

AIDS - Semiparametric Mixed Model

February 8, 2012

The "AIDS"-data from "catdata" are loaded.

```
> library(catdata)
> data(aids)
```

As for normal GAMs for GAMMs the package "mgcv" is used.

```
> library(mgcv)
```

The Semiparametric Mixed Model (or Generalized Additive Mixed Model) for "AIDS"-Data is fitted by the function "gamm". Here the only random effect is the random intercept.

```
> gammmaids<-gamm(cd4 ~ s(time) + drugs + partners + s(cesd) + s(age),
+                 random=list(person=~1), family=poisson(link=log), data=aids)
```

Maximum number of PQL iterations: 20

The summary of the fixed effects is printed.

```
> summary(gammmaids$gam)
```

Family: poisson
Link function: log

Formula:
cd4 ~ s(time) + drugs + partners + s(cesd) + s(age)

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.52514	0.02524	258.49	<2e-16 ***
drugs	0.03626	0.02318	1.56	0.12
partners	0.00297	0.00262	1.13	0.26

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

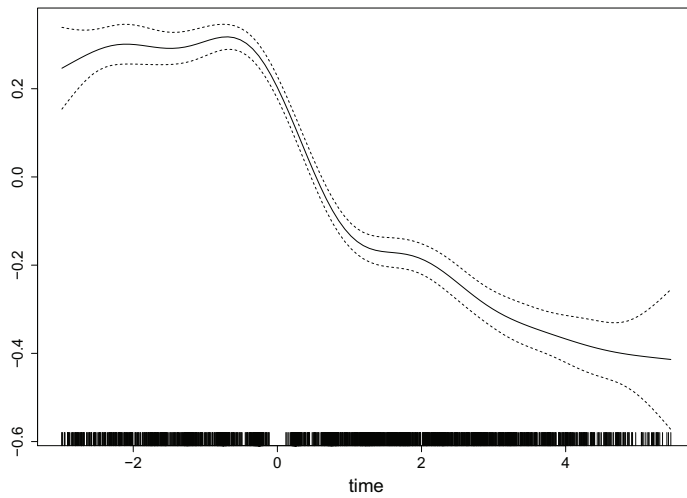
	edf	Ref.df	F	p-value
s(time)	7.79	7.79	119.10	<2e-16 ***
s(cesd)	1.00	1.00	9.57	0.002 **
s(age)	1.00	1.00	0.19	0.663

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

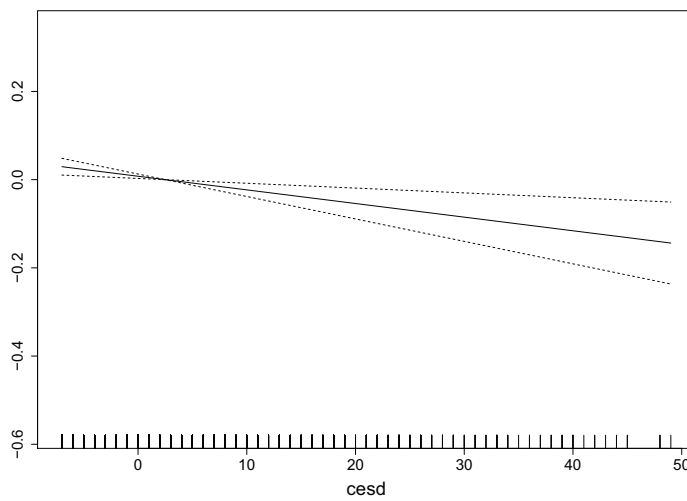
R-sq.(adj) = 0.212 Scale est. = 69.519 n = 2376

Finally the three smooth effects from the gam are plotted.

```
> plot(gammaids$gam,ylab=" ",cex.lab=1.8,cex.axis=1.5,select=1)
```



```
> plot(gammaids$gam,ylab=" ",cex.lab=1.8,cex.axis=1.5,select=2)
```



```
> plot(gammaids$gam,ylab=" ",cex.lab=1.8,cex.axis=1.5,select=3)
```

