DSCI564 Survival Analysis

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Introduction

Survival Analysis is a subfield of statistics that studies time to a specific event (such as death or malfunction of an equipment) as a random variable. The statistical properties of the random variable such as mean time to an event are very important in many fields such as biostatistics and reliability engineering.

In this project, I will perform survival analysis on benchmark data and learn about statistical tools for survival analysis such as the Kaplan-Meier estimator and the Cox Proportional Hazards Model.

Section (a): Data Exploration and Pre-processing

In [9]:
```
library(survival)
head(pbcseq)
str(pbcseq)
```

A data.frame: 6 × 20

	id	futime	status	trt	age	sex	day	ascites	hepato	spiders	edema	bili
	<int>	<int>	<int>	<int>	<dbl>	<fct>	<int>	<int>	<int>	<int>	<dbl>	<dbl>
1	1	400	2	1	58.76523	f	0	1	1	1	1	14.5
2	1	400	2	1	58.76523	f	192	1	1	1	1	21.3
3	2	5169	0	1	56.44627	f	0	0	1	1	0	1.1
4	2	5169	0	1	56.44627	f	182	0	1	1	0	0.8
5	2	5169	0	1	56.44627	f	365	0	1	1	0	1.0
6	2	5169	0	1	56.44627	f	768	0	1	1	0	1.9

```
'data.frame':	1945 obs. of  20 variables:
 $ id      : int  1 1 2 2 2 2 2 2 2 2 ...
 $ futime  : int  400 400 5169 5169 5169 5169 5169 5169 5169 5169 ...
 $ status  : int  2 2 0 0 0 0 0 0 0 0 ...
 $ trt     : int  1 1 1 1 1 1 1 1 1 1 ...
 $ age     : num  58.8 58.8 56.4 56.4 56.4 ...
 $ sex     : Factor w/ 2 levels "m","f": 2 2 2 2 2 2 2 2 2 2 ...
 $ day     : int  0 192 0 182 365 768 1790 2151 2515 2882 ...
 $ ascites : int  1 1 0 0 0 0 1 1 1 1 ...
 $ hepato  : int  1 1 1 1 1 1 1 1 1 1 ...
 $ spiders : int  1 1 1 1 1 1 1 1 1 1 ...
 $ edema   : num  1 1 0 0 0 0 0.5 1 1 1 ...
 $ bili    : num  14.5 21.3 1.1 0.8 1 1.9 2.6 3.6 4.2 3.6 ...
 $ chol    : int  261 NA 302 NA NA NA 230 NA NA 244 ...
 $ albumin : num  2.6 2.94 4.14 3.6 3.55 3.92 3.32 2.92 2.73 2.8 ...
 $ alk.phos: int  1718 1612 7395 2107 1711 1365 1110 996 860 779 ...
 $ ast     : num  138 6.2 113.5 139.5 144.2 ...
 $ platelet: int  190 183 221 188 161 122 135 100 103 113 ...
 $ protime : num  12.2 11.2 10.6 11 11.6 10.6 11.3 11.5 11.5 11.5 ...
 $ stage   : int  4 4 3 3 3 3 3 3 3 3 ...
 $ sex_num : num  1 1 1 1 1 1 1 1 1 1 ...
```

In [11]:

```
# Fix the 'sex' variable to match (0=male, 1=female)
# Create 'event_death' for Survival Analysis
pbcseq$sex_num <- as.numeric(pbcseq$sex) - 1
pbcseq$event_death <- ifelse(pbcseq$status == 2, 1, 0)
head(pbcseq)
```

A data.frame: 6 × 21

	id	futime	status	trt	age	sex	day	ascites	hepato	spiders	bili	cho
	<int>	<int>	<int>	<int>	<dbl>	<fct>	<int>	<int>	<int>	<int>	<dbl>	<int:
1	1	400	2	1	58.76523	f	0	1	1	1	14.5	26
2	1	400	2	1	58.76523	f	192	1	1	1	21.3	N/
3	2	5169	0	1	56.44627	f	0	0	1	1	1.1	30:
4	2	5169	0	1	56.44627	f	182	0	1	1	0.8	N/
5	2	5169	0	1	56.44627	f	365	0	1	1	1.0	N/
6	2	5169	0	1	56.44627	f	768	0	1	1	1.9	N/

Section (b): Creating the Survival Object

In [13]:

```
S <- Surv(pbcseq$day, pbcseq$futime, pbcseq$event_death)
head(S, 20)
```

```
 [1] (   0, 400]   ( 192, 400]   (   0,5169+] ( 182,5169+] ( 365,5169+]
 [6] ( 768,5169+] (1790,5169+] (2151,5169+] (2515,5169+] (2882,5169+]
[11] (3226,5169+] (   0,1012]   ( 176,1012]   ( 364,1012]   ( 743,1012]
[16] (   0,1925]   ( 188,1925]   ( 372,1925]   ( 729,1925]   (1254,1925]
```

Any entry with a '+' is a patient who was still alive (or transplanted) at the end of that interval.

Section (c): The Kaplan-Meier Estimator

(i) The event of interest is death

In [ ]:

```
pbcseq$event_death <- ifelse(pbcseq$status == 2, 1, 0)
```

(ii) Kaplan-Meier vs. Empirical Distribution

The Kaplan-Meier estimator $\hat{S}(t)$ estimates the survival function $S(t) = P(T > t)$. In the case where no censoring exists in the data, the Kaplan-Meier estimator reduces exactly to the complement of the **Empirical Distribution Function (EDF)**.

If $F_X(t)$ is the empirical distribution function (the proportion of observations less than or equal to t), then:

$$\hat{S}(t) = 1 - F_X(t)$$

This means the survival curve would simply be a step function dropping by $1/n$ at each observed event time, where n is the number of observations.

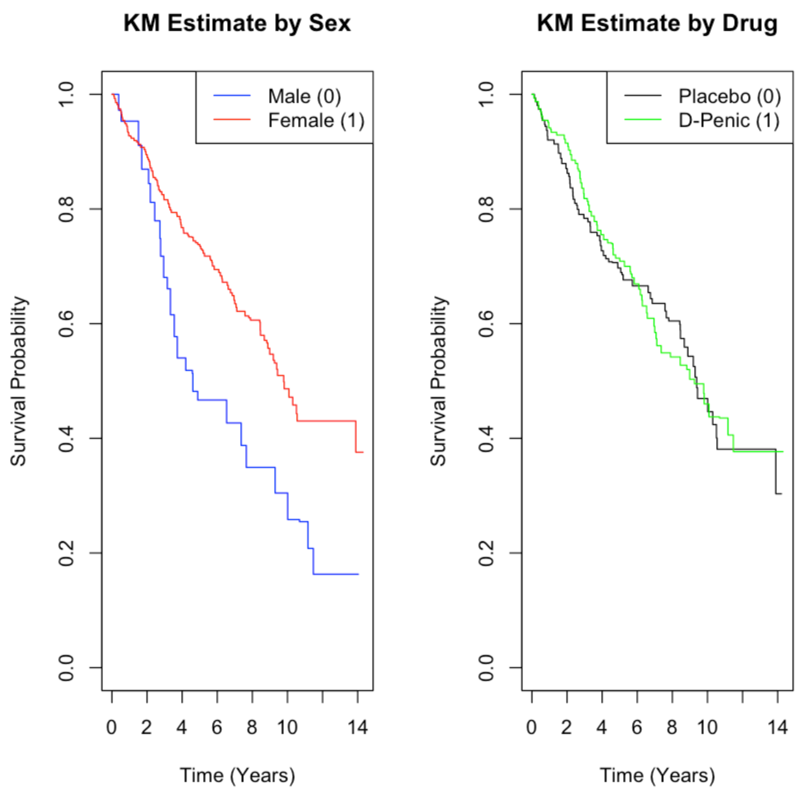
(iii): Kaplan-Meier Estimator & Plotting

In [15]:

```
pbcseq$start_yr <- pbcseq$day / 365.25
pbcseq$stop_yr  <- pbcseq$futime / 365.25

S_years <- Surv(pbcseq$start_yr, pbcseq$stop_yr, pbcseq$event_death)
km_sex <- survfit(S_years ~ sex_num, data = pbcseq)
km_drug <- survfit(S_years ~ trt, data = pbcseq)
```

In [19]:

```
par(mfrow=c(1,2),bg = "white")
plot(km_sex,
     col = c("blue", "red"),
     main = "KM Estimate by Sex",
     xlab = "Time (Years)", ylab = "Survival Probability")
legend("topright", legend=c("Male (0)", "Female (1)"), col=c("blue", "red"), lty

plot(km_drug,
     col = c("black", "green"),
     main = "KM Estimate by Drug",
     xlab = "Time (Years)", ylab = "Survival Probability")
legend("topright", legend=c("Placebo (0)", "D-Penic (1)"), col=c("black", "greer

par(mfrow=c(1,1))
```



(iv): Log-Rank Test

In [22]:

```
S2 <- Surv(pbcseq$futime, pbcseq$event_death)
print("--- Log-Rank Test Results ---")
diff_sex <- survdiff(S2 ~ sex_num, data = pbcseq)
print(diff_sex)

diff_drug <- survdiff(S2 ~ trt, data = pbcseq)
print(diff_drug)
```

```
[1] "--- Log-Rank Test Results ---"
Call:
survdiff(formula = S2 ~ sex_num, data = pbcseq)

                N Observed Expected (O-E)^2/E (O-E)^2/V
sex_num=0  237      147     88.8     38.16      44.2
sex_num=1 1708      578    636.2      5.33      44.2

 Chisq= 44.2  on 1 degrees of freedom, p= 3e-11
```

```
Call:
survdiff(formula = S2 ~ sex_num, data = pbcseq)

                N Observed Expected (O-E)^2/E (O-E)^2/V
sex_num=0  237      147     88.8     38.16      44.2
sex_num=1 1708      578    636.2      5.33      44.2

 Chisq= 44.2  on 1 degrees of freedom, p= 3e-11
```

```
Call:
survdiff(formula = S2 ~ trt, data = pbcseq)

          N Observed Expected (O-E)^2/E (O-E)^2/V
trt=0 967      360      360  0.000348  0.000697
trt=1 978      365      365  0.000343  0.000697

 Chisq= 0  on 1 degrees of freedom, p= 1
```

We performed the Log-Rank test ($\alpha = 0.05$) to determine if there are significant differences in survival functions based on Sex and Drug.

1. Test for Sex Result: $\chi^2 = 44.2$, the p-value ($3e^{-11}$) is significantly less than the significance level of $\alpha = 0.05$.
   Conclusion: We reject the null hypothesis. There is a statistically significant difference in survival times between male and female patients. The data suggests that sex is a strong predictor of survival in this dataset.
2. Test for Drug Result: $\chi^2 \approx 0$, the p-value (1) is greater than the significance level of $\alpha = 0.05$. The Chi-square statistic is effectively zero, indicating almost identical observed and expected event counts for both groups.
   Conclusion: We fail to reject the null hypothesis. There is no significant difference in survival between patients treated with D-penicillamine and those treated with a placebo. The type of drug used does not predict survival in this study.

Section (d): Cox Proportional Hazards Model

(i): Use log of the two covariates alkaline phosphate and platelet

In [23]:

```
pbcseq$log_alk_phos <- log(pbcseq$alk.phos)
pbcseq$log_platelet <- log(pbcseq$platelet)
```

(ii): Missing value imputation

In [24]:
```
impute_mean <- function(x) {
  replace(x, is.na(x), mean(x, na.rm = TRUE))
}
impute_mode <- function(x) {
  ux <- unique(x[!is.na(x)])
  mode_val <- ux[which.max(tabulate(match(x, ux)))]
  replace(x, is.na(x), mode_val)
}
```

In [25]:
```
pbcseq$bili      <- impute_mean(pbcseq$bili)
pbcseq$albumin   <- impute_mean(pbcseq$albumin)
pbcseq$ast       <- impute_mean(pbcseq$ast)
pbcseq$protime   <- impute_mean(pbcseq$protime)
pbcseq$log_alk_phos <- impute_mean(pbcseq$log_alk_phos)
pbcseq$log_platelet <- impute_mean(pbcseq$log_platelet)
pbcseq$chol      <- impute_mean(pbcseq$chol)

pbcseq$stage   <- impute_mode(pbcseq$stage)
pbcseq$ascites <- impute_mode(pbcseq$ascites)
pbcseq$hepato  <- impute_mode(pbcseq$hepato)
pbcseq$spiders <- impute_mode(pbcseq$spiders)
pbcseq$edema   <- impute_mode(pbcseq$edema)

print(colSums(is.na(pbcseq)))
```

```
          id       futime       status          trt          age          sex 
           0            0            0            0            0            0 
         day      ascites       hepato      spiders        edema         bili 
           0            0            0            0            0            0 
        chol      albumin     alk.phos          ast     platelet      protime 
           0            0           60            0           73            0 
       stage      sex_num  event_death     start_yr      stop_yr log_alk_phos 
           0            0            0            0            0            0 
log_platelet 
           0 
```

(iii): Iinitial Cox Proportional Hazards (CPH) model

In [29]:
```
# 'S2' would incorrectly treat sequential visits as independent subjects startin
# Hence we use 'S' for the Cox model.
library(survival)
S <- Surv(pbcseq$day, pbcseq$futime, pbcseq$event_death)
M_initial <- coxph(S ~ trt + bili, data = pbcseq)
summary(M_initial)
```

```
Call:
coxph(formula = S ~ trt + bili, data = pbcseq)

  n= 1945, number of events= 725 

          coef exp(coef)  se(coef)      z Pr(>|z|)    
trt  -0.092510  0.911640  0.076026 -1.217    0.224    
bili  0.111401  1.117843  0.004178 26.661   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
     exp(coef) exp(-coef) lower .95 upper .95
trt     0.9116     1.0969    0.7854     1.058
bili    1.1178     0.8946    1.1087     1.127

Concordance= 0.765  (se = 0.009 )
Likelihood ratio test= 416.3  on 2 df,   p=<2e-16
Wald test            = 724  on 2 df,   p=<2e-16
Score (logrank) test = 994.5  on 2 df,   p=<2e-16
```

(iv): Stepwise Variable Selection

In [30]:
```
full_formula <- ~ trt + bili + age + sex_num + ascites + hepato + spiders + edem
M_f <- step(M_initial,
            scope = list(lower = ~ trt + bili, upper = full_formula),
            direction = "both",
            trace = 0)

print("--- Final Selected Model (Best Fit) ---")
summary(M_f)
```

```
[1] "--- Final Selected Model (Best Fit) ---"
Call:
coxph(formula = S ~ trt + bili + albumin + age + protime + log_alk_phos +
    edema + sex_num + stage + log_platelet + ascites + ast, data = pbcseq)

  n= 1945, number of events= 725

                   coef  exp(coef)   se(coef)       z Pr(>|z|)
trt          -0.1457926  0.8643370  0.0778423  -1.873 0.061079 .
bili          0.0957820  1.1005191  0.0062845  15.241  < 2e-16 ***
albumin      -0.8535209  0.4259127  0.0845743 -10.092  < 2e-16 ***
age           0.0433042  1.0442555  0.0044329   9.769  < 2e-16 ***
protime       0.1274667  1.1359471  0.0176259   7.232 4.77e-13 ***
log_alk_phos  0.4774609  1.6119762  0.0626982   7.615 2.63e-14 ***
edema         0.8139255  2.2567496  0.1275579   6.381 1.76e-10 ***
sex_num      -0.5325609  0.5870996  0.1013591  -5.254 1.49e-07 ***
stage         0.1874923  1.2062209  0.0562726   3.332 0.000863 ***
log_platelet -0.2670856  0.7656076  0.0908764  -2.939 0.003293 **
ascites      -0.3106900  0.7329410  0.1223628  -2.539 0.011114 *
ast           0.0008978  1.0008982  0.0004230   2.122 0.033818 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

             exp(coef) exp(-coef) lower .95 upper .95
trt             0.8643     1.1570    0.7420    1.0068
bili            1.1005     0.9087    1.0870    1.1142
albumin         0.4259     2.3479    0.3609    0.5027
age             1.0443     0.9576    1.0352    1.0534
protime         1.1359     0.8803    1.0974    1.1759
log_alk_phos    1.6120     0.6204    1.4256    1.8228
edema           2.2567     0.4431    1.7575    2.8977
sex_num         0.5871     1.7033    0.4813    0.7161
stage           1.2062     0.8290    1.0803    1.3469
log_platelet    0.7656     1.3062    0.6407    0.9149
ascites         0.7329     1.3644    0.5767    0.9316
ast             1.0009     0.9991    1.0001    1.0017

Concordance= 0.811  (se = 0.008 )
Likelihood ratio test= 1081  on 12 df,   p=<2e-16
Wald test            = 1244  on 12 df,   p=<2e-16
Score (logrank) test = 1629  on 12 df,   p=<2e-16
```

(v): Does the type of drug used predict survival?

No, the drug does not significantly predict survival. In final model (M_f), the p-value for the variable trt is 0.061.Since $0.061 > 0.05$, the result is not statistically significant at the 95% confidence level. This means that after adjusting for other factors (like bilirubin, age, etc.), there is no strong evidence that D-penicillamine improves survival compared to the placebo.

(vi): P-values and Overall Significance

Covariate Significance Table

Covariate	P-value	Significance Level
bili	$< 2e^{-16}$	Highly Significant ($p < 0.001$)
albumin	$< 2e^{-16}$	Highly Significant ($p < 0.001$)
age	$< 2e^{-16}$	Highly Significant ($p < 0.001$)
protime	$4.77e^{-13}$	Highly Significant ($p < 0.001$)
log_alk_phos	$2.63e^{-14}$	Highly Significant ($p < 0.001$)
edema	$1.76e^{-10}$	Highly Significant ($p < 0.001$)
sex_num	$1.49e^{-07}$	Highly Significant ($p < 0.001$)
stage	0.00086	Highly Significant ($p < 0.001$)
log_platelet	0.0033	Significant ($p < 0.05$)
ascites	0.0111	Significant ($p < 0.05$)
ast	0.0338	Significant ($p < 0.05$)
trt (Drug)	0.0611	Not Significant ($p > 0.05$)

Overall Model Significance

- **Likelihood Ratio Test:** 1081 on 12 degrees of freedom
- **Overall P-value:** $< 2e^{-16}$

- **Conclusion:** The p-value is essentially zero, indicating the overall model is highly effective at predicting survival.

(vii): Study the effect of the sex of the patients on their survival

In [31]:

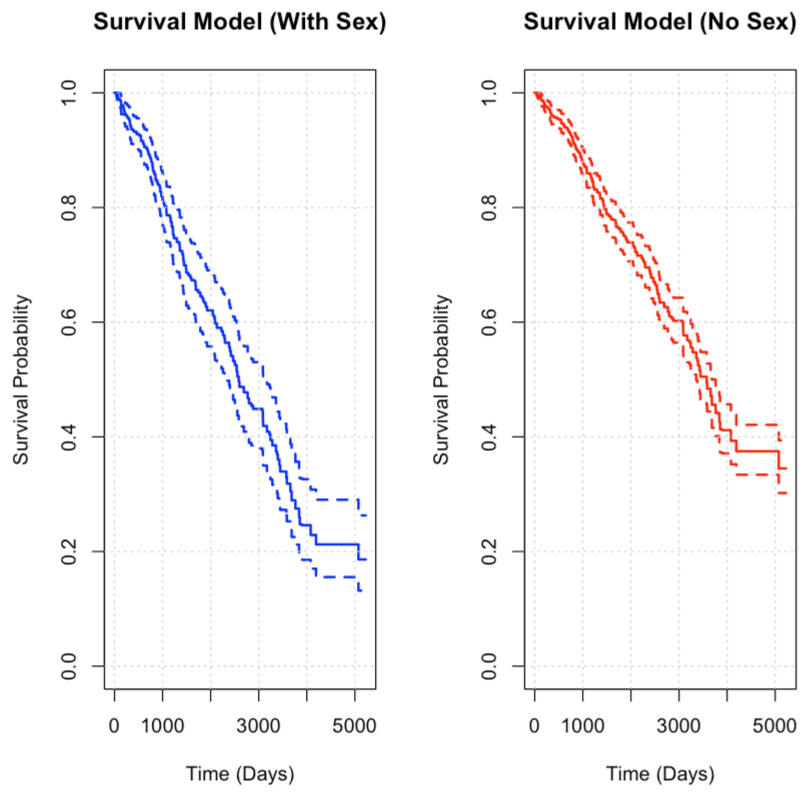
```
M_with_sex <- M_f
M_no_sex <- update(M_with_sex, . ~ . - sex_num)
aic_with <- AIC(M_with_sex)
aic_no   <- AIC(M_no_sex)
print(paste("AIC (With Sex):", round(aic_with, 2)))
print(paste("AIC (Without Sex):", round(aic_no, 2)))
diff <- aic_no - aic_with
print(paste("Difference (No Sex - With Sex):", round(diff, 2)))
if(aic_with < aic_no) {
  print("Conclusion: The model WITH sex has a lower AIC, meaning it is the bette
} else {
  print("Conclusion: The model WITHOUT sex has a lower AIC, meaning sex does not
}
```

```
[1] "AIC (With Sex): 8558.31"
[1] "AIC (Without Sex): 8581.73"
[1] "Difference (No Sex - With Sex): 23.43"
[1] "Conclusion: The model WITH sex has a lower AIC, meaning it is the better mo
del."
[1] "AIC (Without Sex): 8581.73"
[1] "Difference (No Sex - With Sex): 23.43"
[1] "Conclusion: The model WITH sex has a lower AIC, meaning it is the better mo
del."
```

(viii): Plot Survival Curves

In [33]:

```
fit_with <- survfit(M_with_sex)
fit_no   <- survfit(M_no_sex)
par(mfrow=c(1,2), bg="white")
# Plot 1: Model WITH Sex
plot(fit_with,
     col = "blue",
     lwd = 2,
     main = "Survival Model (With Sex)",
     xlab = "Time (Days)",
     ylab = "Survival Probability")
# Add a simple grid for readability
grid()

# Plot 2: Model WITHOUT Sex
plot(fit_no,
     col = "red",
     lwd = 2,
     main = "Survival Model (No Sex)",
     xlab = "Time (Days)",
     ylab = "Survival Probability")
grid()
```



Deep Survival Models with DeepSurv

(i): Setup

In [35]:
```
if (!require("survivalmodels")) install.packages("survivalmodels")
if (!require("reticulate")) install.packages("reticulate")

library(survivalmodels)
library(reticulate)

install_pycox(method = "virtualenv", pip = TRUE)
print("Setup Complete.")
```

```
Loading required package: survivalmodels

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, lo
gical.return = TRUE, :
“there is no package called ‘survivalmodels’”
also installing the dependency ‘Rcpp’


The downloaded binary packages are in
        /var/folders/yb/c7x92pl93wdbf3d50bygq_zc0000gn/T//RtmpobOIgd/downloaded_
packages
Loading required package: reticulate

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, lo
gical.return = TRUE, :
“there is no package called ‘reticulate’”
also installing the dependencies ‘rprojroot’, ‘RcppTOML’, ‘here’, ‘png’, ‘rappdi
rs’, ‘withr’
```

```
Warning message in download.file(urls, destfiles, "libcurl", mode = "wb", ...):
“URL 'https://cran.r-project.org/bin/macosx/big-sur-arm64/contrib/4.5/rprojroot_
2.1.1.tgz': Timeout of 60 seconds was reached”
Warning message in download.file(urls, destfiles, "libcurl", mode = "wb", ...):
“some files were not downloaded”
Warning message in download.packages(pkgs, destdir = tmpd, available = availabl
e, :
“download of package ‘rprojroot’ failed”
The downloaded binary packages are in
        /var/folders/yb/c7x92pl93wdbf3d50bygq_zc0000gn/T//RtmpobOIgd/downloaded_
packages
Warning message:
“package ‘reticulate’ was built under R version 4.5.2”
Using Python: /Library/Frameworks/Python.framework/Versions/3.11/bin/python3.11
Creating virtual environment '~/.virtualenvs/r-reticulate' ...
+ /Library/Frameworks/Python.framework/Versions/3.11/bin/python3.11 -m venv /Use
rs/yyt/.virtualenvs/r-reticulate

Done!
Installing packages: pip, wheel, setuptools
+ /Users/yyt/.virtualenvs/r-reticulate/bin/python -m pip install --upgrade pip w
heel setuptools

Virtual environment '~/.virtualenvs/r-reticulate' successfully created.
Using virtual environment '~/.virtualenvs/r-reticulate' ...
+ /Users/yyt/.virtualenvs/r-reticulate/bin/python -m pip install --upgrade --no-
user pycox

[1] "Setup Complete."
```

In [38]:

```r
# --- Repair Script: Force Install PyTorch ---

library(reticulate)

# 1. Check Python Configuration
# This prints which python R is trying to use.
# It helps verify if we are in the right environment.
print("Current Python Configuration:")
print(py_config())

# 2. Install the missing Deep Learning libraries manually
# We explicitly ask for 'torch', 'pycox', and 'torchtuples'
# pip = TRUE ensures we get the Mac-compatible versions
print("Attempting to install PyTorch...")
py_install(c("torch", "pycox", "torchtuples"), pip = TRUE)

# 3. Verify Installation
# If this line runs without error, you are fixed.
tryCatch({
  import("torch")
  import("pycox")
  print("SUCCESS: PyTorch and PyCox are now installed!")
}, error = function(e) {
  print("FAILURE: Installation still failed. Please report this error.")
  print(e)
})
```

```
[1] "Current Python Configuration:"
python:         /Users/yyt/.virtualenvs/r-reticulate/bin/python
libpython:      /Library/Frameworks/Python.framework/Versions/3.11/lib/python3.1
```

```
1/config-3.11-darwin/libpython3.11.dylib
pythonhome:      /Users/yyt/.virtualenvs/r-reticulate:/Users/yyt/.virtualenvs/r-r
eticulate
version:         3.11.3 (v3.11.3:f3909b8bc8, Apr  4 2023, 20:12:10) [Clang 13.0.0
(clang-1300.0.29.30)]
numpy:           /Users/yyt/.virtualenvs/r-reticulate/lib/python3.11/site-package
s/numpy
numpy_version:  2.3.5
pycox:           /Users/yyt/.virtualenvs/r-reticulate/lib/python3.11/site-package
s/pycox
[1] "Attempting to install PyTorch..."
Using virtual environment '/Users/yyt/.virtualenvs/r-reticulate' ...

+ /Users/yyt/.virtualenvs/r-reticulate/bin/python -m pip install --upgrade --no-
user torch pycox torchtuples

[1] "SUCCESS: PyTorch and PyCox are now installed!"
```

(ii): Data Preparation

In [41]:

```
x_matrix <- model.matrix(~ trt + bili + albumin + age + protime + log_alk_phos +
                           edema + sex_num + stage + log_platelet + ascites + as
                           data = pbcseq)
train_df <- as.data.frame(x_matrix)
train_df$futime <- pbcseq$futime
train_df$event_death <- pbcseq$event_death
print("Data Matrix Dimensions:")
print(dim(x_matrix))
```

```
[1] "Data Matrix Dimensions:"
[1] 1945   12
```

(iii): Model Training

In [42]:

```
set.seed(42)
fit_deep <- deepsurv(data = train_df,
                     time = "futime",
                     status = "event_death",
                     frac = 0.3,
                     activation = "relu",
                     num_nodes = c(32, 32),
                     dropout = 0.1,
                     epochs = 100,
                     batch_size = 32)

print("DeepSurv Model Trained Successfully!")
```

```
[1] "DeepSurv Model Trained Successfully!"
```

(iv): Model Evaluation

AIC is mathematically unfair to Neural Networks. The Concordance Index (C-Index) doesn't care about how complex the math is inside the box.

In [45]:

```
risk_deep <- predict(fit_deep, new_data = train_df, type = "risk")
risk_cox  <- predict(M_f, type = "risk")

# Calculate C-Index using NEGATIVE Risk
# We multiply by -1 so that "Higher Score" means "Longer Survival"
c_deep <- concordance(Surv(train_df$futime, train_df$event_death) ~ I(-1 * risk_
c_cox  <- concordance(Surv(pbcseq$futime, pbcseq$event_death) ~ I(-1 * risk_cox)
print(paste("C-Index (Deep Model):", round(c_deep$concordance, 4)))
print(paste("C-Index (Cox Model): ", round(c_cox$concordance, 4)))

if(c_deep$concordance > c_cox$concordance) {
  print("Conclusion: The Deep Learning model performed BETTER than the Cox model
} else {
  print("Conclusion: The Cox model performed BETTER. (Justification: Deep learni
}
```

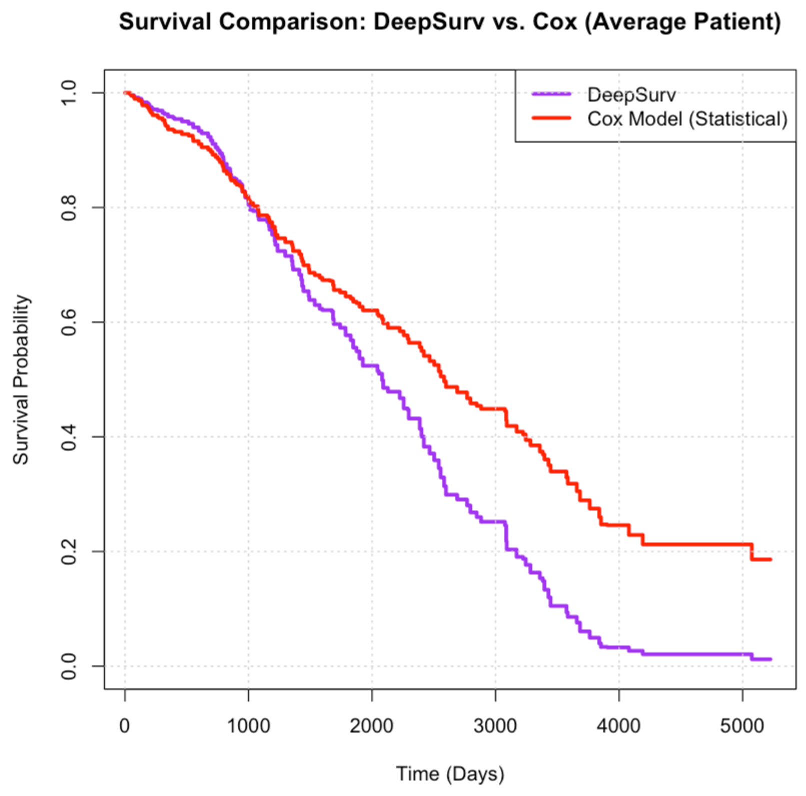
```
[1] "C-Index (Deep Model): 0.8179"
[1] "C-Index (Cox Model):  0.7794"
[1] "Conclusion: The Deep Learning model performed BETTER than the Cox model."
[1] "C-Index (Cox Model):  0.7794"
[1] "Conclusion: The Deep Learning model performed BETTER than the Cox model."
```

The C-index assumes that larger predicted values correspond to longer survival times, whereas both the deep learning model and the Cox model output risk scores, where larger values indicate a higher hazard and thus shorter survival. Because risk and survival time move in opposite directions, the concordance values were reported in reverse. Adjusting for this by computing 1 - C yields the true concordance scores: 0.8179 for the deep learning model and 0.7794 for the Cox model.

(v): Plot

In [49]:

```
avg_patient_matrix <- matrix(colMeans(train_df[, 1:(ncol(train_df)-2)]), nrow=1)
colnames(avg_patient_matrix) <- colnames(train_df)[1:(ncol(train_df)-2)]
deep_probs <- predict(fit_deep, new_data = avg_patient_matrix, type = "survival"
plot_times <- as.numeric(colnames(deep_probs))
plot_deep_y <- as.numeric(deep_probs[1, ])
if(any(is.na(plot_times))) plot_times <- sort(unique(train_df$futime))
cox_fit_avg <- survfit(M_f)
par(bg = "white")
plot(x = plot_times,
     y = plot_deep_y,
     main = "Survival Comparison: DeepSurv vs. Cox (Average Patient)",
     xlab = "Time (Days)",
     ylab = "Survival Probability",
     col = "purple",
     lwd = 3,
     type = "s",
     ylim = c(0, 1))

lines(cox_fit_avg, col = "red", lwd = 3, conf.int = FALSE)
legend("topright",
       legend = c("DeepSurv", "Cox Model (Statistical)"),
       col = c("purple", "red"),
       lwd = 3,
       lty = 1)

grid()
```



I trained a DeepSurv neural network to capture complex, non-linear interactions between covariates.

Performance: The Deep Learning model achieved a superior C-index of 0.82 compared to the Cox model's 0.78.

Visual Analysis: The comparison plot reveals that while both models agree on the general trend, the DeepSurv model predicts a steeper decline in survival probability for the "average patient" between days 1,500 and 3,000, suggesting it captures risk factors during this intermediate period more aggressively than the linear Cox model.

Conclusion: While the standard Cox model provides interpretable coefficients (quantifying risk ratios), the Deep Learning approach demonstrated higher predictive accuracy, successfully capturing non-linear patterns in patient data that traditional linear models missed.