Why use the Weibull model?

SURVIVAL ANALYSIS IN R

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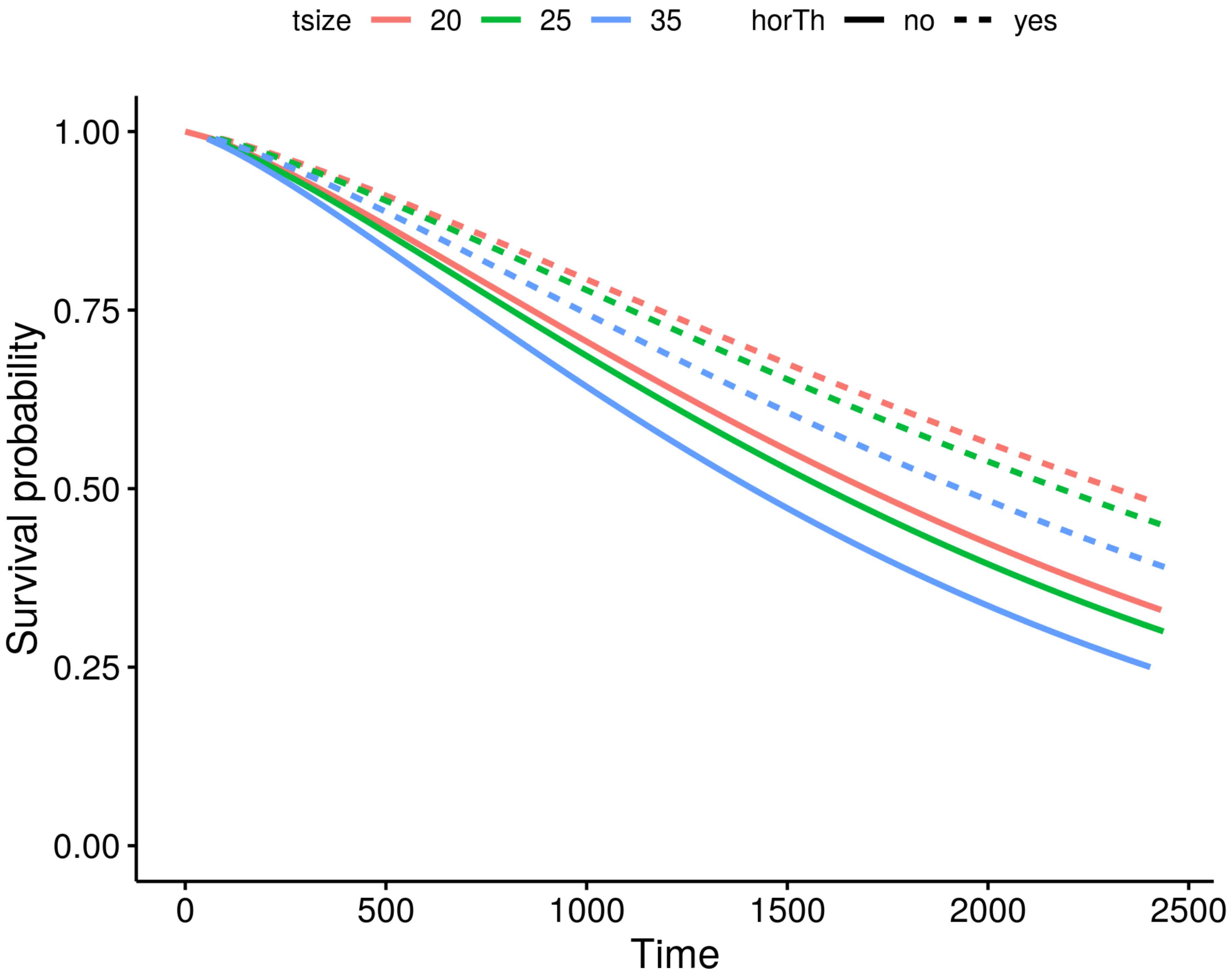
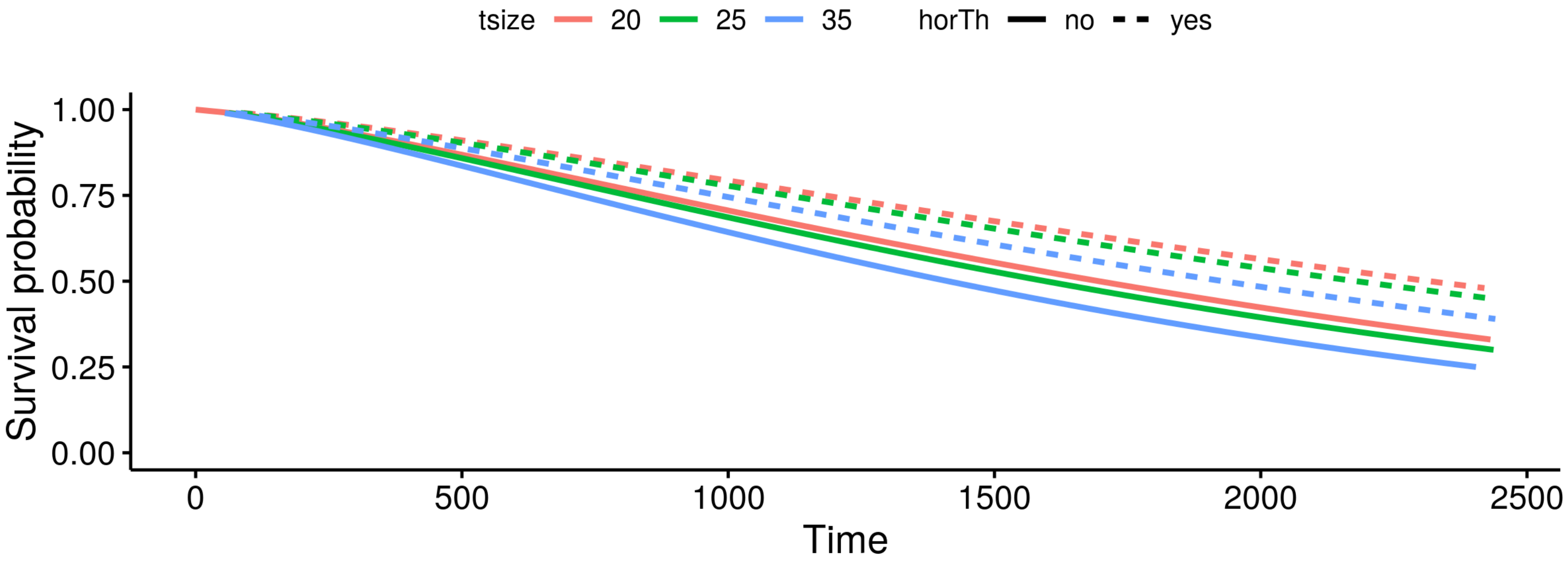

tsize
20
25
35
horTh
no
yes
Survival probability
1.00
0.75
0.50
0.25
0.00
0
500
1000
1500
2000
2500
Time

Computing a Weibull model in R

```
wbmod <- survreg(Surv(time, cens) ~ horTh + tsize, data = GBSG2)
coef(wbmod)
```

```
(Intercept)    horThyes       tsize
 7.96069769  0.31175602 -0.01218073
```



Let's practice!

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Visualising Weibull models

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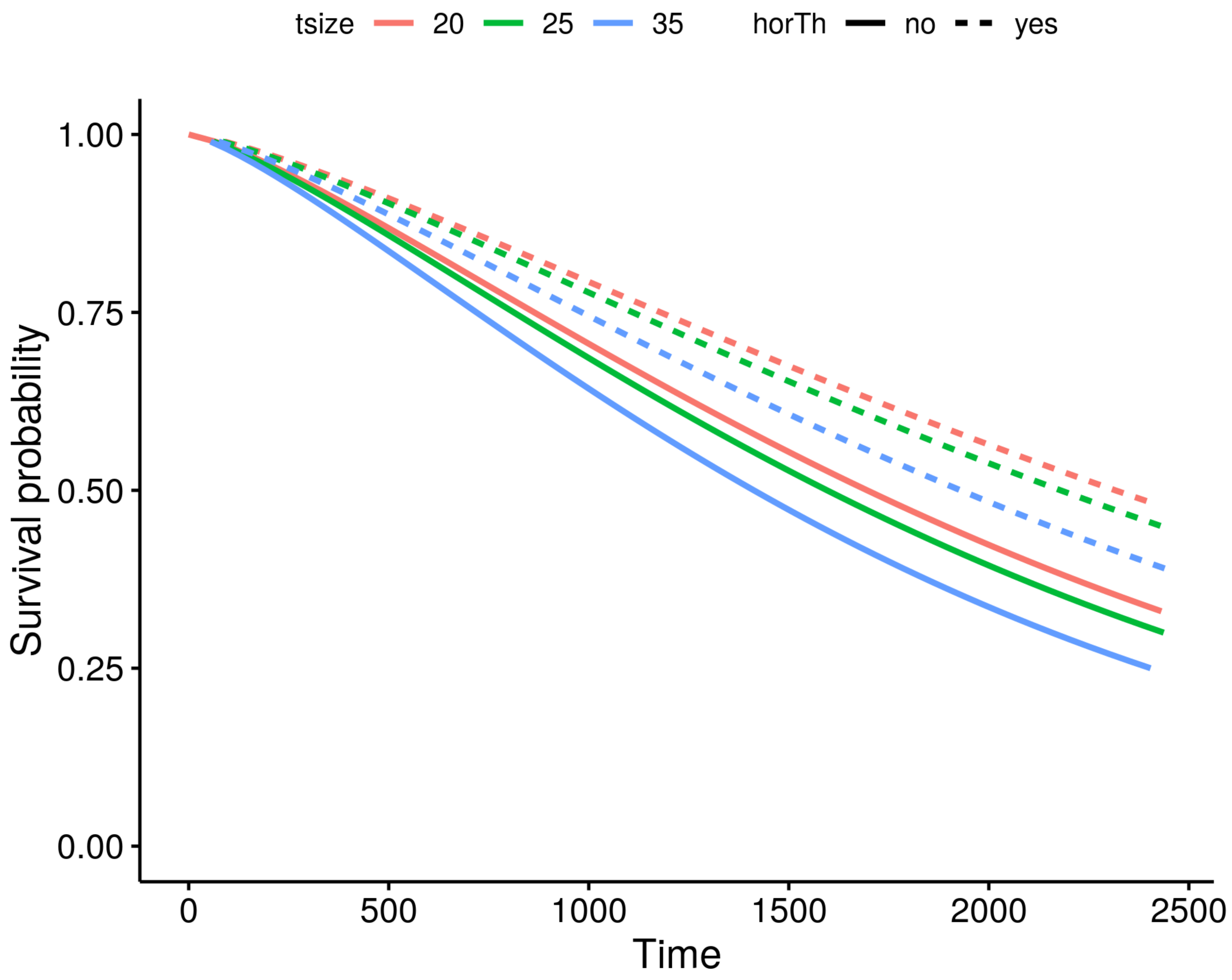
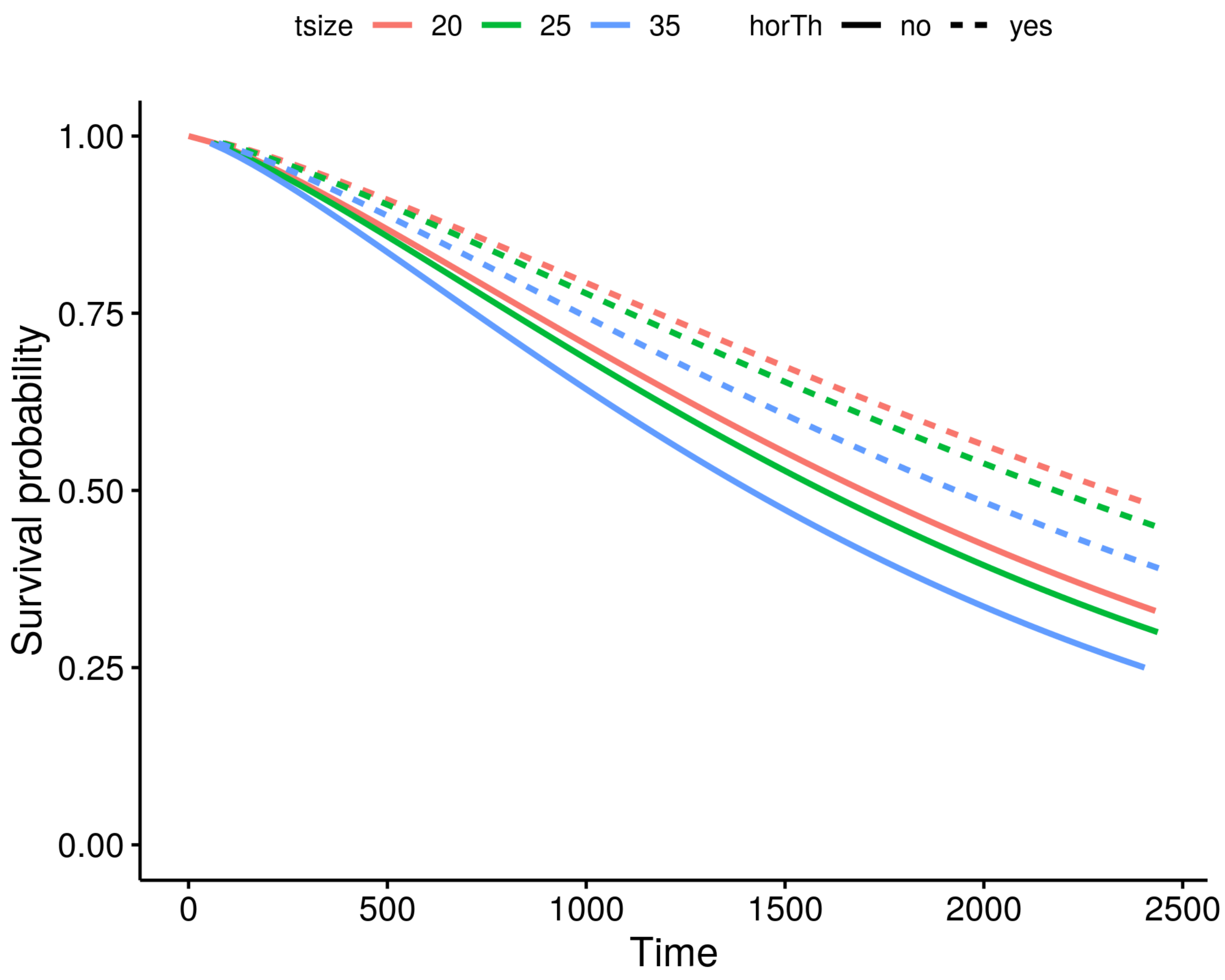

tsize
20
25
35
horTh
no
yes
Survival probability
1.00
0.75
0.50
0.25
0.00
0
500
1000
1500
2000
2500
Time

Steps to produce visualization

- Compute Weibull model
- Decide on "imaginary patients"
- Compute survival curves
- Create `data.frame` with survival curve information
- Plot



Step 1 and 2

- Compute Weibull model

```
wbmod <- survreg(Surv(time, cens) ~ horTh + tsize, data = GBSG2)
```

- Decide on Decide on covariate combinations ("imaginary patients")

```
newdat <- expand.grid(
  horTh = levels(GBSG2$horTh),
  tsize = quantile(GBSG2$tsize, probs = c(0.25, 0.5, 0.75))  )
newdat
```

```
#>   horTh tsize
#> 1    no    20
#> 2   yes    20
#> 3    no    25
...
```

Step 3

- Compute survival curves

```r
surv <- seq(.99, .01, by = -.01)
t <- predict(wbmod, type = "quantile", p = 1 - surv, newdata = newdat)
dim(t)
t[, 1:7]
```

```
6 99
```

```
         [,1]      [,2]     [,3]     [,4]     [,5]     [,6]     [,7]
[1,] 65.86524 112.54061 154.2116 193.0603 230.0268 265.6298 300.1952
[2,] 89.96016 153.71037 210.6256 263.6858 314.1755 362.8029 410.0131
[3,] 61.97352 105.89102 145.0999 181.6531 216.4354 249.9348 282.4579
[4,] 84.64477 144.62823 198.1805 248.1057 295.6121 341.3663 385.7870
[5,] 54.86634  93.74733 128.4597 160.8209 191.6144 221.2720 250.0653
[6,] 74.93762 128.04211 175.4530 219.6526 261.7110 302.2180 341.5445
```

Step 4

- Create `data.frame` with survival curve information

```
surv_wbmod_wide <- cbind(newdat, t)
```

```
library("reshape2")
surv_wbmod <- melt(surv_wbmod_wide, id.vars = c("horTh", "tsize"),
   variable.name = "surv_id",  value.name = "time")
```

```
surv_wbmod$surv <- surv[as.numeric(surv_wbmod$surv_id)]
```

```
surv_wbmod[, c("upper", "lower", "std.err", "strata")] <- NA
```

Step 4

```
str(surv_wbmod)
```

```
'data.frame':    594 obs. of  9 variables:
 $ horTh  : Factor w/ 2 levels "no","yes": 1 2 1 2 1 2 1 2 1 2 ...
 $ tsize  : num  20 20 25 25 35 35 20 20 25 25 ...
 $ surv_id: Factor w/ 99 levels "1","2","3","4",..: 1 1 1 1 1 1 2 2 2 2 ...
 $ time   : num  65.9 90 62 84.6 54.9 ...
 $ surv   : num  0.99 0.99 0.99 0.99 0.99 0.99 0.98 0.98 0.98 0.98 ...
 $ strata : logi  NA NA NA NA NA NA ...
 $ std.err: logi  NA NA NA NA NA NA ...
 $ lower  : logi  NA NA NA NA NA NA ...
 $ upper  : logi  NA NA NA NA NA NA ...
```

If this was too fast...

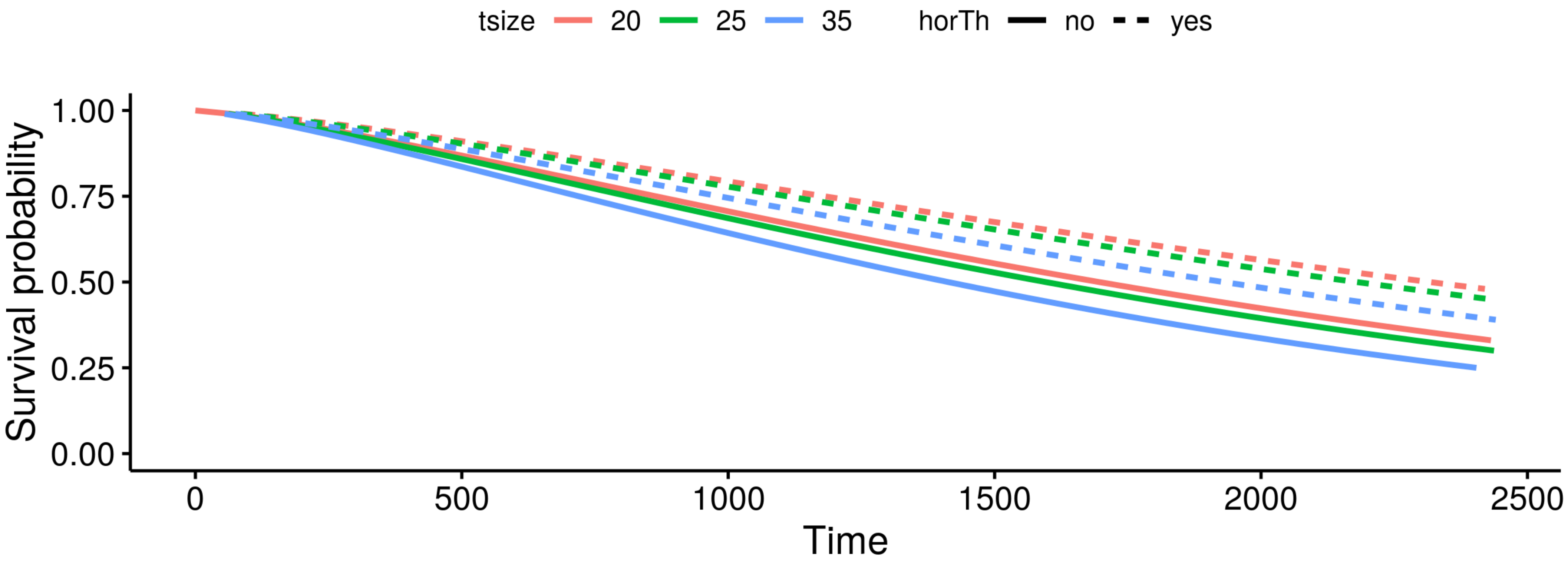
```
library("reshape2")
surv_wbmod <- melt(surv_wbmod_wide, id.vars = names(newdat),
   variable.name = "surv_id",  value.name = "time")
```

```
?melt
```

Step 5

- Plot

```
ggsurvplot_df(surv_wbmod, surv.geom = geom_line,
  linetype = "horTh", color = "tsize", legend.title = NULL)
```



You can do it too! All you need is practice.

Other distributions than Weibull

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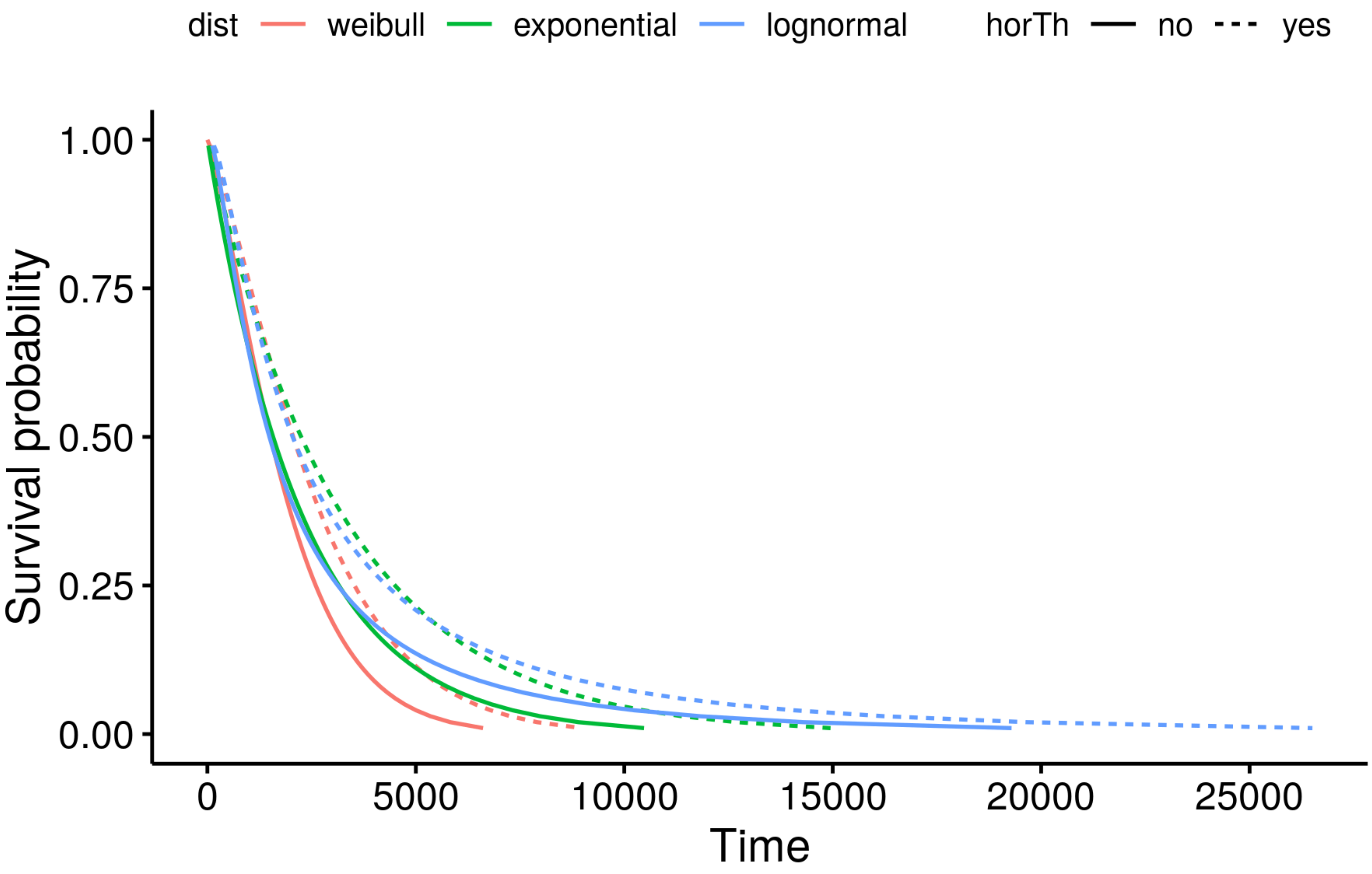
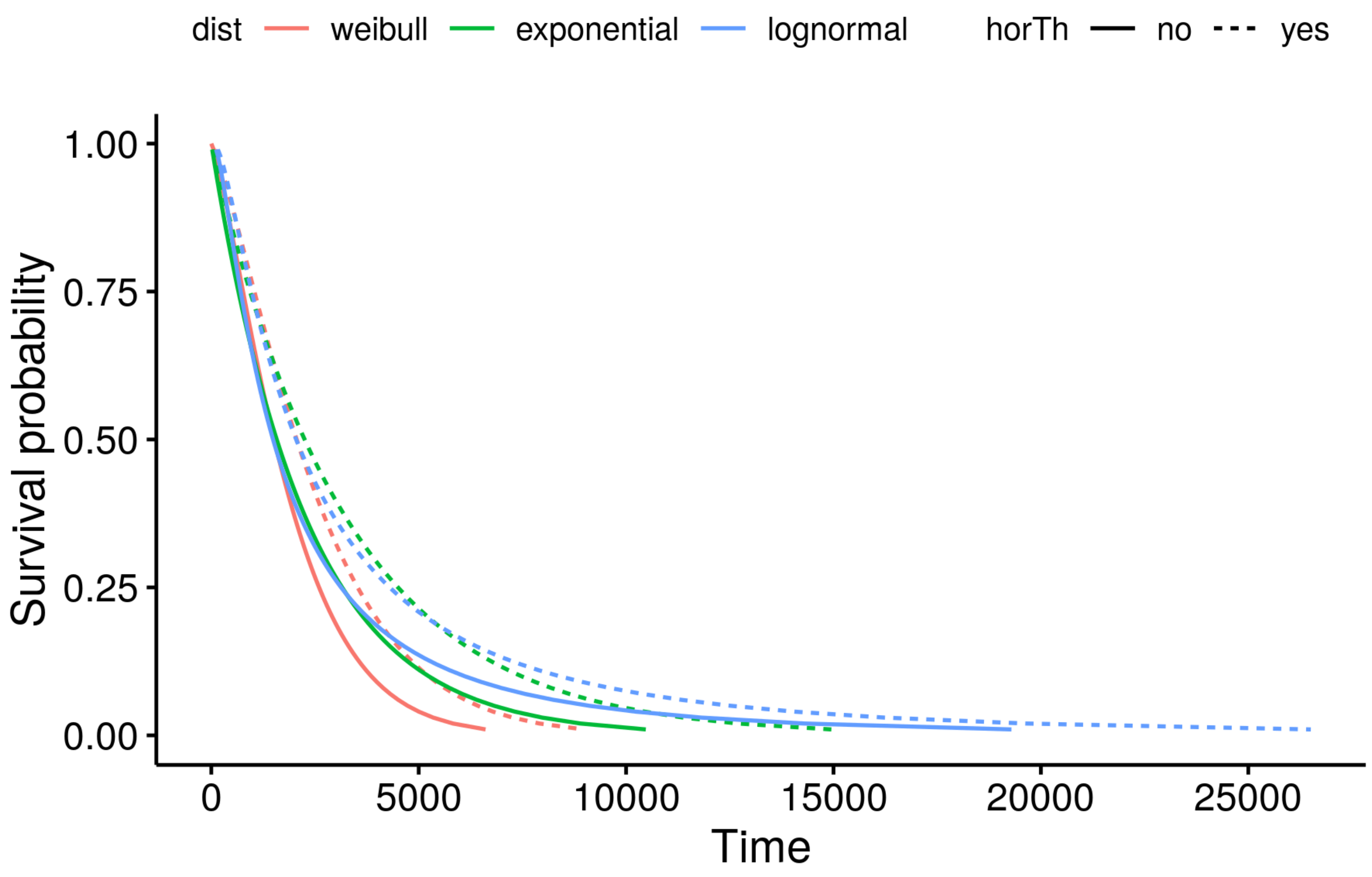

dist
weibull
exponential
lognormal
horTh
no
yes
Survival probability
1.00
0.75
0.50
0.25
0.00
0
5000
10000
15000
20000
25000
Time

survreg() options

```
survreg(Surv(time, cens) ~ horTh,
   data = GBSG2)

survreg(Surv(time, cens) ~ horTh,
   data = GBSG2,
   dist = "exponential")

survreg(Surv(time, cens) ~ horTh,
   data = GBSG2,
   dist = "lognormal")
```



More info:

```
?survreg
```

Let's try working with different models

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