BS Hazard

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BSHazard for exponential hazard rate with sinusoidal fvt

Here, the $\text{mean}(\lambda_3(t)) = \text{mean}(\frac{0.05}{e} * e^{\text{fvt}_2(t)})$, which is just used to find the mean true hazard rate for all the currently alive individuals at each time step.

Simulate and Convert Data

The following simulates 1000 organisms in both cases where fvt influences or does not influence the hazard rate. The data also needed to be converted with `convert_list.R` for the `bshazard` function. Here we also found the average hazard rate at each time step.

```r
out = sim_exp_sin(1000)
fvt.data = out$fvt
nat.data = out$nat
# Calculate average hazard rate accross entire population
# from each individual's fvt
true.fvt.hazard = as.vector(apply(fvt.data, 2, function(col) {
  col = na.omit(col)
  mean((0.05 / exp(1)) * exp(col))
}))[-1]

surv.data.fvt = convert_list(fvt.data)
surv.data.fvt$time0 = surv.data.fvt$time - 1

surv.data.nat = convert_list(nat.data)
surv.data.nat$time0 = surv.data.nat$time - 1
```

Run `bshazard`

```r
bs.fvt = bshazard(Surv(time0, time, status)~1, data=surv.data.fvt, phi=1)
bs.nat = bshazard(Surv(time0, time, status)~1, data=surv.data.nat, phi=1)
```

We also tested for `Surv(time0, time, status)~trait`, but it takes much longer to run `bshazard` this way and there was not much of a difference in the results.

Make Plots

```r
nat.toplot = data.frame(
  "fit"=bs.nat$hazard,
  "time"=bs.nat$time,
  "true"=rep(0.05, length=length(bs.nat$time)),
  "lower.ci"=bs.nat$lower.ci,
```

```r
    "upper.ci"=bs.nat$upper.ci
    )
fvt.toplot = data.frame(
    "fit"=bs.fvt$hazard,
    "time"=bs.fvt$time,
    "true"=true.fvt.hazard,
    "lower.ci"=bs.fvt$lower.ci,
    "upper.ci"=bs.fvt$upper.ci
    )

p1 = ggplot(nat.toplot) +
    geom_line(aes(x=time, y=fit, color="Fitted"), size=1) +
    geom_line(aes(x=time, y=true, color="Actual"), size=1) +
    geom_ribbon(aes(x=time, ymin=lower.ci, ymax=upper.ci), alpha=0.15) +
    theme_bw() +
    scale_color_manual("", breaks=c("Fitted", "Actual"), values=c("Fitted"="black", "Actual"="red")) +
    ggtitle("Trait Does Not Influence Survival") +
    xlab("Time") +
    ylab("Hazard Rate") +
    theme(plot.title = element_text(size=18, hjust=0.5), axis.title=element_text(size=12), legend.text=ele

p2 = ggplot(fvt.toplot) +
    geom_line(aes(x=time, y=fit, color="Fitted"), size=1) +
    geom_line(aes(x=time, y=true, color="Actual"), size=1) +
    geom_ribbon(aes(x=time, ymin=lower.ci, ymax=upper.ci), alpha=0.15) +
    theme_bw() +
    scale_color_manual("", breaks=c("Fitted", "Actual"), values=c("Fitted"="black", "Actual"="red")) +
    ggtitle("Trait Does Influence Survival") +
    xlab("Time") +
    ylab("Hazard Rate") +
    theme(plot.title = element_text(size=18, hjust=0.5), axis.title=element_text(size=12), legend.text=ele

grid.arrange(p1,p2, nrow=2)
```
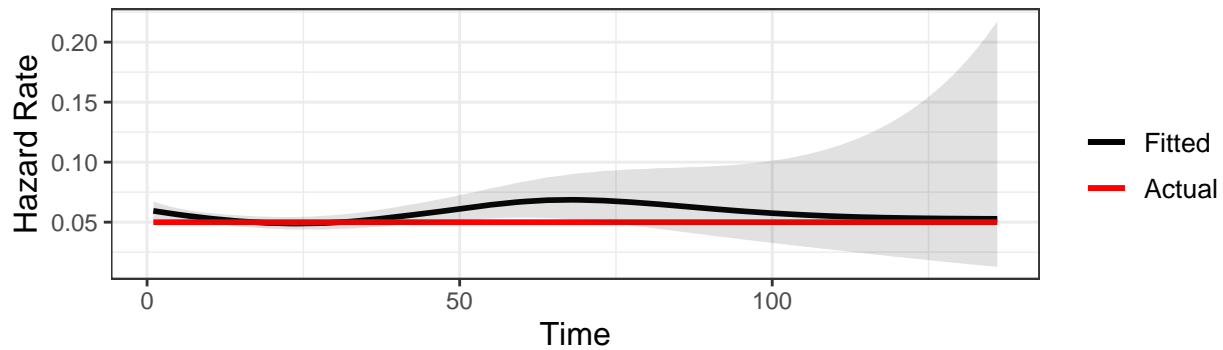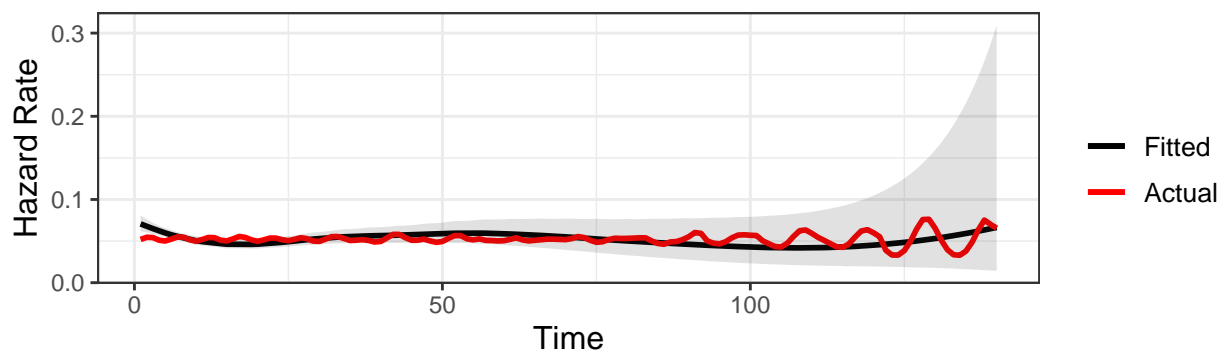
Trait Does Not Influence Survival

Trait Does Influence Survival

Above, the actual hazard rate become more varied towards the end because there are less organisms alive, so the average hazard rate has a greater bias towards specific organisms.

BSHazard for linear hazard rate with Holling type 2

Here, the $\mathrm{mean}(\lambda_1(t)) = \mathrm{mean}(0.05 + 0.001 * \mathrm{fvt}_1(t))$.

Simulate and Convert Data

Like above, except we simulate for Holling Type II, and calculate the average hazard rate of the population differently.

```r
out = sim_hollings(1000)
fvt.data = out$fvt
nat.data = out$nat
# Calculate average hazard rate accross entire population
# from each individual's fvt
true.fvt.hazard = as.vector(apply(fvt.data, 2, function(col) {
  col = na.omit(col)
  mean(0.05 + 0.001* col)
}))[-1]

surv.data.fvt = convert_list(fvt.data)
surv.data.fvt$time0 = surv.data.fvt$time - 1

surv.data.nat = convert_list(nat.data)
surv.data.nat$time0 = surv.data.nat$time - 1
```

Run bshazard

```
bs.fvt = bshazard(Surv(time0, time, status)~1, data=surv.data.fvt, phi=1)
bs.nat = bshazard(Surv(time0, time, status)~1, data=surv.data.nat, phi=1)
```
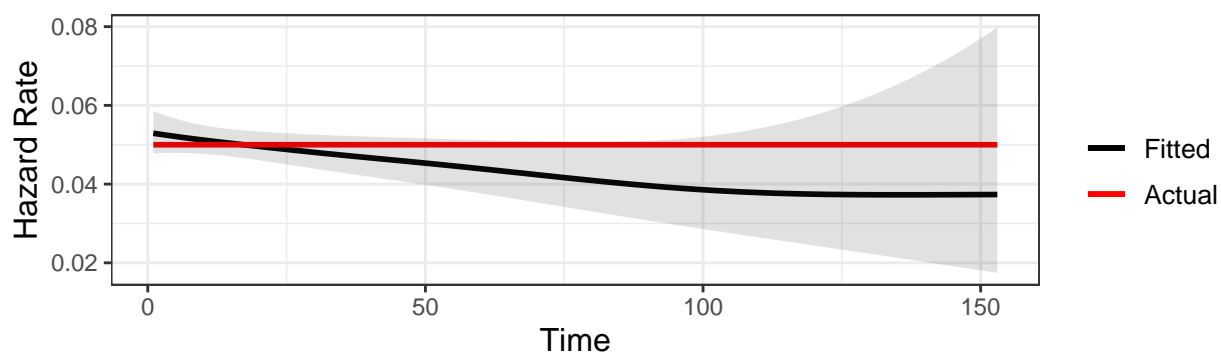
Make Plots

```
nat.toplot = data.frame(
  "fit"=bs.nat$hazard,
  "time"=bs.nat$time,
  "true"=rep(0.05, length=length(bs.nat$time)),
  "lower.ci"=bs.nat$lower.ci,
  "upper.ci"=bs.nat$upper.ci
  )
fvt.toplot = data.frame(
  "fit"=bs.fvt$hazard,
  "time"=bs.fvt$time,
  "true"=true.fvt.hazard,
  "lower.ci"=bs.fvt$lower.ci,
  "upper.ci"=bs.fvt$upper.ci
  )

p1 = ggplot(nat.toplot) +
  geom_line(aes(x=time, y=fit, color="Fitted"), size=1) +
  geom_line(aes(x=time, y=true, color="Actual"), size=1) +
  geom_ribbon(aes(x=time, ymin=lower.ci, ymax=upper.ci), alpha=0.15) +
  theme_bw() +
  scale_color_manual("", breaks=c("Fitted", "Actual"), values=c("Fitted"="black", "Actual"="red")) +
  ggtitle("Trait Does Not Influence Survival") +
  xlab("Time") +
  ylab("Hazard Rate") +
  theme(plot.title = element_text(size=18, hjust=0.5), axis.title=element_text(size=12), legend.text=el

p2 = ggplot(fvt.toplot) +
  geom_line(aes(x=time, y=fit, color="Fitted"), size=1) +
  geom_line(aes(x=time, y=true, color="Actual"), size=1) +
  geom_ribbon(aes(x=time, ymin=lower.ci, ymax=upper.ci), alpha=0.15) +
  theme_bw() +
  scale_color_manual("", breaks=c("Fitted", "Actual"), values=c("Fitted"="black", "Actual"="red")) +
  ggtitle("Trait Does Influence Survival") +
  xlab("Time") +
  ylab("Hazard Rate") +
  theme(plot.title = element_text(size=18, hjust=0.5), axis.title=element_text(size=12), legend.text=el
grid.arrange(p1,p2)
```