

Attachment B

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Statistical analysis about tumours counting data comparasion of 12 months before COVID and 12 months after, in Modena province.

Import of the datasets

```
df_pre <- read.csv("df_pre.csv")
df_post <- read.csv("df_post.csv")
```

```
df_pre = query(
" SELECT *
  FROM df_pre
  ORDER BY Year, Month;"
)
df_pre_m = query(
" SELECT Month,Year, COUNT(*)
  FROM df_pre
  GROUP BY Year,Month;"
)

df_post = query(
" SELECT *
  FROM df_post
  ORDER BY Year, Month;"
)
df_post_m = query(
" SELECT Month,Year, COUNT(*)
  FROM df_post
  GROUP BY Year,Month;"
)

df_h = as.data.frame(cbind(df_pre_m[,3],df_post_m[,3]))
colnames(df_h) = c("before","after") # columns names
```

horizontal monthly dataframe

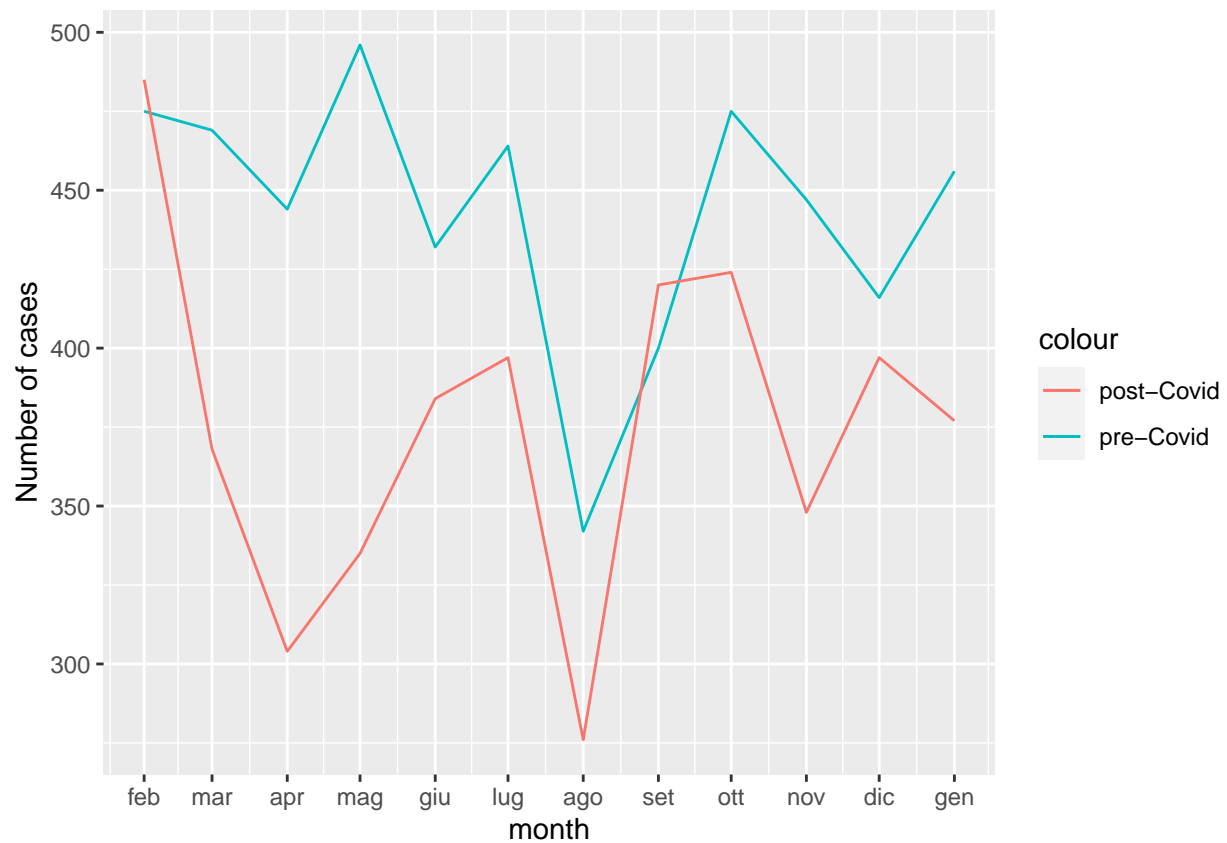
```
#### Vertical Dataframe
df_v = as.data.frame(matrix(data=c(df_h[,1],df_h[,2],rep(0,12),rep(1,12)),
                             nrow = 24,ncol = 2, byrow =F))

colnames(df_v) =c("count","covid")
df_v$covid = as.factor(df_v$covid)
```

from horizontal to vertical monthly dataframe

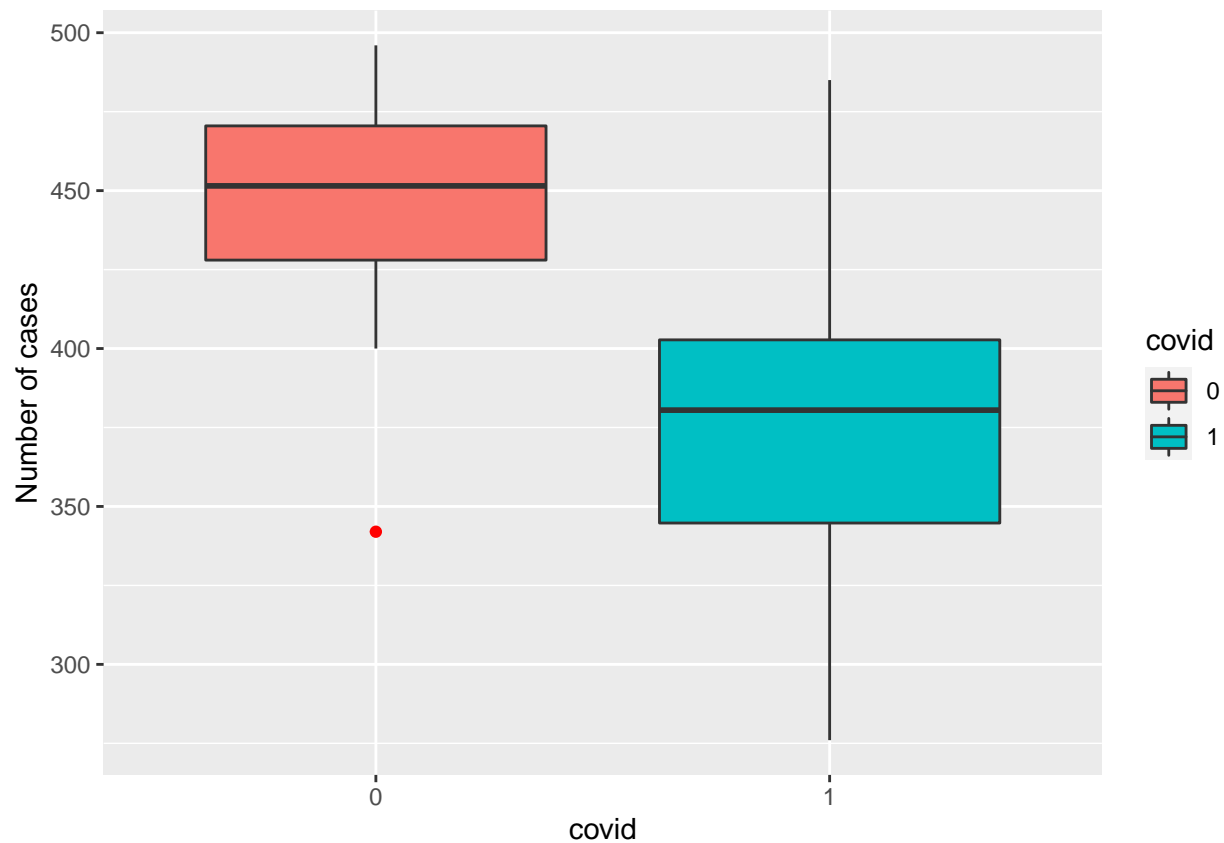
Plot of comparison of the two years of observations

```
time_mesi=seq(as.Date("2019-2-1"), as.Date("2020-1-1"), by = "months")
ggplot(df_h, aes(time_mesi)) +
  geom_line(aes(y = before, colour = "pre-Covid")) +
  geom_line(aes(y = after, colour = "post-Covid")) +
  xlab("month") +
  ylab("Number of cases") +
  scale_x_date(breaks = '1 month',
               date_labels = "%b") +
  theme(plot.title = element_text(size = 11))
```



Boxplot of the two periods

```
ggplot(df_v, aes(x=covid,y=count,fill=covid)) + # boxplot dei 12 mesi pre covid - ROSSO
  geom_boxplot(outlier.colour = "red",) +
  ylab("Number of cases") +
  theme(plot.title = element_text(size = 11))
```



Noticeable difference in mean, the outlier that is seen in the boxplot for 2019/20 corresponds to the observation of August

Total case in the two periods

```
sum(df_h$before)
```

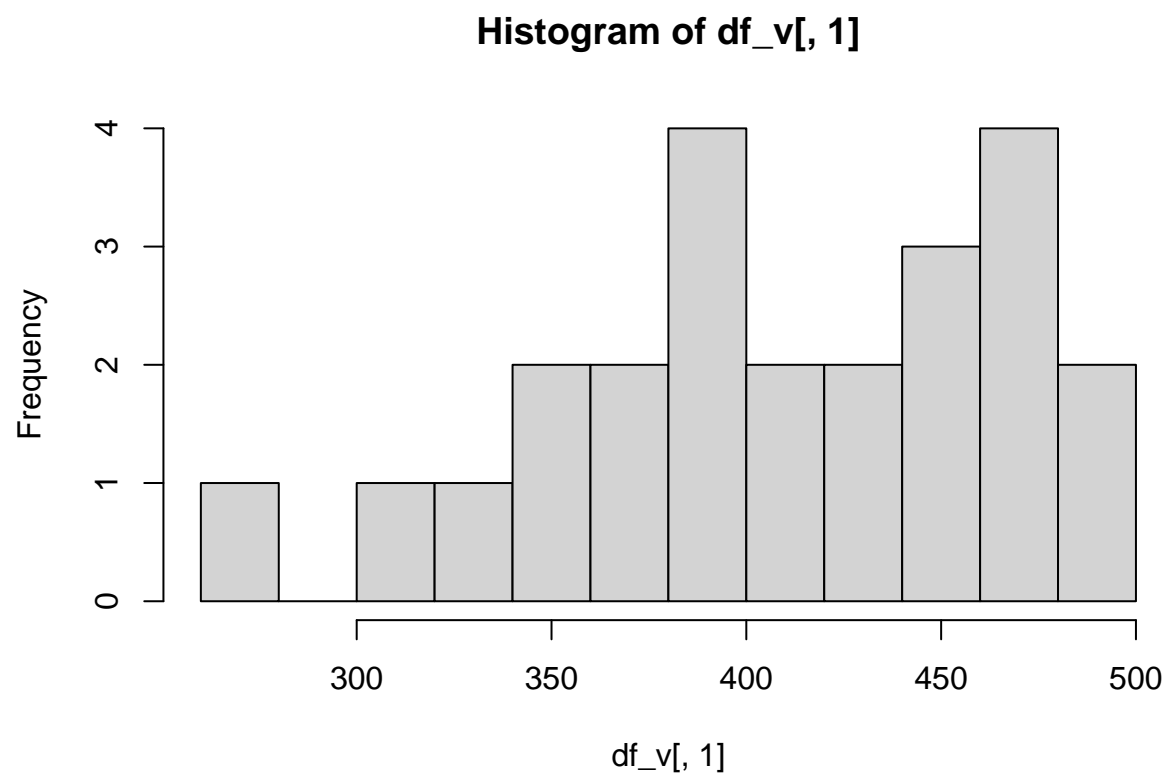
```
## [1] 5316
```

```
sum(df_h$after)
```

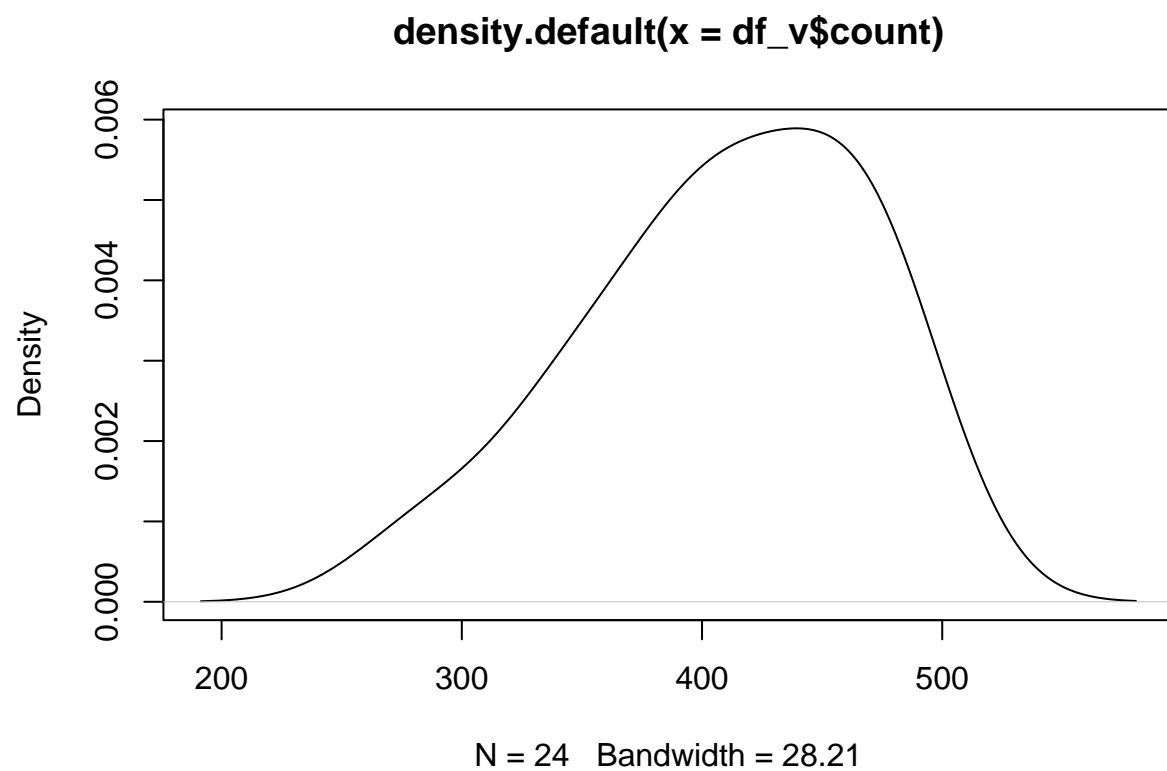
```
## [1] 4515
```

Data distribution analysis

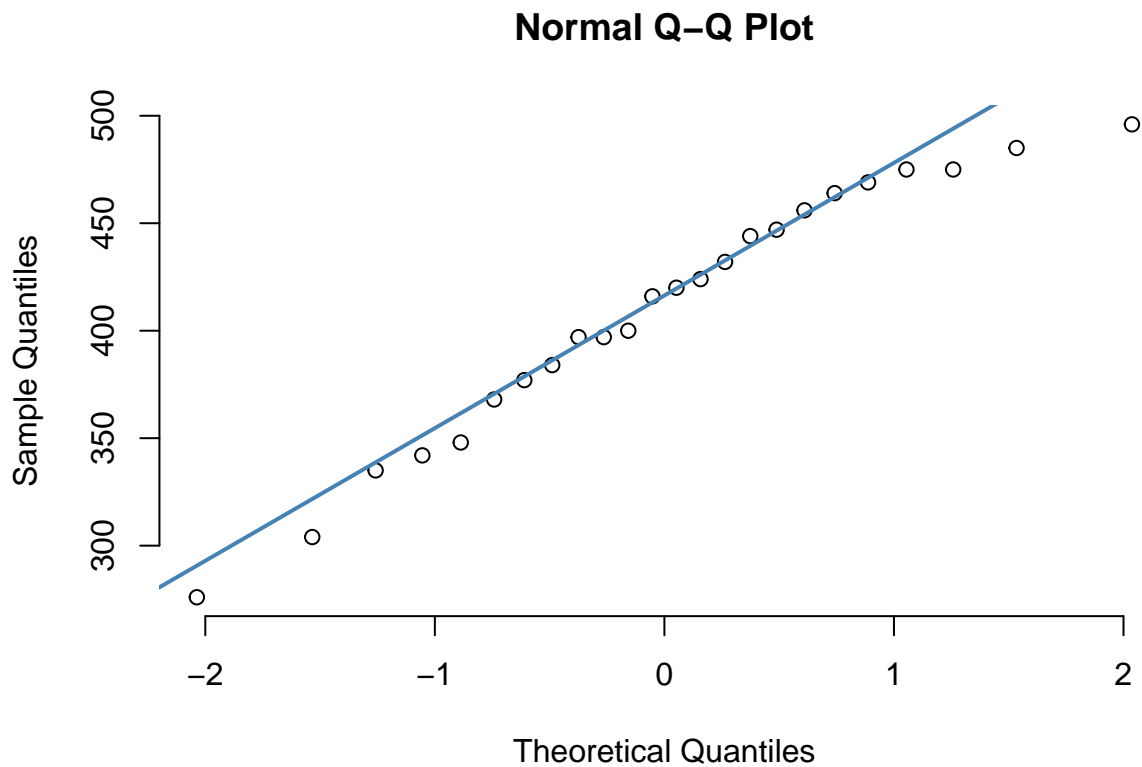
```
hist(df_v[,1],breaks = 8)
```



```
# Kernel Density Plot  
d <- density(df_v$count) # returns the density data  
plot(d) # plots the results
```



```
qqnorm(df_v$count, pch = 1, frame = FALSE)  
qqline(df_v$count, col = "steelblue", lwd = 2)
```



```
# qqplot(df_1920v$conteggio)
shapiro.test(df_v$count)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df_v$count
## W = 0.95976, p-value = 0.4335
shapiro.test(df_h$before)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df_h$before
## W = 0.90154, p-value = 0.1661
shapiro.test(df_h$after)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df_h$after
## W = 0.98335, p-value = 0.9937
```

```
# Test for equal variance in both the sample
```

```
bartlett.test(df_v$count~df_v$covid)
```

```
##
## Bartlett test of homogeneity of variances
##
## data: df_v$count by df_v$covid
## Bartlett's K-squared = 0.93756, df = 1, p-value = 0.3329
```

There is empirical evidence about violation of normality, the nature of the data, the dimension of the sample and the previous graphics analytics suggest to consider a distribution for positive counting data like Poisson or Negative Binomial.

In our case Poisson can't be used because the variance is much bigger compared to the mean of the distribution. (violation of one of the assumption for the Poisson distribution)

Checking mean and variance difference

```
mean(df_h$before)
```

```
## [1] 443
```

```
mean(df_h$after)
```

```
## [1] 376.25
```

```
var(df_h$before)
```

```
## [1] 1732.727
```

```
var(df_h$after)
```

```
## [1] 3161.841
```

Dummy variables

Dummy variables for model the strong seasonality of august

```
# dummy
dm=make.dummy(length(df_v[,1]),start=2, freq=12)
# dm[1:6,]
# give names to the dummies
nomi=c("dm4","dm5","dm6","dm7","dm8","dm9","dm10","dm11","dm12","dm1","dm2","dm3")
dimnames(dm)=list(NULL,nomi)
colnames(dm)<-nomi
```

Test for difference between periods

Linear model with normal assumption, t-test and Wilconox-Mann test

```
# 12 month
# Linear model
summary(lm(df_v$count~df_v$covid+dm[,8]))
```

```
##
## Call:
## lm(formula = df_v$count ~ df_v$covid + dm[, 8])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -81.40 -18.09   0.00  18.35  99.60
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)    452.15      11.48  39.397 < 2e-16 ***
## df_v$covid1   -66.75      15.87  -4.205 0.000398 ***
## dm[, 8]       -109.77     28.72  -3.823 0.000992 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 38.88 on 21 degrees of freedom
## Multiple R-squared:  0.606, Adjusted R-squared:  0.5684
## F-statistic: 16.15 on 2 and 21 DF,  p-value: 5.663e-05

# T test:
t.test(df_v$count~df_v$covid, var.equal =T)

##
## Two Sample t-test
##
## data:  df_v$count by df_v$covid
## t = 3.3051, df = 22, p-value = 0.003223
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  24.86594 108.63406
## sample estimates:
## mean in group 0 mean in group 1
##      443.00      376.25

# Wilcoxon-Mann-Whitney test:
wilcox.test(df_v$count~df_v$covid)

## Warning in wilcox.test.default(x = c(475, 469, 444, 496, 432, 464, 342, : cannot
## compute exact p-value with ties
##
## Wilcoxon rank sum test with continuity correction
##
## data:  df_v$count by df_v$covid
## W = 121, p-value = 0.005089
## alternative hypothesis: true location shift is not equal to 0

The diminution of response correlated with Covid months is highly significant (p-value < 0.001) in all above
test.

Test with negative binomial regression model for overdispersed counting data

# 12 month
bn_covid = glm.nb(df_v$count~df_v$covid+dm[,8]) # negative binomial regression model
summary(bn_covid)

##
## Call:
## glm.nb(formula = df_v$count ~ df_v$covid + dm[, 8], init.theta = 173.8636152,
## link = log)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.44331  -0.48980   0.02804   0.42578   2.67190
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
```



```
## (Intercept)  6.11611    0.02639 231.716 < 2e-16 ***
## df_v$covid1 -0.16404    0.03701  -4.432 9.35e-06 ***
## dm[, 8]      -0.30542    0.06981  -4.375 1.21e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(173.8636) family taken to be 1)
##
##      Null deviance: 62.314  on 23  degrees of freedom
## Residual deviance: 24.176  on 21  degrees of freedom
## AIC: 249.35
##
## Number of Fisher Scoring iterations: 1
##
##
##              Theta: 173.9
##             Std. Err.: 72.2
##
## 2 x log-likelihood: -241.352
```

Same conclusion, the coefficient Covid is highly significant (p-value < 0.0001), the months during the Covid pandemic shows a significant diminution of the diagnosed tumours.

Interpretation of the model parameter Covid

```
# percentage difference after covid can be calculated with
perce= (1-exp(-0.16404))*100
```

15.129% is the percentage difference between the two periods correlated with the change of period between pre and post Covid periods.

Confidence interval for the model parameter Covid

Profile Confidence interval and diminution in percentage correlated with the pandemic period

```
# "profile" confidence interval with 95% confidence for the Covid parameter
bn_CI = c( (1-exp(confint(bn_covid)[2,1]))*100 , (1-exp(confint(bn_covid)[2,2]))*100); bn_CI
```

```
## Waiting for profiling to be done...
## Waiting for profiling to be done...
## [1] 21.068872  8.743037
```

The months during the Covid pandemic shows a significant diminution of the diagnosed tumours between 8.74% and 21.06% with a confidence of 95%

Both models confirm the mean difference between the two sample. Same conclusion.

Check for correct assumption of Negative binomial model instead of Poisson model.

```
# comparison between poisson and negative binomial regression with log-likelihood, possible because Neg
poi_covid <- glm(df_v$count ~ df_v$covid, family = "poisson")
pchisq(2 * (logLik(bn_covid) - logLik(poi_covid)), df = 1, lower.tail = FALSE)
```

```
## 'log Lik.' 3.066798e-20 (df=4)
```

the p-value ≈ 0 confirm the correct assumption of negative binomial instead of Poisson. (presence of overdispersion in the data)

Estimation of lost cases nationally

Assuming a percentage decrease due to the Covid equal among all health structures equal to that observed in ours, using the national incidence to estimate the total cases from which to calculate the decrease of 15,13% in the months during the Covid period, recorded in Modena. This is a very strong assumption and the estimated case data must be taken with caution, but it could correspond to reality.

```
NUMBER_CANCERS_ITALY_2020_F = 181857
NUMBER_CANCERS_ITALY_2020_M = 194754
total_c=NUMBER_CANCERS_ITALY_2020_F+NUMBER_CANCERS_ITALY_2020_M

lost_cases = (total_c/100*perce);lost_cases
```

```
## [1] 56978.2
```

```
# confidence interval prediction
c( (total_c/100*bn_CI[1]), (total_c/100*bn_CI[2]))
```

```
## [1] 79347.69 32927.24
```

Estimated lost cases: 56978

From 32927 to 79347 lost cases with a “profile” confidence interval.