

# AIDS - Semiparametric Mixed Model

February 5, 2020

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.

```
> gammaids<-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(gammaids$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)	6.525238	0.018212	358.29	< 2e-16 ***
drugs	0.010478	0.003066	3.42	0.00064 ***
partners	0.005987	0.000343	17.48	< 2e-16 ***

---

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

Approximate significance of smooth terms:

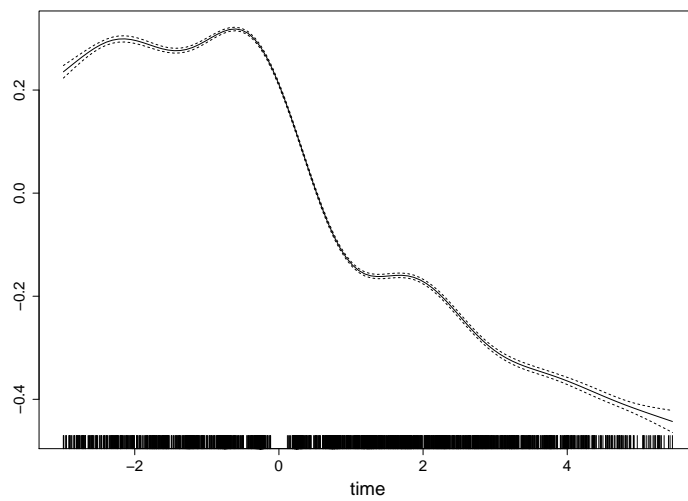
	edf	Ref.df	F	p-value
s(time)	8.98	8.98	6652.23	<2e-16 ***
s(cesd)	8.93	8.93	205.37	<2e-16 ***
s(age)	1.00	1.00	0.07	0.79

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

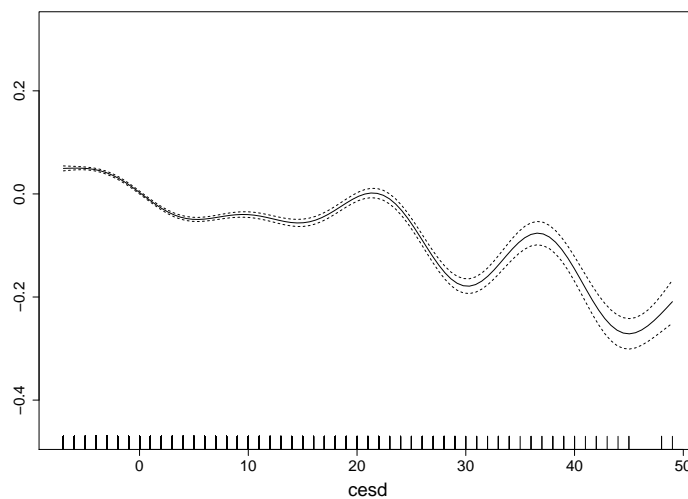
```
R-sq.(adj) =  0.203
Scale est. = 1          n = 2376
```

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)
```

