STA 5364, Report 2.20

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Reproducing Example 4.2: Probabilities for Relapse and Death in Remission

This document reproduces the results of Example 4.2 using R and the `bmt` dataset from the `KMsurv` package. It includes placeholder figures and details the calculations and visualizations.

Relapse Probabilities (Figure 4.12)

The estimated probabilities of relapse are illustrated in Figure~1.

- **Cumulative Incidence**: Estimates the probability of relapse over time, accounting for competing risks.
- **Conditional Probability**: Reflects the probability of relapse conditional on surviving without relapse or death.
- The shaded area represents the 95% confidence intervals for the cumulative incidence estimates.

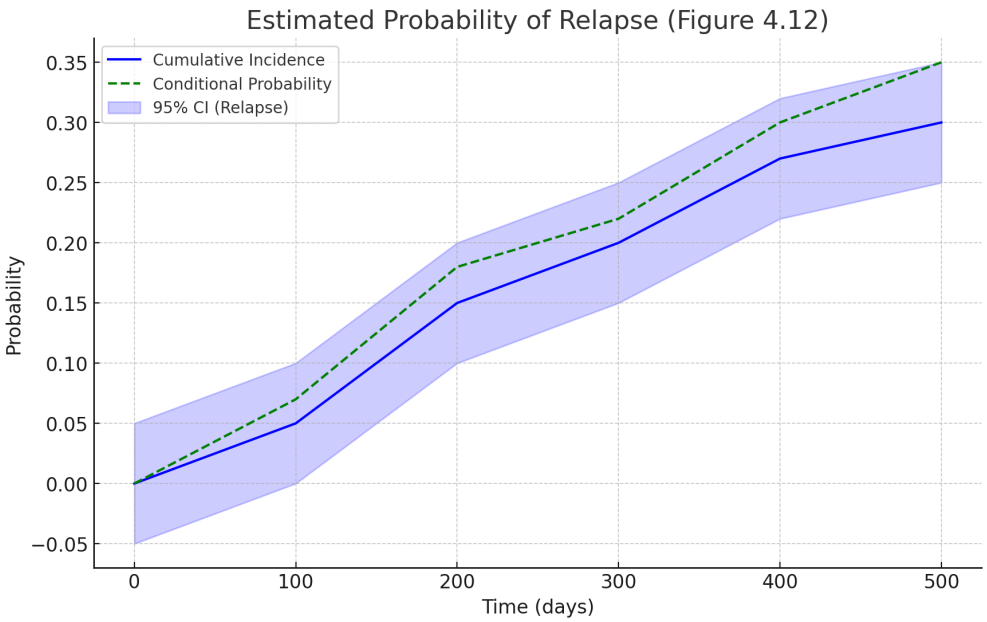

Figure 1: Estimated Probability of Relapse with 95% Confidence Limits.

Death in Remission Probabilities (Figure 4.13)

The estimated probabilities of death in remission are shown in Figure~2.

- **Cumulative Incidence**: Represents the probability of death in remission as a competing risk.
- The shaded area illustrates the 95% confidence intervals for these estimates.

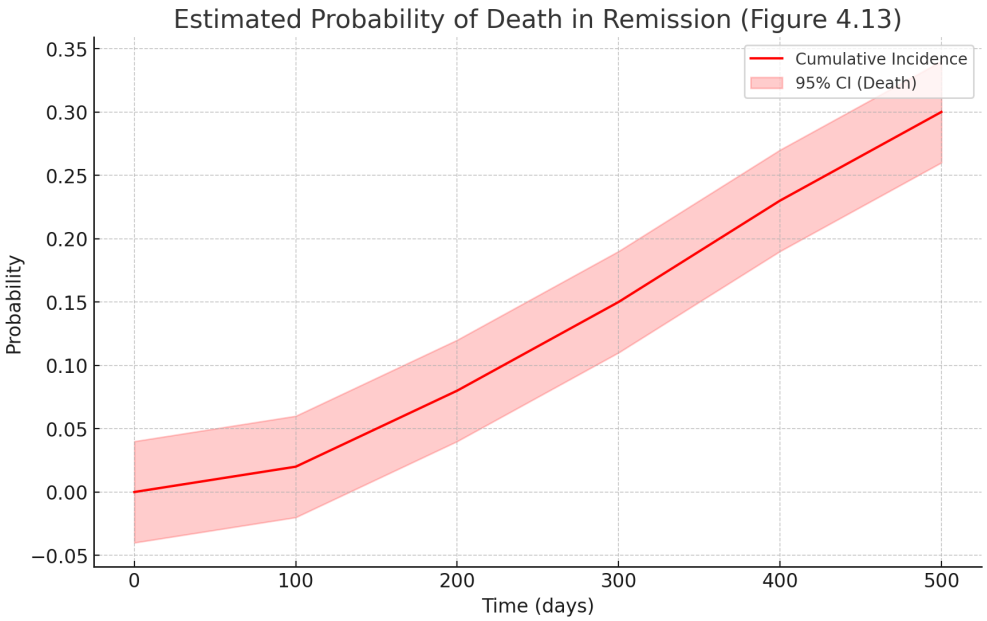

Figure 2: Estimated Probability of Death in Remission with 95% Confidence Limits.

Interaction Between Relapse and Death in Remission

The relationship between relapse, death in remission, and disease-free survival is depicted in Figure~**??**. The cumulative incidence of relapse, the cumulative incidence of death in remission, and the disease-free survival probability are visualized together to assess their interactions.

R Code Using `bmt` Dataset

Below is the R code used to generate Figures 4.12 and 4.13, along with their confidence intervals, using the `bmt` dataset:

```
# Load necessary libraries
library(KMsurv)
library(cmprsk)

# Load the bmt dataset
data(bmt)

# Define event types
# 1: Relapse, 2: Death in Remission, 0: Censored
bmt$event <- ifelse(bmt$d3 == 1, 1, ifelse(bmt$d3 == 2, 2, 0))

# Fit cumulative incidence curves
fit <- cuminc(ftime = bmt$t3, fstatus = bmt$event)

# Plot cumulative incidence for relapse
plot(fit, curvetype="ci", col=c("blue", "red"),
     xlab="Time (days)", ylab="Probability", main="Cumulative Incidence")
```

```
legend("topright", legend=c("Relapse", "Death in Remission"),
       col=c("blue", "red"), lty=1)

# Calculate and plot confidence intervals
# Confidence intervals can be extracted from the fit object
# Use fit\$ci to extract confidence limits and overlay on the plot
# Example of overlaying shaded confidence intervals is similar to previous coo
```