Explaining the differences between ICU's by using APACHEII

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ABSTRACT

Introduction: *When comparing ICU departments, one can find large differences in mortality ratios. The question is if this difference can be explained by the fact that these ICUs have different patient populations.*
Methods: *We used linear regression and linear mixed effects modeling to analyze mortality differences between various ICUs*
Results: *There is a significant difference between models that do not incorporate the medical situation of the patients and models that do take the medical status of the patient into account*
Conclusion: *The severity of patients' medical conditions can be used to explain the differences in mortality between various ICUs.*
Discussion: *It has not been researched if the data can be described using non-linear techniques.*

Introduction

Many Dutch hospitals supply information about their Intensive Care Unit (ICU) patients to the National Intensive Care Evaluation (NICE) registry, maintained by the department of Medical Informatics of the University of Amsterdam. With these data it is possible to determine the number of patients that did not survive their stay at a given ICU. This information could be used to compare the quality of one ICU to the others. However, as the number of non-survivors depends on more parameters than the quality of an ICU, it is necessary to correct for these parameters before quality between different ICUs can be compared. The APACHEII score, which indicates how severe a patient's general medical condition is, is one of these parameters.

We have investigated if the mortality differences between ICUs can be explained by a difference in APACHEII scores of their patients alone.

Methods

We used an aggregation of a sample of the NICE registration data. This dataset contained, per week, per ICU, the amount of patients admitted to the ICU, the amount of patients that died that week and a summation of all that ICU's patients APACHEII score.

We have used SPSS 14.0 and the R Program for Statistical Computing to analyze these data. The R commands used to obtain our results are listed in Appendix A. We used scatter plots, linear regression analysis, and linear regression analysis with mixed-effects to determine the best model to describe our data, and to see if the mortality rate is affected by the medical status of the patients of an ICU.

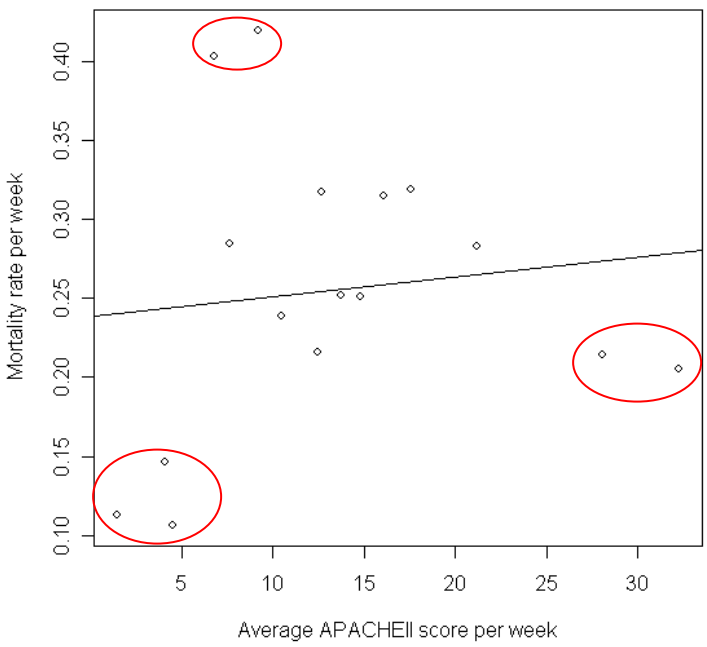
Results

The dataset contained information from 16 ICUs. Basic statistics about these ICUs is displayed in Table 1. This table contains, per ICU, the total number of weeks the ICU was monitored, the average number of patients present per week (Patients/Week), the average APACHEII score per week and the mortality rate per week (Mortality rate/Week). A scatter plot of the APACHEII/Week and Mortality rate/Week is displayed in Figure 1.

ICU	Weeks	Patients/Week	APACHEII/Week	Mortality rate/Week
1	44	21	6.8	0.40

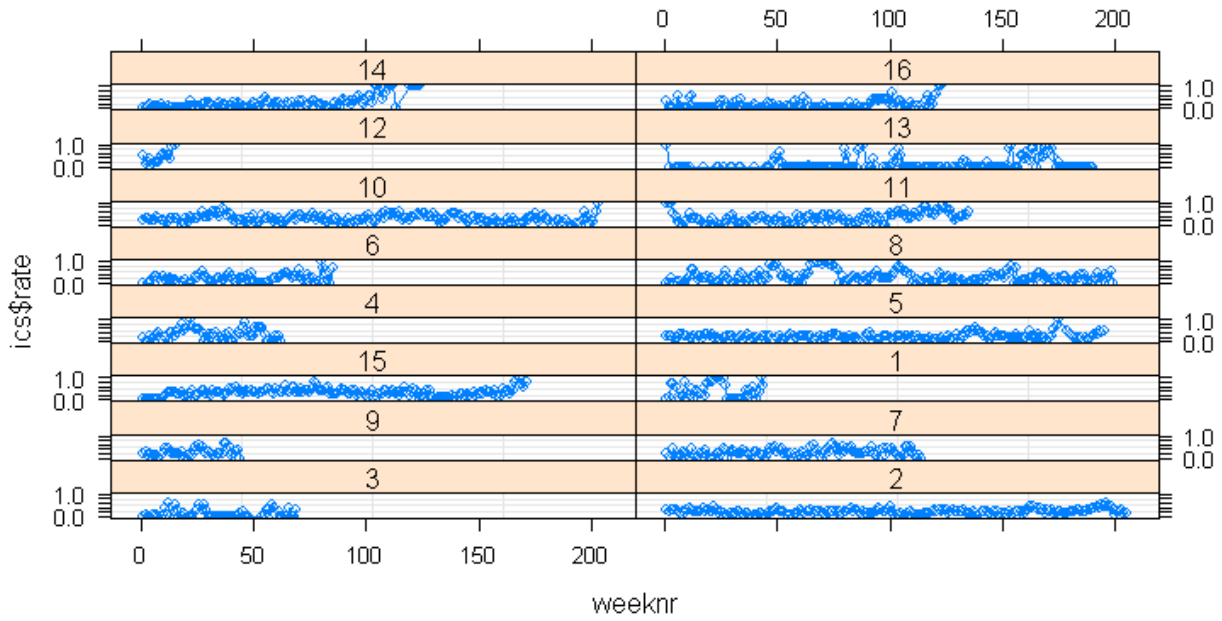
2	205	92	32.3	0.20
3	69	16	4.5	0.10
4	62	29	12.7	0.32
5	195	89	28.1	0.21
6	85	37	12.5	0.22
7	114	34	10.5	0.24
8	199	33	7.6	0.28
9	44	33	13.7	0.25
10	203	46	21.2	0.28
11	135	41	16.1	0.31
12	15	34	9.2	0.42
13	190	7	1.5	0.11
14	124	43	14.8	0.25
15	171	43	17.6	0.32
16	123	14	4.1	0.15

Table 1 – Basic statistics and mortality rate per week



Scatter plotting the average APACHEII score per week against the mortality rate per week shows that these two parameters are not very strongly related. The three marked groups with outliers are interesting in that the group near the origin and the group around point (8, 0.4) deal with the lowest number of patients per week, and the group around point (30, 0.2) deals with the highest number of patients. The group nearest to the origin with very low APACHEII scores contains ICUs with very few patients per week which were included in the registration for the shortest amount of time: these ICUs could be considered anomalies and not representative for the average ICU.

A graphical display of the mortality over time shows that mortality greatly varies with time, and that mortality changes more rapidly in some ICUs than in others. It also clearly shows that some ICUs were included in the registry for a much longer time than others.



Grouping the data on hospital, and performing a linear regression analysis (see appendix A) yields a loglikelihood of 235.8 and an AIC value of –467.6. Using a linear mixed-effects (LME) regression analysis with the hospital ID as random effect yields a loglikelihood of 305.1 and an AIC value of –604.2 with a p-value of 0. When this LME-model is extended with an autoregressive error covariance structure the loglikelihood and AIC value change to 840.5 and –1673.1 respectively, also with a p-value of 0. When the regression model is made dependent on the severity of the average patient in a hospital (through the sum of each patient's APACHEII score per individual (weekly) measurement per hospital) the loglikelihood and AIC value change slightly to 845.0 and –1679.9 with a p-value of 0.0028.

The same mixed-effects analysis with the sum of the APACHEII scores, but now with a Poisson distribution instead of a normal distribution changes the loglikelihood and AIC value to –103.0 and 212.0 respectively, with a p-value of $6.25*10^{-13}$.

Conclusion

From the groups of outliers in the scatter plot (at least the group with very low APACHEII scores and high mortality, and the group with very high APACHEII scores and low mortality) it could be concluded that ICUs with few patients have higher mortality than ICUs with a high throughput of patients. This seems logical in that it has been proven that for example a particular surgical treatment has higher success rates in institutions where that treatment is performed more often than in other institutions. This however is not the main conclusion of our research, and has not been scientifically proven.

What can be concluded from our research is that the straight linear model used to describe our data was not very good when compared to the other three models. The models improve significantly when linear mixed effects modeling is used, and the model which also takes into account the difference between the various ICUs best describes our data. It appears that the difference in mortality between the various ICUs can be attributed to the differences in their patients' medical situations.

The model best describing our data, however, appears to be the model in which the Poisson distribution is used instead of a normal distribution. This model produces a positive AIC which when combined with the AICs of the other models produces the largest ΔAIC, favoring the Poisson model over the other three normally distributed models. Also, the Poisson based model has a much smaller p-value than the normal distribution based model (6.25×10^{-13} and 0.0028) indicating this model better describes our data.

Discussion

We have used linear regression techniques to analyze our data. We did not research if perhaps our data would be better described by non-linear techniques. Also, the status of the three ICUs that lie closely to the origin of the scatter plot of the APACHEII scores versus the mortality rate is not known. These three ICUs appear not to resemble any of the other 13 ICUs, and it could be questioned whether these should be used in this research.

Appendix A – R Commands

In blue the output of R, in dark-blue the input in R

 # 1. Obtaining basic statistics for Table 1 – Basic Statistics and mortality per week per hospital

```
ics = read.csv("ics.csv")

nmetingen = seq(1:16)
for(i in 1:16) {
   nmetingen[i] = max(ics$weeknr[ics$ziekhno==i])
}
```

 # Obtain basic mortality, per hospital, per week

```
ics$rate = mortality_rate_per_week = ics$died / ics$present
mort_rate_week = seq(1:16)
for(i in 1:16) {
   mort_rate_week[i] = sum(ics$rate[ics$ziekhno==i]) / nmetingen[i]
}
mort_rate_week
 [1] 0.4026321 0.2055967 0.1060259 0.3169098 0.2141207 0.2154688 0.2389692
 [8] 0.2842458 0.2518236 0.2831030 0.3149606 0.4195732 0.1126138 0.2505721
[15] 0.3189553 0.1465255
```

 # Obtaining average APACHEII score per week per hospital

```
apacheII_week = seq(1:16)
for(i in 1:16) {
   apacheII_week[i] = sum(ics$sumapache[ics$ziekhno==i]) / nmetingen[i]
}
apacheII_week
 [1]  6.776364 32.268293  4.515362 12.701935 28.093846 12.493412 10.494561
 [8]  7.615729 13.737273 21.219310 16.071704  9.242000  1.458526 14.832581
[15] 17.589532  4.095610
```

 # Obtaining the scatter plot and linear regression for APACHEII/Week and Mortality rate/Week

```
model = lm(mort_rate_week ~ apacheII_week)
plot(apacheII_week, mort_rate_week, xlab="Average APACHEII score per week",
ylab="Mortality rate per week")
abline(model)
```

 # 2. Obtaining the plot with mortality per week, per hospital.

```
icsx <- groupedData(rate~weeknr|ziekhno,data=ics)
plot(icsx)
```

 # 3. Obtaining linear mixed-effects regression model, calculating loglikelihood and aic

```
rate = ics$died_icu/ics$present

h0=lm(rate~1,data=icsx)
h0

Coefficients:
(Intercept)
     0.2455

summary(h0)

Call:
lm(formula = rate ~ 1, data = icsx)

Residuals:
```

```
     Min       1Q   Median       3Q      Max
-0.24551 -0.15676 -0.03122  0.10449  0.75449

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.245510   0.004879   50.32   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2142 on 1926 degrees of freedom
```

```
logl0 = sum(-0.5 * log(2*pi*0.2142^2) - 0.5 * (icsx$rate-0.24551)^2/0.2142^2)
logl0
235.7960
aic0 = -2*logl0+2*2
aic0
-467.5919
```

 # 4. Obtaining a linear mixed effects regression analysis, loglikelihood and aic

```
h1=lme(rate~1,random=~1,data=icsx,method="ML")
summary(h1)

Linear mixed-effects model fit by maximum likelihood
 Data: icsx
       AIC       BIC   logLik
  -604.1745 -587.4833 305.0872

Random effects:
 Formula: ~1 | ziekhno
        (Intercept)  Residual
StdDev:   0.0755549 0.2042361

Fixed effects: mortality ~ 1
                Value  Std.Error   DF  t-value p-value
(Intercept) 0.2549255 0.01974755 1911 12.90922       0

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.8684070 -0.7060122 -0.1763444  0.4094116  4.1902827

Number of Observations: 1927
Number of Groups: 16

logl1 = h1$logLik
logl1
305.0872
aic1 = -2*logl1+2*3
aic1
-604.1745
```

 # 5. Obtaining LME-model on hospital ID, with autoregressive error covariance

```
h2=lme(rate~1,random=~1,data=icsx,method="ML",corr=corAR1())
summary(h2)

Linear mixed-effects model fit by maximum likelihood
 Data: icsx
       AIC       BIC   logLik
  -1673.086 -1650.832 840.5432

Random effects:
 Formula: ~1 | ziekhno
```

```
        (Intercept)  Residual
StdDev:  0.05058885 0.2123324

Correlation Structure: AR(1)
 Formula: ~1 | ziekhno
 Parameter estimate(s):
      Phi
0.6809078
Fixed effects: rate ~ 1
               Value Std.Error   DF  t-value p-value
(Intercept) 0.2524962 0.0173312 1911 14.56888       0

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.4212155 -0.7838348 -0.1736120  0.3981098  3.8286681

Number of Observations: 1927
Number of Groups: 16

logl2 = h2$logLik
logl2
840.5432
aic2 = -2*logl2+2*4
aic2
-1673.086
```

 # 6. Obtaining LME-model on hospital ID, with autoregressive error covariance extended with sumapache

```
h3=lme(rate~sumapache,random=~1,data=icsx,method="ML",corr=corAR1())
summary(h3)

Linear mixed-effects model fit by maximum likelihood
 Data: icsx
       AIC       BIC   logLik
  -1679.947 -1652.128 844.9733

Random effects:
 Formula: ~1 | ziekhno
        (Intercept)  Residual
StdDev:  0.04975266 0.2134771

Correlation Structure: AR(1)
 Formula: ~1 | ziekhno
 Parameter estimate(s):
     Phi
0.686821
Fixed effects: rate ~ sumapache
                Value   Std.Error   DF   t-value p-value
(Intercept) 0.22179149 0.020094623 1910 11.037355  0.0000
sumapache   0.00216623 0.000723007 1910  2.996141  0.0028
 Correlation:
          (Intr)
sumapache -0.51

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.4985221 -0.7889778 -0.2082469  0.3827400  3.8634025

Number of Observations: 1927
Number of Groups: 16

logl3 = h3$logLik
```

```
logl3
844.9733
aic3 = -2*logl3+2*5
aic3
-1679.947
```

 # The last three comparisons could be done with a (simple) ANOVA

```
anova(h1,h2,h3)

Model df        AIC        BIC   logLik   Test   L.Ratio p-value
h1     1  3  -604.1745  -587.4833 305.0872
h2     2  4 -1673.0865 -1650.8316 840.5432 1 vs 2 1070.9120  <.0001
h3     3  5 -1679.9466 -1652.1280 844.9733 2 vs 3    8.8601  0.0029
```

 # Enthussiasts: Poisson-distributed LMER analysis with the APACHEII scores as fixed effect

```
## package lme4 required
## (1|died_icu) is the random effect
## rate~sumapache is the fixed effect
## we use the ML (maximum likelihood)
pois <- lmer(rate~sumapache + (1|died_icu), family = "poisson", data = icsx,
method="ML", corr=corAR1())
summary(pois)

Generalized linear mixed model fit using Laplace
Formula: rate ~ sumapache + (1 | died_icu)
   Data: icsx
 Family: poisson(log link)
 AIC   BIC logLik deviance
 212 228.7   -103      206
Random effects:
 Groups   Name        Variance Std.Dev.
 died_icu (Intercept) 0.64781  0.80486
number of obs: 1927, groups: died_icu, 48

Estimated scale (compare to  1 )  0.270105

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.446918   0.173790  -2.572   0.0101 *
sumapache   -0.039236   0.005453  -7.195 6.25e-13 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
          (Intr)
sumapache -0.596
```