# flexsurv: flexible parametric survival modelling in R. Supplementary examples

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#### Abstract

This vignette of examples supplements the main flexsurv user guide.

Keywords: survival.

# 1. Examples of custom distributions

## 1.1. Proportional hazards generalized gamma model

Crowther and Lambert (2013) discuss using the **stgenreg** Stata package to construct a proportional hazards parameterisation of the three-parameter generalised gamma distribution. A similar trick can be used in **flexsurv**. A four-parameter custom distribution is created by defining its hazard (and cumulative hazard) functions. These are obtained by multiplying the built-in functions hgengamma and Hgengamma by an extra dummy parameter, which is used as the location parameter of the new distribution. The intercept of this parameter is fixed at 1 when calling flexsurvreg, so that the new model is no more complex than the generalized gamma AFT model fs3, but covariate effects on the dummy parameter are now interpreted as hazard ratios.

```
+ })
> fs7 <- flexsurvreg(Surv(recyrs, censrec) ~ group, data=bc,
+ dist=custom.gengammaPH, fixedpars=1)</pre>
```

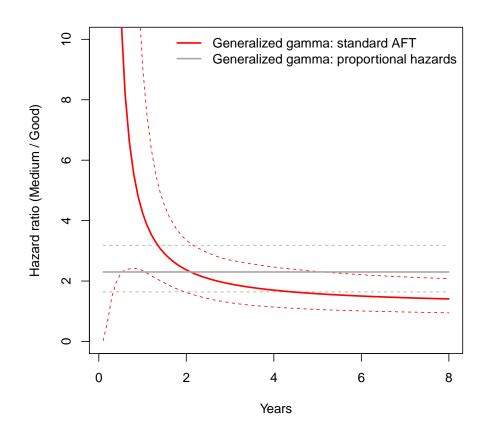
# 2. Examples of custom model summaries

## 2.1. Plotting a hazard ratio against time

The following code plots the hazard ratio (Medium versus Good prognostic group) against time for both the proportional hazards model fs7 and the better-fitting accelerated failure time model fs2. It illustrates the use of the following functions.

- summary.flexsurvreg for generating the estimated hazard at a series of times, for particular covariate categories.
- normboot.flexsurvreg for generating a bootstrap-style sample from the sampling distribution of the parameter estimates, for particular covariate categories.
- do.call for constructing a function call by supplying a list containing the function's arguments. This is used throughout the source of **flexsurv**.

```
> fs2 <- flexsurvreg(Surv(recyrs, censrec) ~ group + sigma(group),</pre>
                     data=bc, dist="gengamma")
> B <- 5000
> t <- seq(0.1, 8, by=0.1)
> hrAFT.est <-
      summary.flexsurvreg(fs2, t=t, type="hazard",
                          newdata=data.frame(group="Medium"),ci=FALSE)[[1]][,"est"] /
      summary.flexsurvreg(fs2, t=t, type="hazard",
                          newdata=data.frame(group="Good"),ci=FALSE)[[1]][,"est"]
> pars <- normboot.flexsurvreg(fs2, B=B, newdata=data.frame(group=c("Good","Medium")))</pre>
> hrAFT <- matrix(nrow=B, ncol=length(t))</pre>
> for (i in seq_along(t)){
      haz.medium.rep <- do.call(hgengamma, c(list(t[i]), as.data.frame(pars[[2]])))
      haz.good.rep <- do.call(hgengamma, c(list(t[i]), as.data.frame(pars[[1]])))
      hrAFT[,i] <- haz.medium.rep / haz.good.rep</pre>
+ }
> hrAFT <- apply(hrAFT, 2, quantile, c(0.025, 0.975))
> hrPH.est <-
      summary.flexsurvreg(fs7, t=t, type="hazard",
                          newdata=data.frame(group="Medium"),ci=FALSE)[[1]][,"est"] /
      summary.flexsurvreg(fs7, t=t, type="hazard",
                          newdata=data.frame(group="Good"),ci=FALSE)[[1]][,"est"]
> pars <- normboot.flexsurvreg(fs7, B=B, newdata=data.frame(group=c("Good","Medium")))
> hrPH <- matrix(nrow=B, ncol=length(t))</pre>
```



References

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Crowther MJ, Lambert PC (2013). "stgenreg: A Stata package for general parametric survival analysis." *Journal of Statistical Software*, **53**, 1–17.