

R code

```
> install.packages("BuyseTest", quiet = TRUE)
> library(BuyseTest)
```

R output

```
Loading required package: Rcpp
BuyseTest version 3.0.6
```

R code

```
> set.seed(10)
> data <- simBuyseTest(100, n.strata = 2)
> head(data)
```

R output

	id	treatment	eventtime	status	toxicity	score	strata
	<num>	<fctr>	<num>	<num>	<fctr>	<num>	<fctr>
1:	1	C	0.17392093	1	yes	-2.1250686	a
2:	2	C	0.16255166	0	yes	0.5211787	a
3:	3	C	0.08302502	1	yes	-0.0464229	b
4:	4	C	0.22204972	0	no	-1.1494717	b
5:	5	C	0.11669726	1	no	0.6293383	a
6:	6	C	0.11885540	1	yes	-0.7264715	a

R code

```
> e.BT <- BuyseTest(treatment ~ tte(eventtime, status = status),
  data = data)
```

R output

Generalized Pairwise Comparisons

Settings

- 2 groups : Control = C and Treatment = T
- 1 endpoint:

priority	endpoint	type	operator	event
1	eventtime	time to event	higher is favorable	status (0 1)

- right-censored pairs: probabilistic score based on the survival curves

Point estimation and calculation of the iid decomposition

Estimation of the estimator's distribution

- method: moments of the U-statistic

Gather the results in a S4BuyseTest object

R code

```
> summary(e.BT)
```

R output

```
Generalized pairwise comparisons with 1 endpoint

- statistic      : net treatment benefit (delta: endpoint specific, Delta: global)
- null hypothesis : Delta == 0
- confidence level: 0.95
- inference      : H-projection of order 1 after atanh transformation
- treatment groups: T (treatment) vs. C (control)
- censored pairs : probabilistic score based on the survival curves
- results
endpoint total(%) favorable(%) unfavorable(%) neutral(%) uninf(%) Delta CI [2.5% ; 97.5%] p.v
eventtime      100          57.39          42.61          0          0 0.1479 [-0.0293;0.3161] 0.1
```

R code

```
> confint(e.BT, statistic = "winRatio")
```

R output

	estimate	se	lower.ci	upper.ci	null	p.value
eventtime	1.347081	0.2450411	0.9430953	1.924118	1	0.1014458

R code

```
> e.BThalf <- BuyseTest(treatment ~ tte(eventtime, status),
                        data = data, add.halfNeutral = TRUE, trace = FALSE)
> model.tables(e.BThalf, statistic = "favorable")
```

R output

	endpoint	total	favorable	unfavorable	neutral	uninf	Delta	lower.ci	upper.ci	p.value
1 eventtime	100	57.39388	42.60612	0	0	0.5739388	0.4852354	0.6581263	0.1019135	

R code

```
> coef(e.BThalf, statistic = "winRatio")
```

R output

```
[1] 1.347081
```

R code

```
> e.MBT <- BuyseTest(treatment ~ tte(eventtime, status, threshold = 1) + bin(toxicity, operator = "gt",
                                data = data, trace = 0)
> model.tables(e.MBT)
```

R output

	endpoint	threshold	total	favorable	unfavorable	neutral	uninf	delta	Delta	lower.ci	upper.ci
1	eventtime	1e+00	100.0	10.2	2.55	87.2	0	0.0768	0.0768	-0.00928	0.15588
3	toxicity	1e-12	87.2	18.8	24.72	43.7	0	-0.0590	0.0178	-0.13396	0.10816

R code

```
plot(e.MBT)
```

R code

```
plot(e.MBT, type = "racetrack")
```

$$\widehat{U} - U = \underbrace{\frac{1}{m} \sum_{i=1}^m h_E(i)}_{\text{Experimental group}} + \underbrace{\frac{1}{n} \sum_{j=1}^n h_C(j)}_{\text{Control group}} + \underbrace{\frac{1}{mn} \sum_{i=1}^n \sum_{j=1}^m h_{EC}(i, j)}_{\text{Second order term}}$$

where for $i \in \{1, \dots, m\}$, $h_E(i) = \mathbb{E}[\mathbb{1}_{Y_i > X_j} - \mathbb{1}_{X_i > Y_j} \mid X_i] - U$
 $j \in \{1, \dots, n\}$, $h_C(j) = \mathbb{E}[\mathbb{1}_{Y_i > X_j} - \mathbb{1}_{X_i > Y_j} \mid Y_j] - U$

$$\widehat{\sigma}_{\widehat{U}} \underbrace{\approx}_{\text{First order}} \frac{1}{m^2} \sum_{i=1}^2 h_E^2(i) + \frac{1}{n^2} \sum_{j=1}^n h_C^2(j)$$