili uyarı bulunmasından ötürü 2019 olarak daralttım.
- Yaş : 13+
- Irk/Etnik Köken : Beyaz
- Cinsiyet : Kadın
- Bulaşma Kategorisi : Tüm kategoriler
    - Enjeksiyonla uyuşturucu alımı
    - Heteroseksüel ilişki
    - Diğer







```
> library(readr)
> HIV_deaths2 <-
read_csv("D:/GitRepository/big-data-in-fs/final/HIV_deaths2.csv")
```

Veri Keşfi ve Görselleştirme (Data Exploration and Visualization)

Veri setinin boyutunu öğrenme: `dim()`

```
> dim(HIV_deaths2)
[1] 36  6
```

Veri setindeki değişken adlarını öğrenme: `names()`

```
> names(HIV_deaths2)
[1] "Indicator"       "Year"            "Geography"       "FIPS"            "Cases"           "Rate per 100000"
```

Veri setinin yapısını ve niteliklerini öğrenme: `str()` ve `attributes()`

```
> str(HIV_deaths2)
spc_tbl_ [36 × 6] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
 $ Indicator      : chr [1:36] "HIV deaths" "HIV deaths" "HIV deaths" "HIV deaths" ...
 $ Year           : num [1:36] 2008 2009 2010 2011 2012 ...
 $ Geography      : chr [1:36] "Midwest" "Midwest" "Midwest" "Midwest" ...
 $ FIPS           : num [1:36] 83002 83002 83002 83002 83002 ...
 $ Cases          : num [1:36] 114 98 114 106 123 93 83 83 115 124 ...
 $ Rate per 100000: num [1:36] 0.5 0.4 0.5 0.5 0.5 0.4 0.4 0.4 0.5 0.5 ...
 - attr(*, "spec")=
  .. cols(
  ..   Indicator = col_character(),
  ..   Year = col_double(),
  ..   Geography = col_character(),
  ..   FIPS = col_double(),
  ..   Cases = col_double(),
  ..   `Rate per 100000` = col_double()
  .. )
 - attr(*, "problems")=<externalptr>
```

```
> attributes(HIV_deaths2)
$row.names
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

$names
[1] "Indicator"       "Year"            "Geography"       "FIPS"            "Cases"           "Rate per 100000"

$spec
cols(
  Indicator = col_character(),
  Year = col_double(),
  Geography = col_character(),
  FIPS = col_double(),
  Cases = col_double(),
  `Rate per 100000` = col_double()
)

$problems
<pointer: 0x000002bc23a29cf0>

$class
[1] "spec_tbl_df" "tbl_df"      "tbl"         "data.frame"

> |
```

Verinin minimum, maksimum, ortalama, medyan, birinci ve üçüncü çeyrek değerlerini içeren özeti inceleme: *summary()*

```
> summary(HIV_deaths2)
  Indicator              Year       Geography             FIPS          Cases        Rate per 100000
 Length:36          Min.   :2008   Length:36          Min.   :83002   Min.   : 83.0   Min.   :0.4
 Class :character   1st Qu.:2011   Class :character   1st Qu.:83002   1st Qu.:113.8   1st Qu.:0.5
 Mode  :character   Median :2014   Mode  :character   Median :83003   Median :126.5   Median :0.7
                    Mean   :2014                      Mean   :83003   Mean   :199.6   Mean   :0.8
                    3rd Qu.:2016                      3rd Qu.:83004   3rd Qu.:345.2   3rd Qu.:1.1
                    Max.   :2019                      Max.   :83004   Max.   :414.0   Max.   :1.3
```

Verinin çeyreklerini inceleme: *quantile()*

```
> quantile(HIV_deaths2$Cases)
    0%    25%    50%    75%   100%
 83.00 113.75 126.50 345.25 414.00
> quantile(HIV_deaths2$`Rate per 100000`)
  0%  25%  50%  75% 100%
 0.4  0.5  0.7  1.1  1.3
```

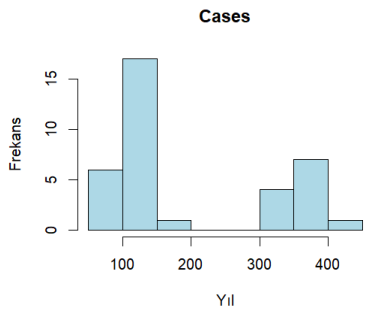
Verinin varyansını inceme: *var()*

100 bin kişi başına ölüm oranındaki sapmanın sonucu:

```
> var(HIV_deaths2$`Rate per 100000`)
[1] 0.09885714
```

Verinin histogram grafiği: *hist()*

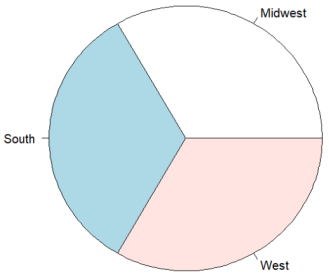
200-300 arasında vaka bulunan bölge olmadığını görüyoruz.




```
> hist(
+   HIV_deaths2$Cases,
+   main = "Cases",
+   xlab = "Yıl",
+   ylab = "Frekans",
+   col = "lightblue",
+ )
```

Verinin pie chartı: `pie(table())`

```
> pie(table(HIV_deaths2$Geography))
```

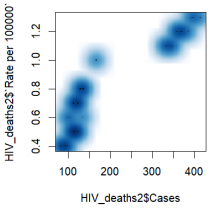


Verinin kovaryans ve korelasyon: `cov()` ve `cor()`

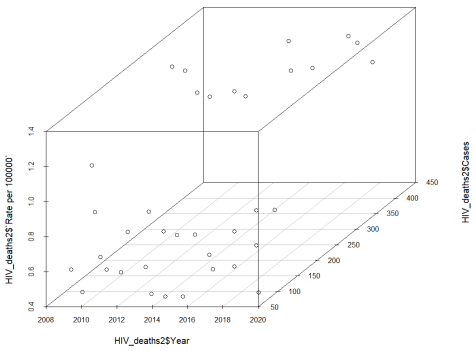
```
> cov(HIV_deaths2$Cases, HIV_deaths2$`Rate per 100000`)
[1] 36.04
> cor(HIV_deaths2$Cases, HIV_deaths2$`Rate per 100000`)
[1] 0.9409925
```

Verinin düzgün dağılım grafiği (renk yoğunluğu): `smoothScatter()`

```
> smoothScatter(HIV_deaths2$Cases, HIV_deaths2$`Rate per 100000`)
```



Verinin üç boyutlu dağılım grafiği: `scatterplot3d()`



Verinin ısı haritası: `heatmap()`

Isı haritası kullanımını gerektiren sayıda veri satırı bulunmamaktadır.

Decision Tree: train data

Başlangıçta `Geography`nin değişkenin türü değiştirildi: chracter → factor

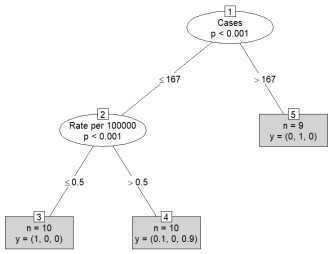
Tekrarlanabilirlik için seed girdisi yapıldı. Aynı sürümde farklı bilgisayarda bile aynı sonuçların tekrar edilebilmesi için (Aynı rastgelelik).

```
# HIV_deaths2$Geography<-as.factor(HIV_deaths2$Geography)

set.seed(444)
ind <- sample(2, nrow(HIV_deaths2), replace=TRUE, prob=c(0.7, 0.3))
trainData <- HIV_deaths2[ind==1,]
testData <- HIV_deaths2[ind==2,]

library(party)
myFormula <- Geography ~ Year + Cases + `Rate per 100000`
hiv_ctree <- ctree(myFormula, data=trainData)


# check the prediction >
table(predict(hiv_ctree), trainData$Geography)
```

```
table(predict(hiv_ctree), trainData$Geography)

         Midwest South West
Midwest       10     0    0
South          0     9    0
West           1     0    9
```

```
> print(hiv_ctree)

        Conditional inference tree with 3 terminal nodes

Response:  Geography
Inputs:  Year, Cases, Rate per 100000
Number of observations:  29

1) Cases <= 167; criterion = 1, statistic = 27.393
  2) Rate per 100000 <= 0.5; criterion = 1, statistic = 14.394
    3)*  weights = 10
  2) Rate per 100000 > 0.5
    4)*  weights = 10
1) Cases > 167
  5)*  weights = 9
```

```
plot(hiv_ctree, type="simple")
```



Decision Tree: test data

```
> # predict on test data >
> testPred <- predict(hiv_ctree, newdata = testData)
> table(testPred, testData$Geography)

testPred  Midwest South West
  Midwest       1     0    0
  South         0     3    0
  West          0     0    3
```

Tamamını doğru tahmin etti.

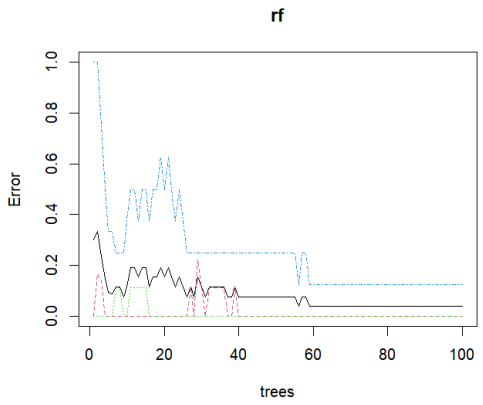
Random Forest

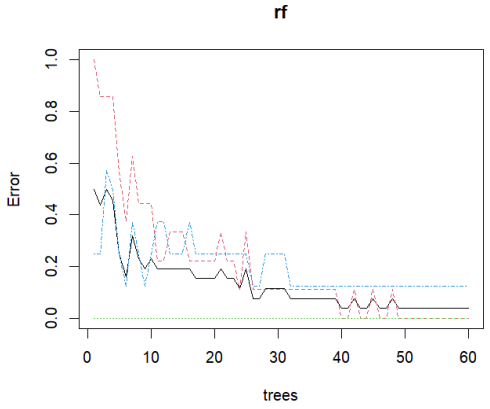
trainData işlemleri:

```
> HIV_deaths3$Geography<-as.factor(HIV_deaths3$Geography)
> ind <- sample(2, nrow(HIV_deaths3), replace=TRUE, prob=c(0.7, 0.3))
> trainData <- HIV_deaths3[ind==1,]
> testData <- HIV_deaths3[ind==2,]
> library(randomForest)
> rf <- randomForest(Geography ~ Year + Cases + `Rate`, data=trainData, ntree=100, proximity=TRUE)
> table(predict(rf), trainData$Geography)

          Midwest South West
  Midwest       9     0    1
  South         0     9    0
  West          0     0    7
```

```
> print(rf)

Call:
 randomForest(formula = Geography ~ Year + Cases + Rate, data = trainData,      ntree = 100, proximity = TRUE)
               Type of random forest: classification
                     Number of trees: 100
No. of variables tried at each split: 1

        OOB estimate of  error rate: 3.85%
Confusion matrix:
        Midwest South West class.error
Midwest       9     0    0       0.000
South         0     9    0       0.000
West          1     0    7       0.125
```

```
> attributes(rf)
$names
 [1] "call"            "type"            "predicted"       "err.rate"        "confusion"       "votes"
 [7] "oob.times"       "classes"         "importance"      "importanceSD"    "localImportance" "proximity"
[13] "ntree"           "mtry"            "forest"          "y"               "test"            "inbag"
[19] "terms"

$class
[1] "randomForest.formula" "randomForest"
```





100 ağaç üretilerek çalıştırılmış modelde 60'tan sonra değişiklik olmadığı gözlemlenerek 60 ağaçla tekralanıp grafik gözlemlendi.

```
> importance(rf)
      MeanDecreaseGini
Year          1.485198
Cases         6.243888
Rate          8.856384
```

Tahmin etmede değişkenlerin önemine dair tablo.

Random Forest: test data

```
> hivPred <- predict(rf, newdata=testData)
> table(hivPred, testData$Geography)

hivPred   Midwest South West
  Midwest       2     0    0
  South         0     3    0
  West          1     0    4
```

3 Mindwest'ten 1 tanesini West olarak tahmin etti.

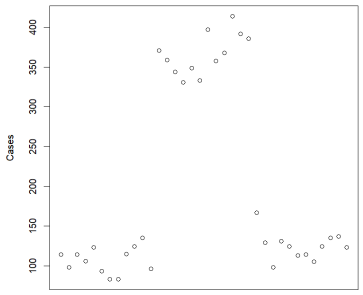
Regresyon

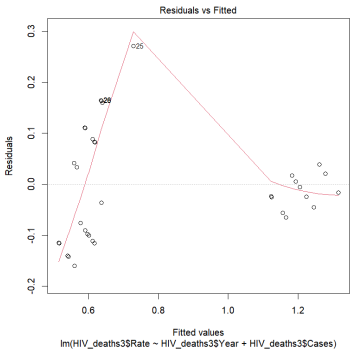
Regresyon, bağımlı bir değişkeni (yanıt olarak da adlandırılır) tahmin etmek için bağımsız değişkenlerin (tahmin ediciler olarak da bilinir) bir fonksiyonunu oluşturmaktır.

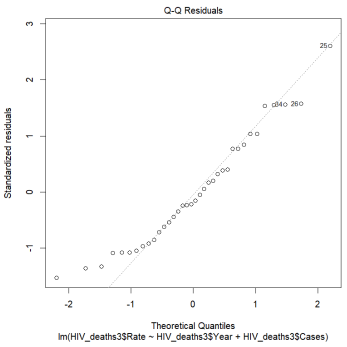
$$y = c_0 + c_1 x_1 + c_2 x_2 + \cdots + c_k x_k,$$

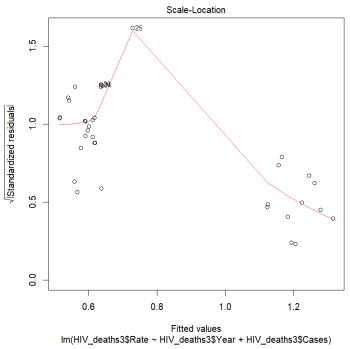
```
> reg <- lm(HIV_deaths3$Rate ~ HIV_deaths3$Year + HIV_deaths3$Cases)
> reg

Call:
lm(formula = HIV_deaths3$Rate ~ HIV_deaths3$Year + HIV_deaths3$Cases)

Coefficients:
      (Intercept)   HIV_deaths3$Year  HIV_deaths3$Cases
          3.31471           -0.00149            0.00243
```

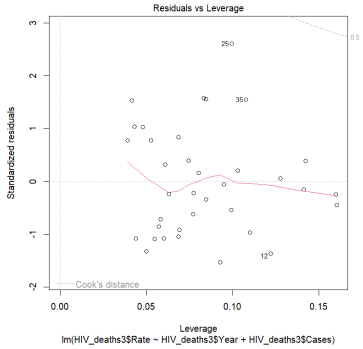
```
> summary(reg)

Call:
lm(formula = HIV_deaths3$Rate ~ HIV_deaths3$Year + HIV_deaths3$Cases)

Residuals:
     Min       1Q   Median       3Q      Max
-0.15975 -0.09226 -0.01945  0.08261  0.27106

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)        3.314705  10.646352   0.311    0.757
HIV_deaths3$Year  -0.001490   0.005288  -0.282    0.780
HIV_deaths3$Cases  0.002430   0.000152  15.991   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.1095 on 33 degrees of freedom
Multiple R-squared:  0.8857,    Adjusted R-squared:  0.8788
F-statistic: 127.9 on 2 and 33 DF,  p-value: 2.852e-16
```



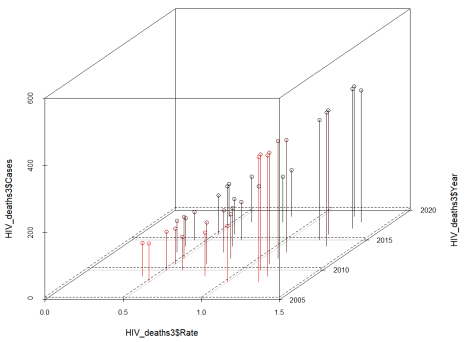









```
> library(scatterplot3d)
> s3d <- scatterplot3d(HIV_deaths3$Rate, HIV_deaths3
$Year, HIV_deaths3$Cases, highlight.3d=T, type="h", l
ab=c(2,3))
> s3d$plane3d(reg)
```



Kümeleme (Clustring)

```
> hiv2 <- HIV_deaths3
> hiv2$Geography <- NULL
> hiv2$Indicator <- NULL
> hiv2$FIPS <- NULL
> (kmeans.result <- kmeans(hiv2, 3))
K-means clustering with 3 clusters of sizes 8, 16, 12

Cluster means:
      Year    Cases     Rate
1 2013.375  95.2500 0.462500
2 2013.562 126.3750 0.675000
3 2013.500 366.8333 1.191667

Clustering vector:
 [1] 2 1 2 1 2 1 1 1 2 2 2 1 3 3 3 3 3 3 3 3 3 3 3 2 2 1 2 2 2 2 1 2 2 2 2

Within cluster sum of squares by cluster:
[1]  609.4337 2956.0175 7704.7358
 (between_SS / total_SS =  97.8 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss" "betweenss"    "size"
[8] "iter"         "ifault"
```

12-12-12 bulamadı.

```
> table(HIV_deaths3$Geography, kmeans.result$cluster)

           1  2  3
  Midwest  6  6  0
  South    0  0 12
  West     2 10  0
```

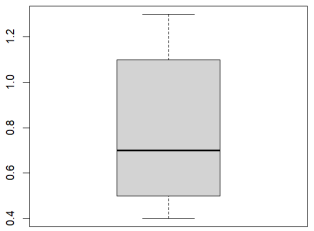
West ve Midwest'in iki ayrı kümeye dağılması hepsini doğru kümeyemediğini gösteriyor.

3 = South. Ama 1 ve 2'yi bilemeyiz.

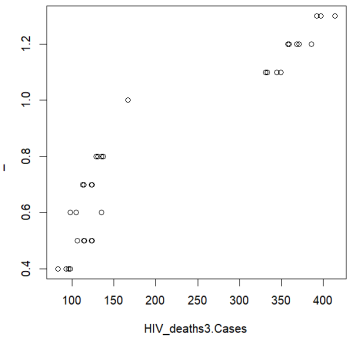
Verinin azlığı sebebiyle kmeans'tan verim alınamadığından diğer metotlar eklenmemiştir.

Aykırı Değer Tespiti (Outlier Detection)

```
> boxplot.stats(HIV_deaths3$Rate)$out
numeric(0)
> boxplot(HIV_deaths3$Rate)
```




```
> attach(df)
The following object is masked from df (pos = 3):

    HIV_deaths3.Rate

The following object is masked from df (pos = 4):

    HIV_deaths3.Rate

> (a <- which(HIV_deaths3$Cases %in% boxplot.stats(HIV_deaths3$Cases)$out))
integer(0)
> detach(df)
> (b <- which(HIV_deaths3$Rate %in% boxplot.stats(HIV_deaths3$Rate)$out))
integer(0)
> (outlier.list1 <- intersect(a,b))
integer(0)
```



Verimde outlier çıkmadığı için bölümün kalanı veri setine uygulanmadı.

Time Series Data in R

```
> # Time Series
> a <- ts(1:12, frequency=1, start=c(2008,1))
> a
Time Series:
Start = 2008
End = 2019
Frequency = 1
 [1]  1  2  3  4  5  6  7  8  9 10 11 12
>
```

Time Series Forecasting

```
install.packages("forecast")
library(forecast)

ts_trainData <- ts(HIV_deaths3$Cases, start = min(HIV_deaths3$Year), end = 2017, frequency = 1)
plot(ts_trainData, main = "Cases Over Time", xlab = "Year", ylab = "Number of Cases")

model <- arima(ts_trainData)
forecast_result <- forecast(model, h = 2)  # 2
plot(forecast_result, main = "Forecasted Cases Over Next 2 Year", xlab = "Year", ylab = "Number of Cases")
```

```
> forecast_result
     Point Forecast    Lo 80    Hi 80   Lo 95    Hi 95
2018          105.3 86.69277 123.9072 76.8427 133.7573
2019          105.3 86.69277 123.9072 76.8427 133.7573
```