Introduction to analysis of aggregate data in the packageapc

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Contents

1 Introduction

The purpose of this vignette is give an introduction the age-period-cohort analysis of tables of aggregate data using R package `apc`.

The apc package uses the canonical parameters suggested by Kuang, Nielsen and Nielsen (2008a) and generalized by Nielsen (2014). These evolve around the second differences of age, period and cohort factors as well as an three parameters (level and two slopes) for a linear plane. The age, period and cohort factors themselves are not identifiable. They could be ad hoc identified by associating the levels and two slopes to the age, period and cohort factors in a particular way. This should be done with great care as such ad hoc identification easily masks which information is coming from the data and which information is coming from the choice of ad hoc identification scheme. An illustration is given below. A short description of the package can be found in Nielsen (2015).

2 Analysis of Belgian lung cancer data

The very first step is to call the package.

```
> library(apc)
```

The data

The data set is taken from table VIII of Clayton and Schifflers (1987a), which contains age-specific incidence rates (per 100,000 person-years observation) of lung cancer in Belgian females during the period 1955-1978. Numerators are also available. The original source was the WHO mortality database.

The package uses a special data format for aggregate data, where the data is kept in a matrix format. This data format also keeps track of the labels of the different time scales. This comes in handy when listing parameters, when plotting and when seeking to truncate the data. The package does not use the vectorized format in the traditional data.frame in R.

The Belgian data are already in the apc.data.list format. Other data can be organized using the apc.data.list function.

```
> data.list   <- data.Belgian.lung.cancer()
> objects(data.list)

 [1] "age1"        "coh1"        "data.format" "dose"        "label"
 [6] "n.decimal"   "per.max"     "per.zero"    "per1"        "response"
[11] "time.adjust" "unit"

> data.list

$response
      1955-1959 1960-1964 1965-1969 1970-1974
```

```
25-29          3          2          7          3
30-34         11         16         11         10
35-39         11         22         24         25
40-44         36         44         42         53
45-49         77         74         68         99
50-54        106        131         99        142
55-59        157        184        189        180
60-64        193        232        262        249
65-69        219        267        323        325
70-74        223        250        308        412
75-79        198        214        253        338

$dose
      1955-1959 1960-1964 1965-1969 1970-1974
25-29 15.789474 15.384615 14.000000 15.789474
30-34 16.666667 16.326531 15.277778 14.084507
35-39 14.102564 16.666667 16.326531 15.243902
40-44 13.483146 13.924051 16.600791 15.680473
45-49 15.909091 13.214286 13.793103 16.363636
50-54 16.060606 15.411765 12.941176 13.408876
55-59 15.154440 15.333333 14.905363 12.552301
60-64 13.075881 14.172266 14.555556 14.147727
65-69 10.667316 11.814159 12.971888 13.357994
70-74  8.498476  9.025271 10.108303 11.153221
75-79  5.915745  6.367153  6.880609  7.736324

$data.format
[1] "AP"

$age1
[1] 25

$per1
[1] 1955

$coh1
[1] 5

$unit
[1] 5

$per.zero
NULL

$per.max
```

```
NULL

$time.adjust
[1] 0

$label
NULL

$n.decimal
NULL
```

Plot the data

The data analysis can be initiated by plotting the data. The package has a number of plots. All plot formats can be called with a single command. Some of plots involve grouping of data. A warning is produced because the defaults settings lead to an unbalanced grouping of data.

```
> apc.plot.data.all(data.list)

[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
```

Alternatively, the plots can be called individually. The first plot contains data sums.

```
> graphics.off()
> apc.plot.data.sums(data.list)
```

A sparsity plot shows where data are thin. In this case, the plots are blank with default settings. We therefore change sparsity.limits.

```
> graphics.off()
> apc.plot.data.sparsity(data.list)
> apc.plot.data.sparsity(data.list,sparsity.limits=c(5,10))
```

The next plots visualize data using different pairs of the three time scales. These plots are done for mortality ratios. All plots appear to have approximately parallel lines. This indicates that interpretation should be done carefully.

```
> graphics.off()
> apc.plot.data.within.all.six(data.list,"m")

[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
[1] "apc.plot.data.within warning: maximal index not divisible by thin, so last group
```

Get a deviance table

A deviance table is constructed. For this, we need to formulated the distribution of the model. The table show that the sub-models "AC" and "Ad" cannot be rejected relative to the unrestricted "APC" model

```
> apc.fit.table(data.list,"poisson.dose.response")
```

```
    deviance df.residual prob(>chi_sq) LR vs.APC df vs.APC prob(>chi_sq)
APC   20.225          18          0.320       NaN       NaN           NaN
AP    25.558          30          0.697     5.333        12         0.946
AC    21.454          20          0.371     1.229         2         0.541
PC    99.228          27          0.000    79.004         9         0.000
Ad    26.584          32          0.737     6.359        14         0.957
Pd   253.562          39          0.000   233.337        21         0.000
Cd   100.712          29          0.000    80.487        11         0.000
A     85.577          33          0.000    65.352        15         0.000
P   6390.146          40          0.000  6369.921        22         0.000
C   1217.030          30          0.000  1196.805        12         0.000
t    254.518          41          0.000   234.293        23         0.000
tA   308.135          42          0.000   287.910        24         0.000
tP  6390.708          42          0.000  6370.483        24         0.000
tC  1612.070          42          0.000  1591.845        24         0.000
1   6499.777          43          0.000  6479.552        25         0.000
         aic
APC  341.397
AP   322.730
AC   338.625
PC   402.400
Ad   319.756
Pd   532.733
Cd   399.884
A    376.749
P   6667.318
C   1514.202
t    529.690
tA   581.307
tP  6663.879
tC  1885.241
1   6770.948
```

Estimate selected models

We consider the "APC" and "Ad" model. We also consider also the sub-model "A", which is not supported by the tests in the deviance table. We get the three fits

```
> fit.apc <- apc.fit.model(data.list,"poisson.dose.response","APC")
> fit.ad  <- apc.fit.model(data.list,"poisson.dose.response","Ad")
> fit.a   <- apc.fit.model(data.list,"poisson.dose.response","A")
```

The coefficients for canonical parameters are found through

```
> fit.apc$coefficients.canonical
```

```
                  Estimate Std. Error     z value      Pr(>|z|)
level          1.957545765 0.06587835 29.71455339 4.980891e-194
age slope      0.504384208 0.07522008  6.70544587  2.007923e-11
cohort slope   0.120878598 0.06799397  1.77778399  7.543934e-02
DD_age_35     -0.497116645 0.42748123 -1.16289700  2.448713e-01
DD_age_40      0.253907149 0.28839948  0.88040084  3.786422e-01
DD_age_45     -0.155115204 0.20515233 -0.75609770  4.495906e-01
DD_age_50     -0.205504949 0.15042595 -1.36615360  1.718908e-01
DD_age_55     -0.043344184 0.11872510 -0.36508022  7.150515e-01
DD_age_60     -0.092603145 0.09711954 -0.95349653  3.403386e-01
DD_age_65      0.023605714 0.08354890  0.28253770  7.775312e-01
DD_age_70     -0.046471233 0.07644644 -0.60789267  5.432587e-01
DD_age_75     -0.077331927 0.07619553 -1.01491426  3.101467e-01
DD_period_1965 -0.065187056 0.06656344 -0.97932225  3.274208e-01
DD_period_1970  0.064058271 0.06211963  1.03120825  3.024432e-01
DD_cohort_1890  0.089055820 0.12918107  0.68938756  4.905794e-01
DD_cohort_1895  0.022794960 0.09524872  0.23932039  8.108572e-01
DD_cohort_1900 -0.009887705 0.07806299 -0.12666316  8.992070e-01
DD_cohort_1905 -0.087602585 0.07716974 -1.13519348  2.562943e-01
DD_cohort_1910  0.070174649 0.08627345  0.81339796  4.159899e-01
DD_cohort_1915  0.005654086 0.10239118  0.05522044  9.559628e-01
DD_cohort_1920  0.015051099 0.12850964  0.11712039  9.067647e-01
DD_cohort_1925 -0.093529779 0.15857808 -0.58980270  5.553229e-01
DD_cohort_1930  0.191506367 0.20187869  0.94862102  3.428134e-01
DD_cohort_1935 -0.214529781 0.28443477 -0.75423192  4.507100e-01
DD_cohort_1940  0.160455202 0.43666159  0.36745894  7.132767e-01
DD_cohort_1945 -0.609263039 0.81479117 -0.74775361  4.546088e-01
```

```
> fit.ad$coefficients.canonical
```

```
                Estimate Std. Error    z value     Pr(>|z|)
level         1.98218357 0.04901861 40.4373684 0.000000e+00
age slope     0.48079205 0.06025798  7.9788936 1.476508e-15
cohort slope  0.08871334 0.01158119  7.6601263 1.857504e-14
DD_age_35    -0.61853253 0.40273616 -1.5358257 1.245811e-01
DD_age_40     0.26923140 0.27445998  0.9809496 3.266176e-01
DD_age_45    -0.18763742 0.19544414 -0.9600565 3.370268e-01
DD_age_50    -0.16690515 0.14277769 -1.1689862 2.424092e-01
```

```
DD_age_55    -0.05010697 0.11368129 -0.4407671 6.593816e-01
DD_age_60    -0.08993029 0.09378346 -0.9589141 3.376020e-01
DD_age_65     0.02072825 0.08101869  0.2558452 7.980703e-01
DD_age_70    -0.04428379 0.07371656 -0.6007305 5.480195e-01
DD_age_75    -0.08566734 0.07233153 -1.1843706 2.362664e-01
```

Residual analysis

We get a number of plots to illustrate the fit. We plot estimators, probability transforms of responses given fit, residuals, fitted values, linear predictors, and data.

In the probability transform plot: Black circle are used for central part of distribution. Triangles are used in tails, green/blue/red as responses are further in tail No sign of mis-specification for "APC" and "Ad": there are many black circles and only few coloured triangles. In comparison the model "A" yields more extreme observations. That model is not supported by the data. To get numerical values see apc.plot.fit.pt

```
> graphics.off()
> apc.plot.fit.all(fit.apc)

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted

> apc.plot.fit.all(fit.ad)

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted

> apc.plot.fit.all(fit.a)

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted
```

Plot estimated coefficients for sub models

We consider the "APC", "Ad" and "A" models and plot the estimated coefficients The first row of plots show double differences of parameters The second row of plots shows level and slope determining a linear plane The third row shows double sums of double differences, all identified to be zero at the begining and at the end. Thus the plots in third row must be interpreted jointly with those in the second row. The interpretation of the third row plots is that they show deviations from linear trends. The third row plots are not invariant to changes to data array.

For the "APC" and "Ad" the estimated coefficients are similar. For the "A" model the coefficients are different, reflecting the misspecification.

```
> graphics.off()
> apc.plot.fit(fit.apc)

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted

> apc.plot.fit(fit.ad)

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted

> apc.plot.fit(fit.a)

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted
```

Recursive analysis

Cut the first period group and redo analysis

```
> data.list.subset.1 <- apc.data.list.subset(data.list,0,0,1,0,0,0)

WARNING apc.data.list.subset: cuts in arguments are:
[1] 0 0 1 0 0 0
have been modified to:
[1] 0 0 1 0 1 0
WARNING apc.data.list.subset: coordinates changed to "AC" & data.format changed to "t

> apc.fit.table(data.list.subset.1,"poisson.dose.response")

    deviance df.residual prob(>chi_sq) LR vs.APC df vs.APC prob(>chi_sq)
APC   12.096           9         0.208       NaN       NaN           NaN
AP    20.876          20         0.404     8.780        11         0.642
AC    13.341          10         0.205     1.244         1         0.265
PC    45.500          18         0.000    33.404         9         0.000
Ad    21.847          21         0.408     9.750        12         0.638
Pd   200.976          29         0.000   188.879        20         0.000
Cd    47.171          19         0.000    35.075        10         0.000
A     45.822          22         0.002    33.725        13         0.001
P   5036.080          30         0.000  5023.983        21         0.000
C    516.272          20         0.000   504.175        11         0.000
t    201.864          30         0.000   189.767        21         0.000
tA   223.070          31         0.000   210.973        22         0.000
tP  5036.598          31         0.000  5024.502        22         0.000
tC   806.013          31         0.000   793.916        22         0.000
1   5081.113          32         0.000  5069.017        23         0.000
         aic
APC  264.065
AP   250.844
AC   263.309
PC   279.468
Ad   249.815
Pd   412.944
Cd   279.139
A    271.790
P   5246.048
C    746.240
t    411.832
tA   431.038
tP  5244.567
tC  1013.981
1   5287.081
```

Effect of ad hoc identification

At first a subset is chosen where youngest age and cohort groups are truncated. This way sparsity is eliminated and ad hoc identification effects are dominated by estimation uncertainty. Then consider Plot 1: parameters estimated from data without first age groups Plot 2: parameters estimated from all data Note that estimates for double difference very similar. Estimates for linear slopes are changed because the indices used for parametrising these are changed Estimates for detrended double sums of age and cohort double differences are changed, because they rely on a particular ad hoc identifications that have changed. Nonetheless these plots are useful to evaulate variation in time trends over and above linear trends.

```
> graphics.off()
> data.list   <- data.Belgian.lung.cancer()
> data.list.subset <- apc.data.list.subset(data.list,2,0,0,0,0,0)

WARNING apc.data.list.subset: cuts in arguments are:
[1] 2 0 0 0 0 0
have been modified to:
[1] 2 0 0 0 0 2
WARNING apc.data.list.subset: coordinates changed to "AC" & data.format changed to "t

> fit.apc     <- apc.fit.model(data.list,"poisson.dose.response","APC")
> fit.apc.subset  <- apc.fit.model(data.list.subset,"poisson.dose.response","APC")
> apc.plot.fit(fit.apc.subset,
+              main.outer="1. Belgian lung cancer: cut first two age groups")

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted

> apc.plot.fit(fit.apc,main.outer="2. Belgian lung cancer data: all data")

WARNING apc.plot.fit: sdv large for plot 5 - possibly not plotted
```

3 References

Clayton, D. and Schifflers, E. (1987a) Models for temperoral variation in cancer rates. I: age-period and age-cohort models. *Statistics in Medicine* 6, 449-467.

Kuang, D., Nielsen, B. and Nielsen, J.P. (2008a) Identification of the age-period-cohort model and the extended chain ladder model. *Biometrika* 95, 979-986. *Download*: Earlier version: http://www.nuffield.ox.ac.uk/economics/papers/2007/w5/KuangNielsenNielsen07.pdf.

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