

Supplementary materials

Tables

Table S1: Parameters calculated in the parametric models and their significance

	Estimate	Std. Error	t value	Pr(> t)	
COVID vaccines					
<i>ZANBI</i>					
eta.mu	1.28446	0.01355	94.8	<2e-16	***
eta.sigma	-1.2099	0.06096	-19.85	<2e-16	***
eta.nu	-20.61	494.30	-0.042	0.967	
<i>ZAPIG</i>					
eta.mu	1.30337	0.01264	103.1	<2e-16	***
eta.sigma	-1.2733	0.06106	-20.85	<2e-16	***
eta.nu	-19.37	250.66	-0.077	0.938	
Other drugs					
<i>ZANBI</i>					
eta.mu	0.14781	0.04808	3.07408	0.00211	**
eta.sigma	0.56955	0.08895	6.40267	1.52e-10	***
eta.nu	-22.55	1482.91	-0.01521	0.987	
<i>ZAPIG</i>					
eta.mu	0.46367	0.02105	22.02865	<2e-16	***
eta.sigma	0.06889	0.05608	1.22856	0.21924	
eta.nu	-22.56	1048.58	-0.02151	0.983	

Figures

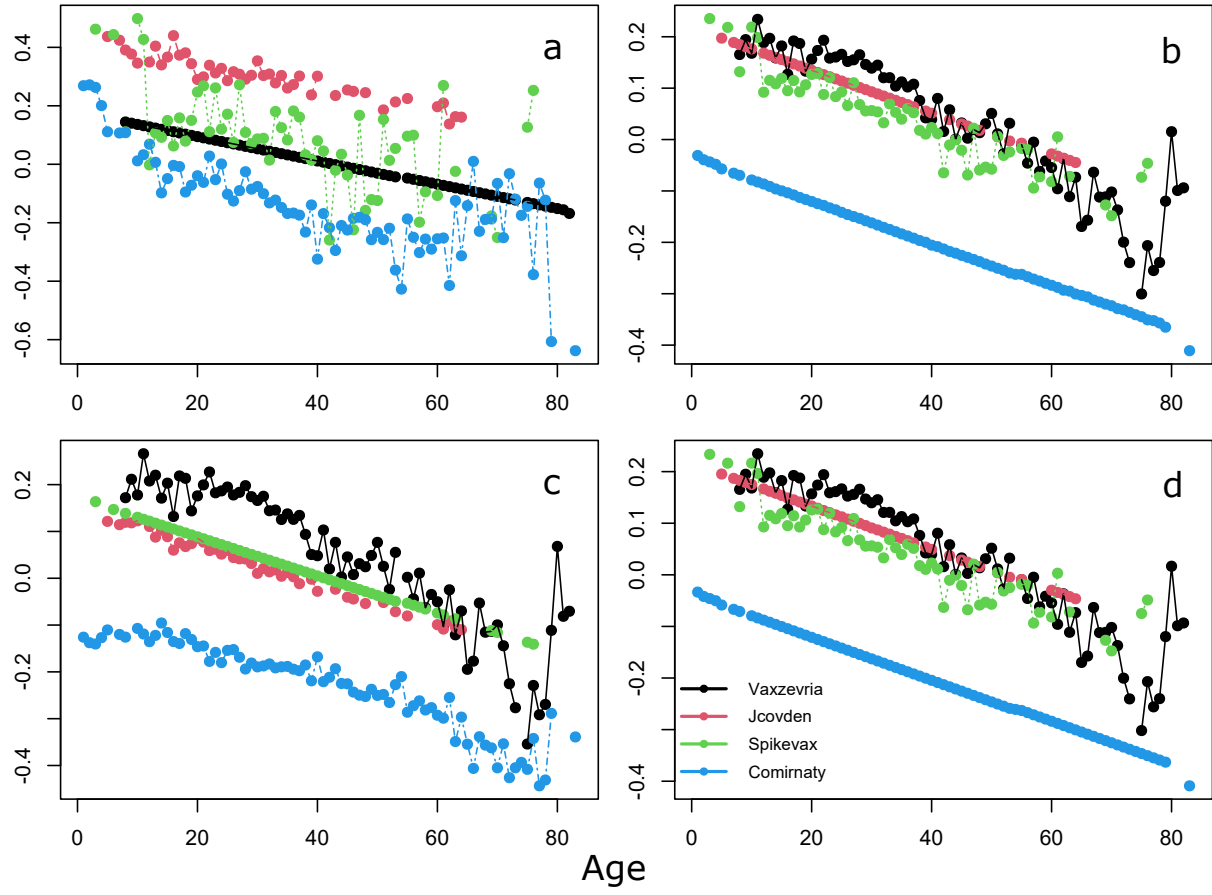


Figure S1: Age dependence of $\log \hat{\mu}$ for the levels of factor Vaccine, for different reference vaccines. Reference vaccine: a, Vaxzevria; b, Jcovden; c, Spikevax; d, Comirnaty.

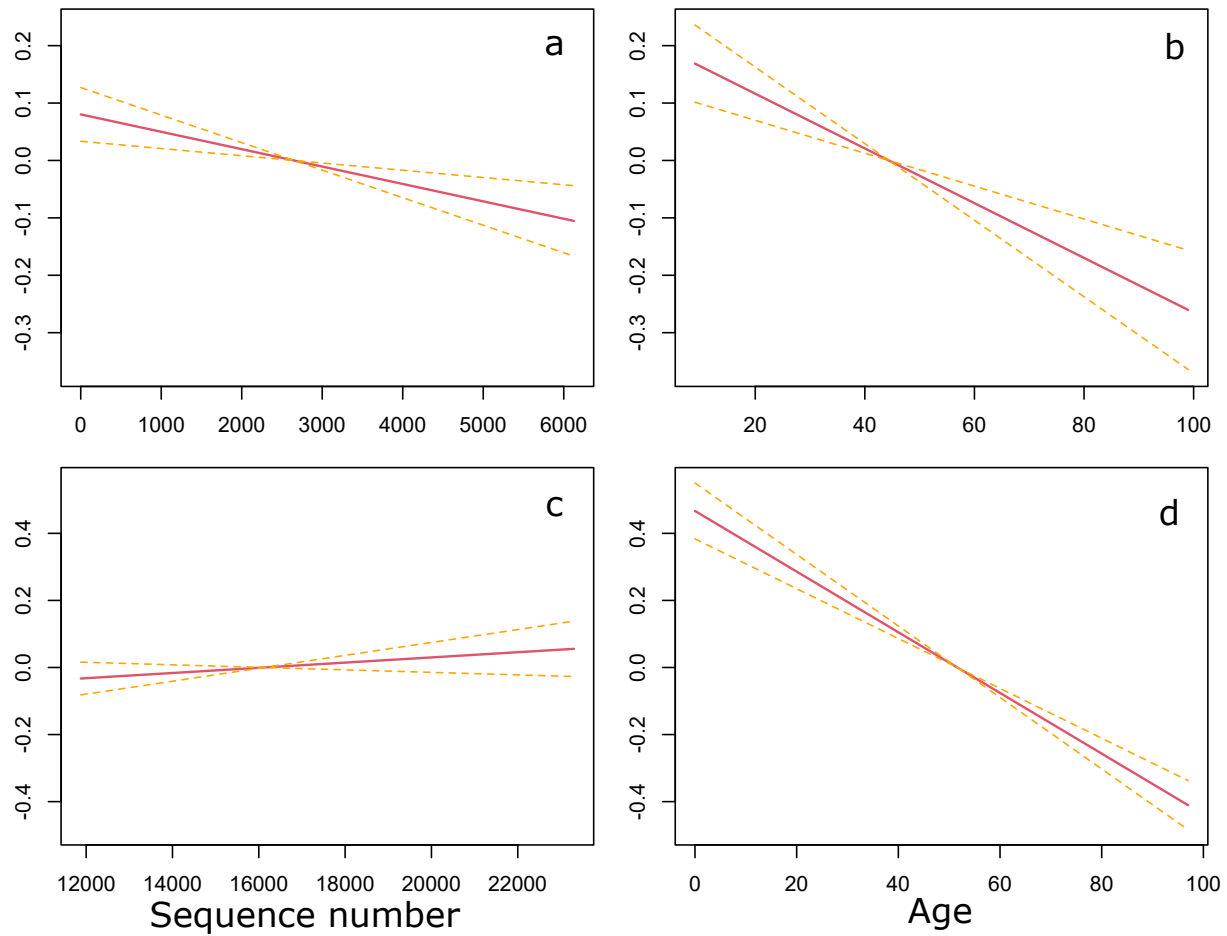


Figure S2: Term plots for Sequence-number and Age dependence of $\log \hat{\mu}$ for COVID-19 vaccines Model 15.6 (a and b) and other drugs data Model 29.6 (c and d).

R code

```
# Load data for COVID-19 vaccines and for Other drugs
library(readxl)
COVID <- read_excel("COVID_Vaccine_data.xlsx")
Other <- read_excel("Other_Drugs_data.xlsx")

# Bespoke function for calculating the Pearson dispersion statistic
overdisp_fun <- function(model) {
  rdf <- df.residual(model)
  rp <- resid(model, type="p")
  Pearson.chisq <- sum(na.omit(rp^2))
  prat <- Pearson.chisq/rdf
  pval <- pchisq(Pearson.chisq, df=rdf, lower.tail=FALSE)
  c(chisq=Pearson.chisq, ratio=prat, rdf=rdf, p=pval)
}
overdisp_fun(Model15.6)
```

```

# Calculating the overdispersion by the Cameron
# and Trivedi (1990, 2013) method
library(overdisp)
overdisp(COVID, dependent.position = 6,
          predictor.position = 1:5, sig = NULL)

# Function for determining outliers and extreme values
library(rstatix)
identify_outliers(COVID, counts)

# Histogram of observed and theoretical distributions
# and parametric coefficients
library(gamlss)
histDist(COVID$counts, family=ZANBI, na.rm=TRUE,
          ylim = 0.20) #or 'family=ZAPIG'

# GAMLSS parametric models
library(gamlss)
COVID_counts <- data.frame(Seq_No=COVID$Seq_No, counts=COVID$counts)
mCOVID<-gamlssML(counts,data=COVID_counts,family=ZANBI
) #similarly, with 'Other' data and with ZAPIG

# Best GAMLSS full models
library(gamlss)
Model15.6<-gamlss(counts~Age+Sex+Serious+Vaccine,data=na.omit(COVID),
sigma.formula=~X+Serious+X*Serious,family=ZANBI)
Model29.6<-gamlss(counts~Age+Serious,data=na.omit(Other),
sigma.formula=~X+Serious,family=ZANBI)

# Diagnostic plots
plot(mCOVID,ts=TRUE) #ACF, density, and Q-Q plots
rqres.plot(mCOVID, howmany=40, plot.type = "all"
) #worm plot with 40 bootstrap iterations

# ggplot2 graphics for covariates with
# linear regression and loess curves
mu_fv <- Model15.6$mu.fv
library(ggplot2)
ggplot(na.omit(COVID), aes(Age, mu_fv)) +
  geom_point(color="dimgray") +
  geom_smooth(method = "lm", color="red") +
  geom_smooth(method = "loess", color = "blue"
) #similar for other models, data, and covariates

# Composite term plots
op<-par(mfrow=c(1,3),mar=c(2,2,1,1)+0.1)

```

```
termplot(Model15.6, what="mu", terms=c(3,4,5), pages=1, se=T,xlabs=""  
) # makes a row with 3 plots for the factors Sex, Serious, Vaccine  
par(op)
```