

Kaplan-Meier Plots

2024-09-30

Loading R packages

```
# install.packages("maicplus")  
library(maicplus)
```

Additional suggested packages for this vignette:

```
library(survminer) # this is used for ggplot version of KM plots
```

Introduction

After conducting an MAIC, the results can be effectively illustrated through visual representations of the weighted and non-weighted data. This can be achieved by plotting Kaplan-Meier (KM) curves and comprehensively depicting the time-to-event data. To generate these curves, it is crucial to obtain pseudo-IPD from the comparator study through the digitization of KM curves from the comparator study. For guidance on this process, refer to the works of Guyot et al. and Liu et al. [1,2]

Unanchored case

```
data(weighted_sat)  
data(adtte_sat)  
data(pseudo_ipd_sat)
```

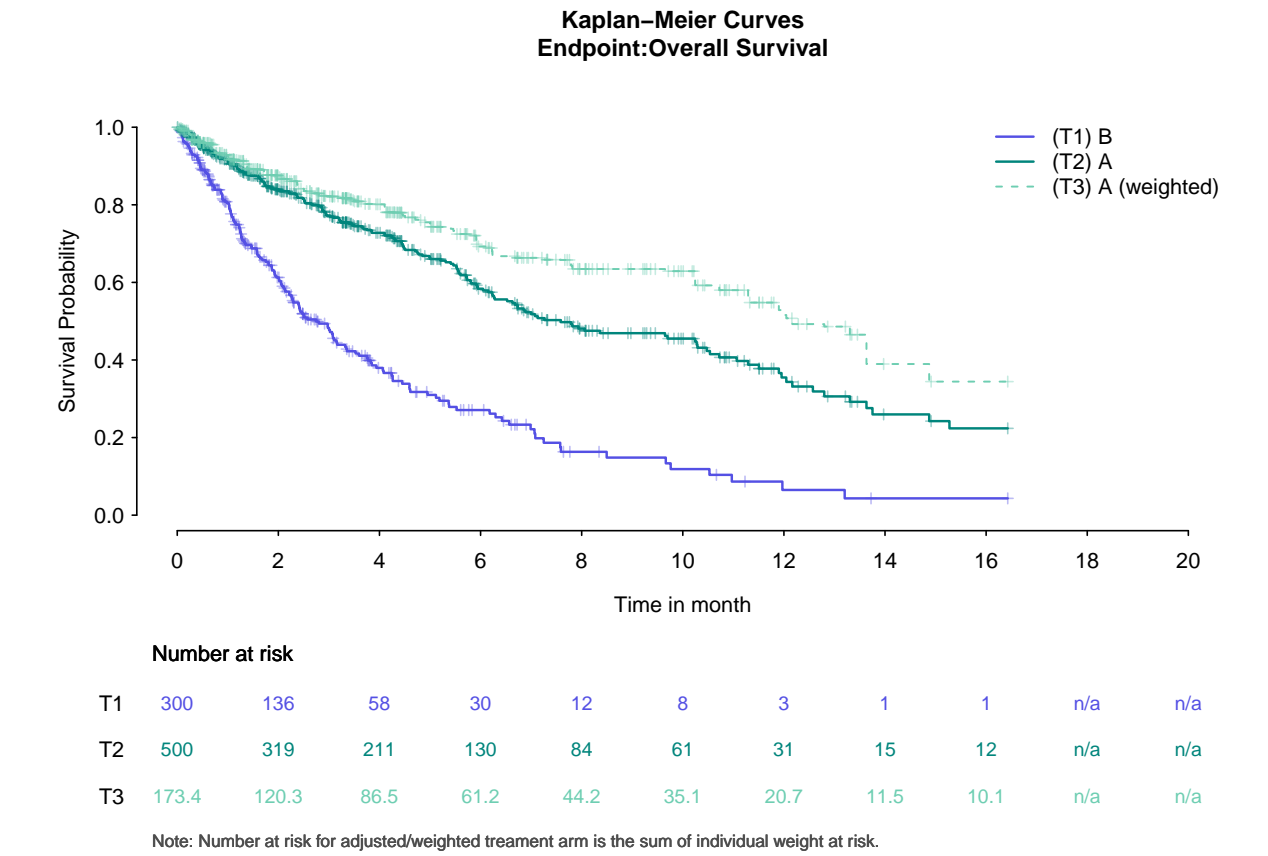
Here is a Kaplan-Meier plot using base R graphics. Note that number at risk for weighted treatment arm is the sum of individual weights at risk. Consequently, number at risk for weighted treatment arm at time 0 is different from calculated ESS. Another important thing to note is that the time input that we specify (i.e. `adtte_sat` in our example) should be in days. `time_scale` component allows us to change days into the analysis unit of preference.

```
kmplot(  
  weights_object = weighted_sat,  
  tte_ipd = adtte_sat,  
  tte_pseudo_ipd = pseudo_ipd_sat,  
  trt_ipd = "A",  
  trt_agd = "B",  
  trt_common = NULL,  
  endpoint_name = "Overall Survival",
```

```

km_conf_type = "log-log",
time_scale = "month",
time_grid = seq(0, 20, by = 2),
use_colors = NULL,
use_line_types = NULL,
use_pch_cex = 0.65,
use_pch_alpha = 100
)

```



There is also a ggplot option for Kaplan-Meier curves using `survminer` R package.

```

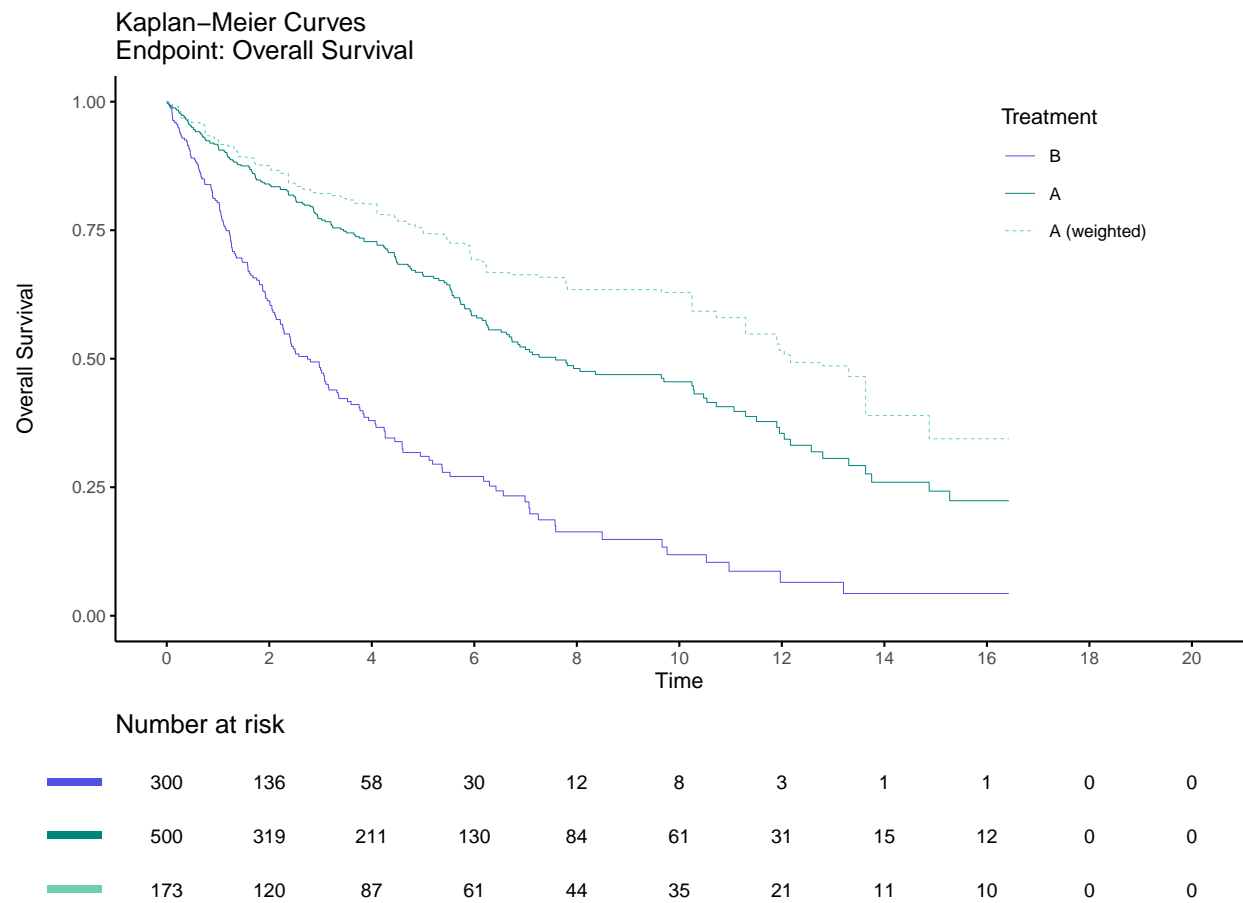
kmplot2(
  weights_object = weighted_sat,
  tte_ipd = addtte_sat,
  tte_pseudo_ipd = pseudo_ipd_sat,
  trt_ipd = "A",
  trt_agd = "B",
  trt_common = NULL,
  endpoint_name = "Overall Survival",
  km_conf_type = "log-log",
  time_scale = "month",
  break_x_by = 2,
  xlim = c(0, 20),

```

```

    censor = FALSE
  )

```



Anchored case

Here is an example for an anchored case.

```

data(weighted_twt)
data(addtte_twt)
data(pseudo_ipd_twt)

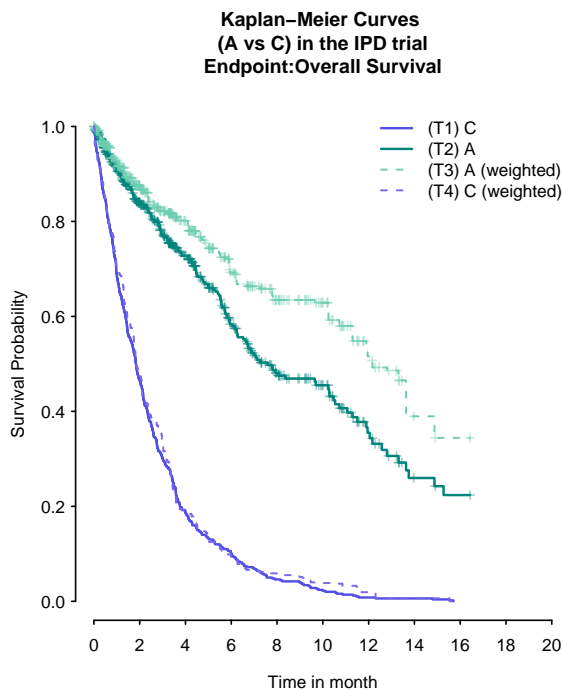
# plot by trial
kmplot(
  weights_object = weighted_twt,
  tte_ipd = addtte_twt,
  tte_pseudo_ipd = pseudo_ipd_twt,
  trt_ipd = "A",
  trt_agd = "B",
  trt_common = "C",
  endpoint_name = "Overall Survival",
  km_conf_type = "log-log",
  km_layout = "by_trial",

```

```

time_scale = "month",
time_grid = seq(0, 20, by = 2),
use_colors = NULL,
use_line_types = NULL,
use_pch_cex = 0.65,
use_pch_alpha = 100
)

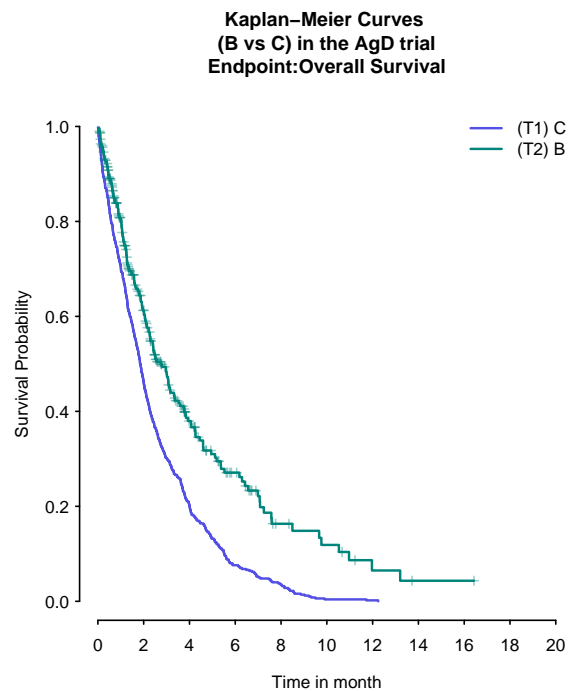
```



Number at risk

T1	500	233	93	50	23	11	4	3	n/a	n/a	n/a
T2	500	319	211	130	84	61	31	15	12	n/a	n/a
T3	173.4	120.3	86.5	61.2	44.2	35.1	20.7	11.5	10.1	n/a	n/a
T4	173.4	84.1	33.1	15.8	10.2	6.7	3.3	1.1	n/a	n/a	n/a

Note: Number at risk for adjusted/weighted treatment arm is the sum of indi



Number at risk

T1	500	230	101	38	18	2	1	n/a	n/a	n/a	n/a
T2	300	136	58	30	12	8	3	1	1	n/a	n/a

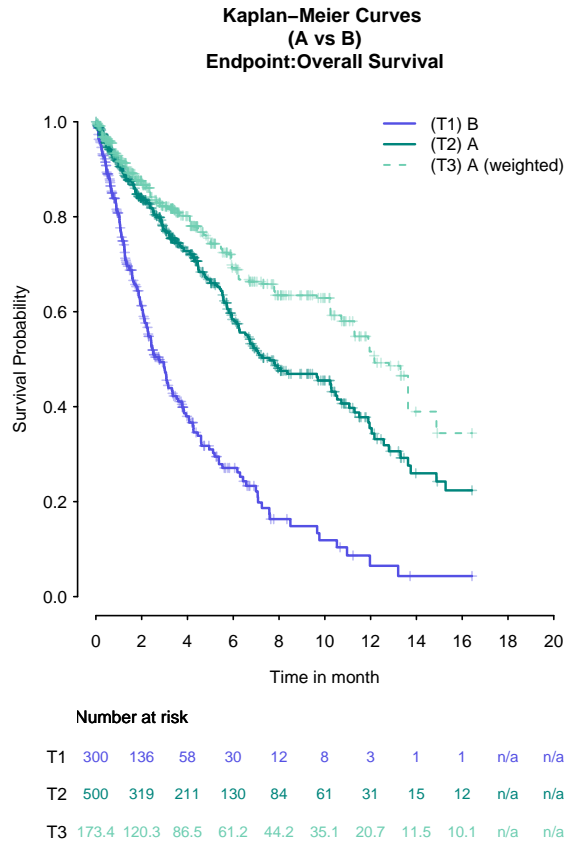
Note: Number at risk for adjusted/weighted treatment arm is the sum of indi

```

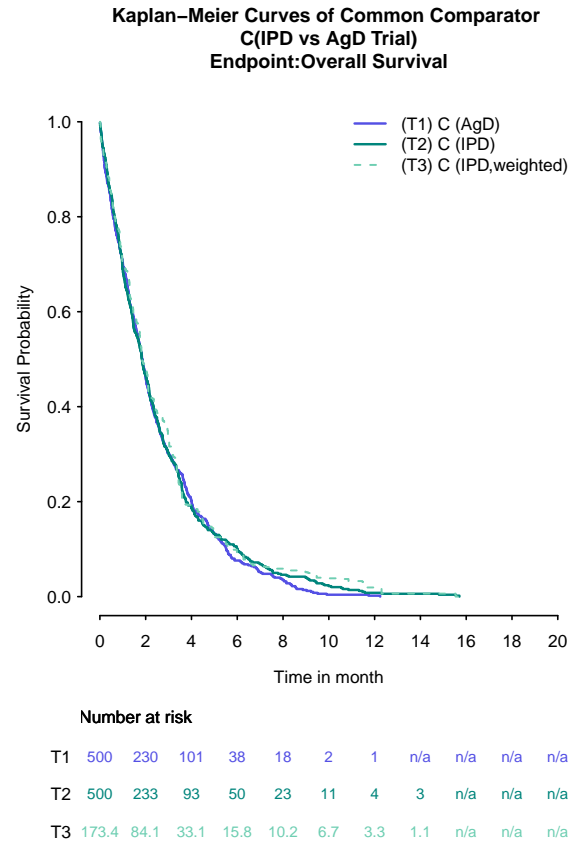
# plot by arm
kmplot(
  weights_object = weighted_twt,
  tte_ipd = addtte_twt,
  tte_pseudo_ipd = pseudo_ipd_twt,
  trt_ipd = "A",
  trt_agd = "B",
  trt_common = "C",
  endpoint_name = "Overall Survival",
  km_conf_type = "log-log",
  km_layout = "by_arm",
  time_scale = "month",
  time_grid = seq(0, 20, by = 2),
  use_colors = NULL,
  use_line_types = NULL,

```

```
use_pch_cex = 0.65,
use_pch_alpha = 100
)
```

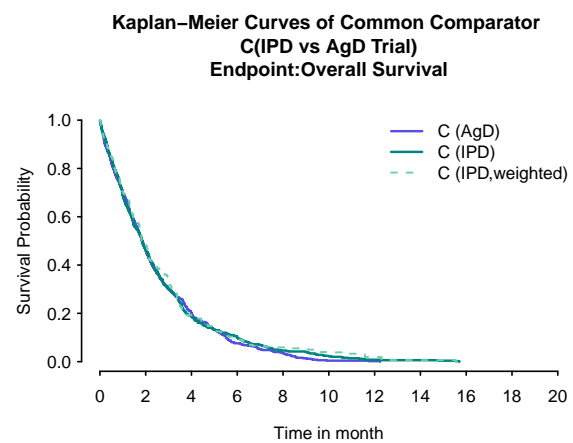
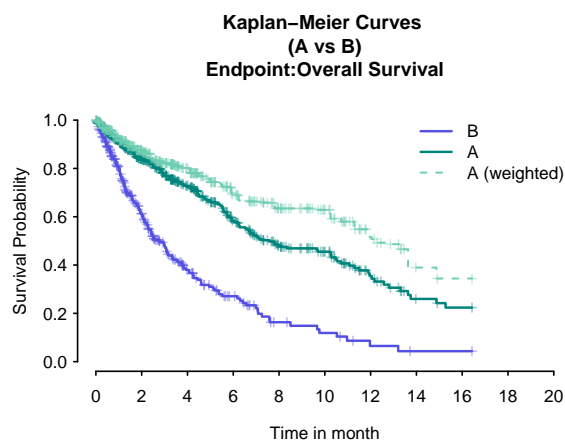
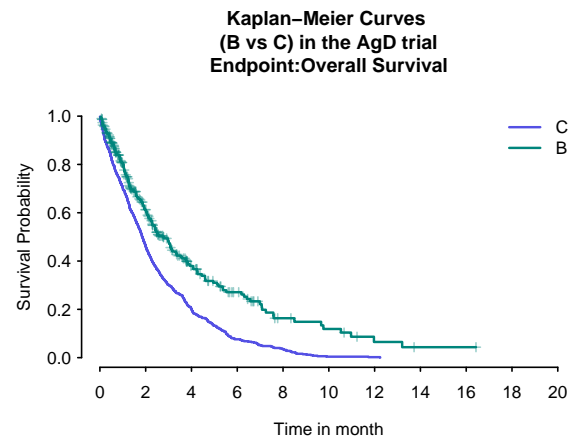
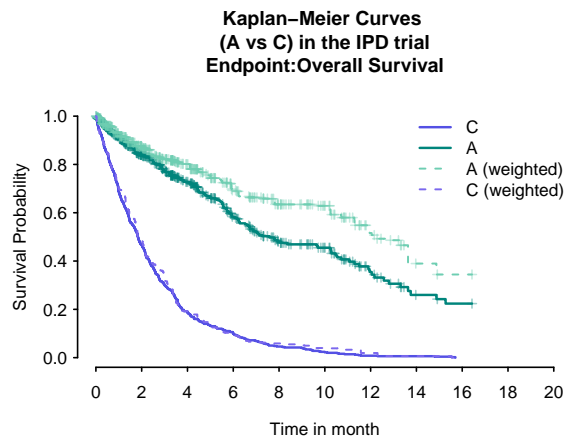


Note: Number at risk for adjusted/weighted treatment arm is the sum of indi



Note: Number at risk for adjusted/weighted treatment arm is the sum of indi

```
# plot all
kmplot(
  weights_object = weighted_twt,
  tte_ipd = adtte_twt,
  tte_pseudo_ipd = pseudo_ipd_twt,
  trt_ipd = "A",
  trt_agd = "B",
  trt_common = "C",
  endpoint_name = "Overall Survival",
  km_conf_type = "log-log",
  km_layout = "all",
  time_scale = "month",
  time_grid = seq(0, 20, by = 2),
  use_colors = NULL,
  use_line_types = NULL,
  use_pch_cex = 0.65,
  use_pch_alpha = 100
)
```



Again there is a ggplot option

```
data(weighted_twt)
data(addtte_twt)
data(pseudo_ipd_twt)

# plot by trial
# kmpplot2(
#   weights_object = weighted_twt,
#   tte_ipd = addtte_twt,
#   tte_pseudo_ipd = pseudo_ipd_twt,
#   trt_ipd = "A",
#   trt_agd = "B",
#   trt_common = "C",
#   endpoint_name = "Overall Survival",
#   km_conf_type = "log-log",
#   km_layout = "by_trial",
#   time_scale = "month",
#   break_x_by = 2
# )

# plot by arm
# kmpplot2(
#   weights_object = weighted_twt,
```

```

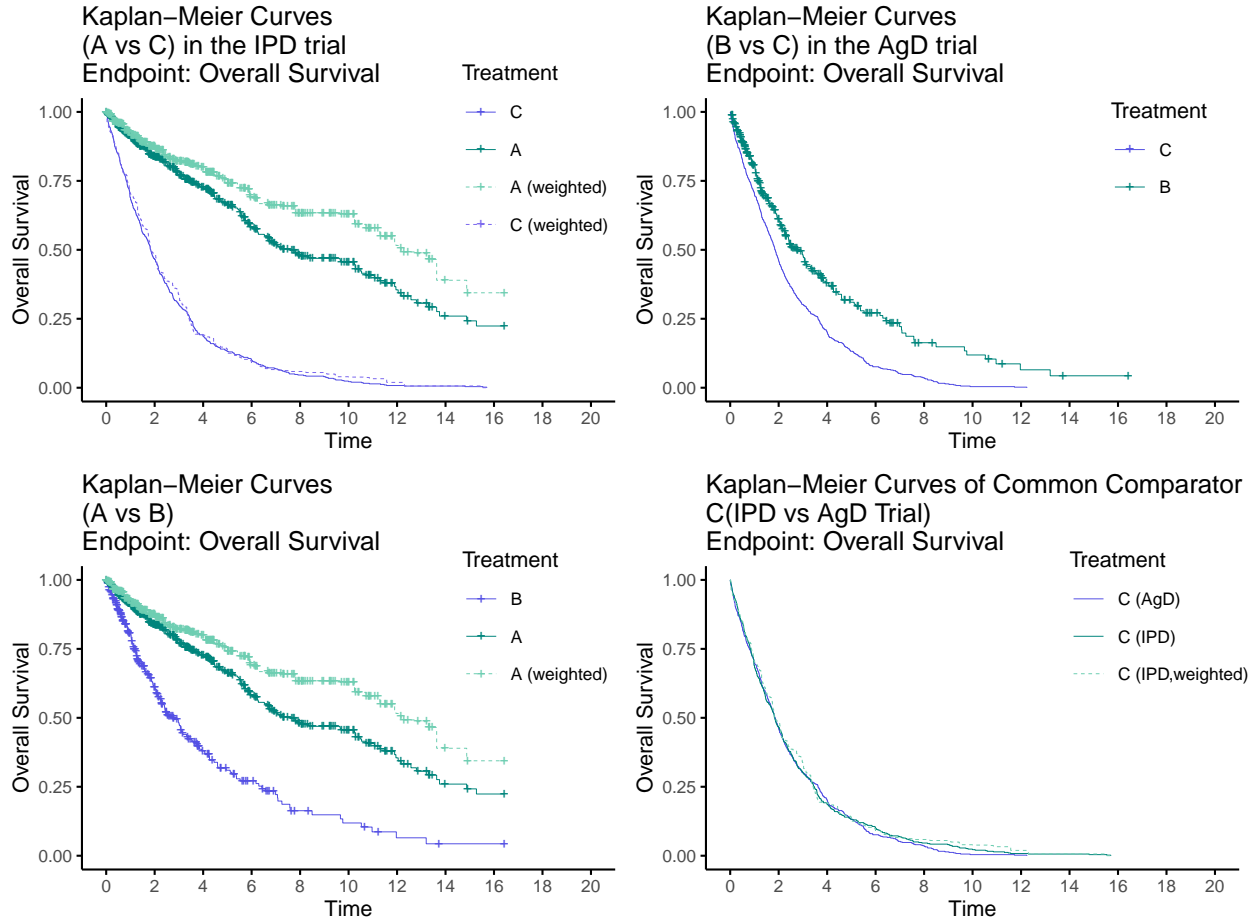
# tte_ipd = adtte_twt,
# tte_pseudo_ipd = pseudo_ipd_twt,
# trt_ipd = "A",
# trt_agd = "B",
# trt_common = "C",
# endpoint_name = "Overall Survival",
# km_conf_type = "log-log",
# km_layout = "by_arm",
# time_scale = "month",
# break_x_by = 2
# )

```

```

# plot all
kmplot2(
  weights_object = weighted_twt,
  tte_ipd = adtte_twt,
  tte_pseudo_ipd = pseudo_ipd_twt,
  trt_ipd = "A",
  trt_agd = "B",
  trt_common = "C",
  endpoint_name = "Overall Survival",
  km_conf_type = "log-log",
  km_layout = "all",
  time_scale = "month",
  break_x_by = 2,
  xlim = c(0, 20),
  show_risk_set = FALSE
)

```



References

- [1] Guyot P, Ades A, Ouwens MJ, Welton NJ. Enhanced secondary analysis of survival data: Reconstructing the data from published kaplan-meier survival curves. *BMC Medical Research Methodology* 2012;12:9.
- [2] Liu N, Yanhong Z, Lee JJ. IPDfromKM: Reconstruct individual patient data from published kaplan-meier survival curves. *BMC Medical Research Methodology* 2021;21:111.