


Performing GPC in a paired design

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This vignette describes how to use Generalized Pairwise comparisons (GPC) in a paired design. This for instance corresponds to the Diabetic Retinopathy Study (DRS) contained in the `survival`  package where 197 patients had one of their eye randomized to laser treatment while the other did not receive any treatment:

```
data(diabetic, package = "survival")
head(diabetic)
```

	id	laser	age	eye	trt	risk	time	status
1	5	argon	28	left	0	9	46.23	0
2	5	argon	28	right	1	9	46.23	0
3	14	xenon	12	left	1	8	42.50	0
4	14	xenon	12	right	0	6	31.30	1
5	16	xenon	9	left	1	11	42.27	0
6	16	xenon	9	right	0	11	42.27	0

The outcome was time to blindness (visual acuity drop below a certain threshold). In the real study `status` equal to 0 mixes death and censoring (due to drop-out or end of study) but this complication will be neglected here for simplicity.

We will replicate some of the analyzes presented in [Matsouaka \(2022\)](#). In this paper they split the dataset into juvenile and adult patients:

```
diabetic$juvenile <- diabetic$age <= 19
library(LMMstar)
summarize(age ~ juvenile, data = diabetic[!duplicated(diabetic$id),])
```

	juvenile	observed	missing	mean	sd	min	q1	median	q3	max
1	FALSE	83	0	35.30120	11.242054	20	25	34	45.00	58
2	TRUE	114	0	10.21053	4.713892	1	7	10	13.75	19

and we will focus on the juvenile patients:

```
diabeticJ <- diabetic[diabetic$juvenile,]
```

1 Wald methods (Gehan scoring rule)

To mimic the methodology underlying the results presented in Table 1 of [Matsouaka \(2022\)](#), we perform GPC stratified by patient using the Gehan scoring rule:

```
library(BuyseTest)
e.BTjuv <- BuyseTest(trt ~ tte(time,status) + strata(id, match = TRUE),
                    data = diabeticJ, trace = FALSE,
                    scoring.rule = "Gehan")
model.tables(e.BTjuv, percentage = FALSE)
```

	endpoint	total	favorable	unfavorable	neutral	uninf	Delta	lower.ci	upper.ci	p.value
1	time	114	39	21	3	51	0.1578947	0.02591623	0.2844633	0.01922741

Indeed this scoring rule does not involve any extra-modeling, only evaluating the patient specific net benefit and averaging them:

```
mean(coef(e.BTjuv, strata = TRUE))
```

```
[1] 0.1578947
```

[Matsouaka \(2022\)](#) propose to estimate the standard error as:

```
N <- nobs(e.BTjuv)["pairs"]
pw <- coef(e.BTjuv, statistic = "favorable")
pl <- coef(e.BTjuv, statistic = "unfavorable")
sqrt((pw + pl - (pw - pl)^2)/N)
```

```
time
0.06631828
```

which matches what BuyseTest output:

```
confint(e.BTjuv)
```

	estimate	se	lower.ci	upper.ci	null	p.value
time	0.1578947	0.06631828	0.02591623	0.2844633	0	0.01922741

By default `confint` uses a hyperbolic tangent to compute confidence intervals (CIs), which will then differ from the 'Wald' discussed in [Matsouaka \(2022\)](#). These 'untransformed Wald' CIs can be retrieved by setting the argument `transform` to `FALSE`:

```
confint(e.BTjuv, transform = FALSE)
```

	estimate	se	lower.ci	upper.ci	null	p.value
time	0.1578947	0.06631828	0.02791329	0.2878762	0	0.01727214

Note: naively one may think to estimate the standard error as:

```
sqrt(var(coef(e.BTjuv, strata = TRUE))/N)
```

```
pairs  
0.06661108
```

This is equivalent (in large samples to the previous formula). Indeed:

$$\begin{aligned} & \mathbb{P}[X > Y] + \mathbb{P}[Y > X] - (\mathbb{P}[X > Y] - \mathbb{P}[Y > X])^2 \\ &= \mathbb{P}[X > Y] + \mathbb{P}[Y > X] - \mathbb{P}[X > Y]^2 - \mathbb{P}[Y > X]^2 + 2\mathbb{P}[X > Y]\mathbb{P}[Y > X] \\ &= \mathbb{P}[X > Y](1 - \mathbb{P}[X > Y]) + \mathbb{P}[Y > X](1 - \mathbb{P}[Y > X]) + 2\mathbb{P}[X > Y]\mathbb{P}[Y > X] \\ &= \mathbb{P}[X > Y](1 - \mathbb{P}[X > Y]) + \mathbb{P}[Y > X](1 - \mathbb{P}[Y > X]) \\ &\quad - 2(0 - \mathbb{P}[X > Y]\mathbb{P}[Y > X] - \mathbb{P}[X > Y]\mathbb{P}[Y > X] + \mathbb{P}[X > Y]\mathbb{P}[Y > X]) \\ &= \text{Var}[\mathbf{1}_{X>Y}] + \text{Var}[\mathbf{1}_{X<Y}] - 2\text{Cov}(\mathbf{1}_{X>Y}, \mathbf{1}_{X<Y}) \\ &= \text{Var}[\mathbf{1}_{X>Y} - \mathbf{1}_{X<Y}] \end{aligned}$$

There is only a factor $N/(N-1)$ difference between the two:

```
sqrt(var(coef(e.BTjuv, strata = TRUE))/N) * sqrt((N-1)/N)
```

```
pairs  
0.06631828
```

2 MOVER method (Gehan scoring rule)

The method recommended by [Matsouaka \(2022\)](#) is the MOVER approach, which has been developed for a binary scoring rule (e.g. Gehan). An experimental function with the same name has been implemented in the `BuyseTest` package:

```
mover(e.BTjuv)
```

```
estimate      lower      upper      pvalue  
0.15789474 0.02540421 0.28317729 0.01967878
```

leading to the same results as those of the table 1 in the original article, up to rounding.

3 Wald methods (Peron scoring rule)

To better account for censoring one could use the Peron scoring rule where the survival is estimated across all subjects within a treatment group. One has to specify the survival model, otherwise, the `BuyseTest` function will estimate a treatment and strata specific survival curve which is impossible to perform here. The `model.tte` argument can be used to specify such survival model:

```
library(prodlim)
e.BTjuv2 <- BuyseTest(trt ~ tte(time,status) + strata(id, match = TRUE),
                     data = diabeticJ, trace = FALSE,
                     model.tte = prodlim(Hist(time,status)~ trt, data = diabeticJ))
model.tables(e.BTjuv2, percentage = FALSE)
```

	endpoint	total	favorable	unfavorable	neutral	uninf	Delta	lower.ci	upper.ci	p.value
1	time	114	47.36525	24.29552	3	39.33923	0.202366	0.05045454	0.3451254	0.009329589

Ignoring the uncertainty of the survival model, the standard would be:

```
c(sqrt(var(coef(e.BTjuv2, strata = TRUE))/N),
  sqrt(var(coef(e.BTjuv2, strata = TRUE))/N) * sqrt((N-1)/N)
)
```

	pairs	pairs
	0.06595510	0.06566518

depending on whether a small sample correction is used or not. This matches the output of `BuyseTest` when ignoring the uncertainty of the survival model:

```
model.tte <- prodlim(Hist(time,status)~ trt, data = diabeticJ)
attr(model.tte, "iidNuisance") <- FALSE
confint(BuyseTest(trt ~ tte(time,status) + strata(id, match = TRUE),
                  data = diabeticJ, trace = FALSE,
                  model.tte = model.tte))
```

	estimate	se	lower.ci	upper.ci	null	p.value
time	0.202366	0.06566518	0.07088227	0.3269375	0	0.002726979

⚠ Because the pairwise win and loss score are no more binary, the previous formula no more simplifies into the formula presented in Matsouaka (2022):

```
pw.peron <- coef(e.BTjuv2, statistic = "favorable")
pl.peron <- coef(e.BTjuv2, statistic = "unfavorable")
sqrt((pw.peron + pl.peron - (pw.peron - pl.peron)^2)/N)
```

	time
	0.07179718

To account for the uncertainty of the survival model, `BuyseTest` outputs a slightly higher standard error:

```
confint(e.BTjuv2)
```

```
      estimate      se  lower.ci  upper.ci null    p.value
time 0.202366 0.07569815 0.05045454 0.3451254    0 0.009329589
```

This is achieved by considering two sources of uncertainty:

- average of a finite number of pairs:

```
pw.peronS <- coef(e.BTjuv2, statistic = "favorable", strata = TRUE)
pl.peronS <- coef(e.BTjuv2, statistic = "unfavorable", strata = TRUE)
Hterm1 <- (pw.peronS - pl.peronS) - (pw.peron - pl.peron)
```

- propagate the uncertainty of the survival model to the net benefit. Because each pair appear twice (control and treatment) the impact of removing a pair on the net benefit is stored in the control and the treated is set to 0:

```
Hterm2.obs <- e.BTjuv2@iidNuisance$favorable - e.BTjuv2@iidNuisance$unfavorable
Hterm2.pair <- Hterm2.obs[diabeticJ$trt==0]
table(Hterm2.obs[diabeticJ$trt==1])
```

```
0
114
```

After rescaling the terms by a factor N (number of pairs, to account for the pooling) we retrieve the uncertainty output by `BuyseTest`:

```
c(average = sqrt(crossprod((Hterm1/N))),
  nuisance = sqrt(crossprod((Hterm2.pair/N))),
  all = sqrt(crossprod((Hterm1/N + Hterm2.pair/N))))
```

```
      average  nuisance      all
0.06566518 0.02084622 0.07569815
```

References

Matsouaka, R. A. (2022). Robust statistical inference for matched win statistics. *Statistical Methods in Medical Research*, 31(8):1423–1438.