

SurvComp: a package for performance assessment and comparison for survival analysis

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Contents

| | | |
|----------|---|-----------|
| 1 | Introduction | 2 |
| 1.1 | Installation | 2 |
| 1.2 | Further help | 2 |
| 1.3 | Citing | 2 |
| 2 | A use case: from expression data to survival analysis | 2 |
| 2.1 | Overview | 3 |
| 2.2 | Computing concordance index, D index and hazard ratio | 4 |
| 2.3 | Combining estimations across datasets | 6 |
| 2.4 | The forestplot.surv | 7 |
| 2.5 | Kaplan Meier survival curves | 18 |
| 2.6 | Meta analysis of estimation values | 21 |
| 3 | Session Info | 24 |
| 4 | Functions within SurvComp | 25 |

1 Introduction

The *SurvComp* package is providing functions to assess and to statistically compare the performance of risk prediction (survival) models. It includes (i) implementation of state-of-the-art statistics developed to measure the performance of risk prediction models and (ii) to combine these statistics estimated from multiple datasets using a meta-analytical framework, functions (iii) to visualize those measurements in a clear and compact way, and (iv) to statistically compare the performance of competitive models.

1.1 Installation

SurvComp requires that *survival*, *ipred*, *prodlm*, *survivalROC*, *SuppDists*, *bootstrap* and *R* ($\geq 2.3.0$) are installed. These should be installed automatically when you install *SurvComp*. To install *SurvComp*, source *biocLite* from *bioconductor*:

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("survcomp")
```

Load the *SurvComp*, into your current workspace:

```
> library(survcomp)
```

1.2 Further help

To view the *SurvComp* description and a summary of all the functions within *SurvComp*, type the following:

```
> library(help = survcomp)
```

1.3 Citing

We are delighted if you use this package. Please do email us if you find a bug or have a suggestion. We would be very grateful if you could cite:

B. Haibe-Kains, C. Desmedt, C. Sotiriou and G. Bontempi (2008) A comparative study of survival models for breast cancer prognostication based on microarray data: does a single gene beat them all? *Bioinformatics* **24(19)**:2200-2208.

2 A use case: from expression data to survival analysis

We will very briefly demonstrate some of the functions in *SurvComp*. We use the *breastCancerData* datafile for demonstration purposes, it includes subsets of the datasets *breastCancerMAINZ*, *breastCancerTRANSBIG*, *breastCancerUPP*, *breastCancerUNT*, *breastCancerVDX* and *breastCancerNKI*, available as experimental datapackages on *Bioconductor*. The six

datasets in `breastCancerData` contain the genes AURKA (also known as STK6, STK7, or STK15), PLAU (also known as uPA), STAT1, VEGF, CASP3, ESR1, and ERBB2, as introduced by Desmedt et al. 2008 [1]. The seven genes represent the proliferation, tumor invasion/metastasis, immune response, angiogenesis, apoptosis phenotypes, and the ER and HER2 signaling, respectively.

2.1 Overview

To use the `ExpressionSet` object we have to load the *Biobase* package. We also make use of the package *xtable* in order to visualize some of the results as tables in this Vignette.

```
> library(Biobase)
> library(xtable)
```

Loading the `breastCancerData` object will result in 6 new objects. If you execute `ls()` you will see `mainz7g`, `transbig7g`, `upp7g`, `unt7g`, `vd7g` and `nki7g`. More details about these datasets are available in the `breastCancerData` manpage (`?breastCancerData`).

```
> data(breastCancerData)
> mainz7g
```

```
ExpressionSet (storageMode: lockedEnvironment)
assayData: 7 features, 200 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: MAINZ_BC6001 MAINZ_BC6002 ... MAINZ_BC6232 (200 total)
  varLabels: samplename dataset ... e.os (21 total)
  varMetadata: labelDescription
featureData
  featureNames: 205225_at 216836_s_at ... 202763_at (7 total)
  fvarLabels: probe Gene.title ... GO.Component.1 (22 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
pubMedIds: 18593943
Annotation: hgu133a
```

Before we can start the analysis, we have to define the annotation for the mentioned seven genes, the datasets we use and a few help-variables. We define the gene symbol list (`gsList`), the entrez-gene ID list (`gidList`), the probe names for the Agilent microarray (`probesNki`), the probe names for the Affymetrix microarray (`probesAffy`), a list containing the dataset names (`datasetList`), spaces for displaying the text in the forestplot at the right place (`myspace` and `mybigspace`) and `tc` for setting the censored time to 10 years. We converted the gene symbols for each gene to lowercase for better separation from the datasets. Table 1 gives an overview of the gene annotation.

| | Gene Symbol | Gene ID | Probes Agilent | Probes Affy |
|---|-------------|---------|----------------|-------------|
| 1 | esr1 | 2099 | NM_000125 | 205225_at |
| 2 | erbb2 | 2064 | NM_004448 | 216836_s_at |
| 3 | aurka | 6790 | NM_003600 | 208079_s_at |
| 4 | plau | 5328 | NM_002658 | 211668_s_at |
| 5 | vegfa | 7422 | NM_003376 | 211527_x_at |
| 6 | stat1 | 6772 | NM_007315 | 209969_s_at |
| 7 | casp3 | 836 | NM_004346 | 202763_at |

Table 1: Overview of the annotation of the seven genes.

```
> gsList <- tolower(fData(mainz7g)[, "Gene.symbol"])
> gidList <- fData(mainz7g)[, "Gene.ID"]
> probesNKI <- as.character(fData(nki7g)[, "probe"])
> probesAffy <- fData(mainz7g)[, "probe"]
> datasetList <- c("MAINZ", "TRANSBIG", "UPP", "UNT", "VDX", "NKI",
+   "", "Overall")
> myspace <- " "
> mybigspace <- "   "
> tc <- 10 * 365
```

2.2 Computing concordance index, D index and hazard ratio

To compute the concordance index [2, 3] for each gene in each dataset, we have to call the `concordance.index()` function for each dataset. See `'?concordance.index'` for details. The following command shows the computation of the concordance index for each gene in the `mainz7g` dataset.

```
> cindexall.mainz.small <- t(apply(X = exprs(mainz7g), MARGIN = 1,
+   function(x, y, z) {
+     tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+       method = "noether", na.rm = TRUE)
+     return(c(cindex = tt$c.index, cindex.se = tt$se, lower = tt$lower,
+       upper = tt$upper))
+   }, y = pData(mainz7g)[, "t.dmfs"], z = pData(mainz7g)[, "e.dmfs"]))
```

To compute the D index [4] for each gene in each dataset, we have to call the `D.index()` function. See `'?D.index'` for details. The following command shows the computation of the D index for each gene in the `mainz7g` dataset.

```
> dindexall.mainz.small <- t(apply(X = exprs(mainz7g), MARGIN = 1,
+   function(x, y, z) {
```

| | Min | Max |
|----------|-------|-------|
| MAINZ | 4.05 | 14.57 |
| TRANSBIG | 4.87 | 15.18 |
| UPP | 4.13 | 11.22 |
| UNT | -5.04 | 3.77 |
| VDX | 2.77 | 15.61 |
| NKI | -1.62 | 0.93 |

Table 2: Overview of the gene expression ranges in the six datasets.

```
+      tt <- D.index(x = x, surv.time = y, surv.event = z, na.rm = TRUE)
+      return(c(dindex = tt$d.index, dindex.se = tt$se, lower = tt$lower,
+              upper = tt$upper))
+    }, y = pData(mainz7g)[, "t.dmfs"], z = pData(mainz7g)[, "e.dmfs"])]
```

To compute the hazard ratio [5] for each gene in each dataset, we have to call the `hazard.ratio()` function. See `?hazard.ratio` for details. Before we compute the hazard ratio, we have to rescale the gene expression data for each dataset to a comparable scale, since the Affymetrix and Agilent microarrays have a different range of their gene expression, which would affect the hazard ratio computation. Table 2 gives an overview of the gene expression ranges in the six datasets that are included in `breastCancerData`.

Therefore we use the following function to rescale the gene expression values to lie approximately in $[-1,1]$, robust to extreme values (possibly outliers).

```
> rescale <- function(x, na.rm = FALSE, q = 0.05) {
+   ma <- quantile(x, probs = 1 - (q/2), na.rm = na.rm)
+   mi <- quantile(x, probs = q/2, na.rm = na.rm)
+   x <- (x - mi)/(ma - mi)
+   return((x - 0.5) * 2)
+ }
```

The following command shows the rescaling and the computation of the hazard ratio for each gene in the `mainz7g` dataset.

```
> hratio.mainz.small <- t(apply(X = rescale(exprs(mainz7g), q = 0.05,
+   na.rm = TRUE), MARGIN = 1, function(x, y, z) {
+   tt <- hazard.ratio(x = x, surv.time = y, surv.event = z,
+   na.rm = TRUE)
+   return(c(hratio = tt$hazard.ratio, hratio.se = tt$se, lower = tt$lower,
+   upper = tt$upper))
+ }, y = pData(mainz7g)[, "t.dmfs"], z = pData(mainz7g)[, "e.dmfs"])]
```

| | cindex | cindex.se | lower | upper |
|-------|--------|-----------|-------|-------|
| esr1 | 0.46 | 0.02 | 0.43 | 0.49 |
| erbb2 | 0.50 | 0.02 | 0.47 | 0.53 |
| aurka | 0.64 | 0.01 | 0.62 | 0.67 |
| plau | 0.52 | 0.01 | 0.49 | 0.55 |
| vegfa | 0.56 | 0.01 | 0.53 | 0.59 |
| stat1 | 0.53 | 0.01 | 0.51 | 0.56 |
| casp3 | 0.52 | 0.01 | 0.50 | 0.55 |

Table 3: Combined concordance indices of each gene for the six datasets.

To get an overall estimate over all datasets for the concordance index from each gene, we iterate over all the concordance indices of all datasets and combine them with the `combine.est()` function [6] and recalculate the lower- and upper border accordingly. We do that for the D indices and the hazard ratios in the same way.

2.3 Combining estimations across datasets

```
> tt <- as.data.frame(NULL)
> for (i in 1:7) {
+   tt <- rbind(tt, combine.est(x = cbind(cindexall.mainz.small[i,
+     "cindex"], cindexall.transbig.small[i, "cindex"], cindexall.upp.small[i,
+     "cindex"], cindexall.unt.small[i, "cindex"], cindexall.vdx.small[i,
+     "cindex"], cindexall.nki.small[i, "cindex"]), x.se = cbind(cindexall.mainz.
+     "cindex.se"], cindexall.transbig.small[i, "cindex.se"],
+     cindexall.upp.small[i, "cindex.se"], cindexall.unt.small[i,
+     "cindex.se"], cindexall.vdx.small[i, "cindex.se"],
+     cindexall.nki.small[i, "cindex.se"]), ))
+ }
> tt$lower <- tt$estimate + qnorm(0.025, lower.tail = TRUE) * tt$se
> tt$upper <- tt$estimate + qnorm(0.025, lower.tail = FALSE) *
+   tt$se
> rownames(tt) <- gsList
> colnames(tt) <- c("cindex", "cindex.se", "lower", "upper")
> ccindex <- tt
```

The combined concordance indices for the six datasets are shown in table 3.

The combined log2 D indices for the six datasets are shown in table 4.

The combined log2 hazard ratios for the six datasets are shown in table 5.

| | dindex | dindex.se | lower | upper |
|-------|--------|-----------|-------|-------|
| esr1 | -0.17 | -3.64 | -0.45 | 0.07 |
| erbb2 | 0.09 | -3.62 | -0.14 | 0.29 |
| aurka | 0.96 | -3.66 | 0.84 | 1.07 |
| plau | 0.24 | -3.63 | 0.03 | 0.42 |
| vegfa | 0.45 | -3.65 | 0.28 | 0.61 |
| stat1 | 0.19 | -3.69 | -0.01 | 0.37 |
| casp3 | 0.19 | -3.66 | -0.02 | 0.37 |

Table 4: Combined log2 D indices of each gene for the six datasets.

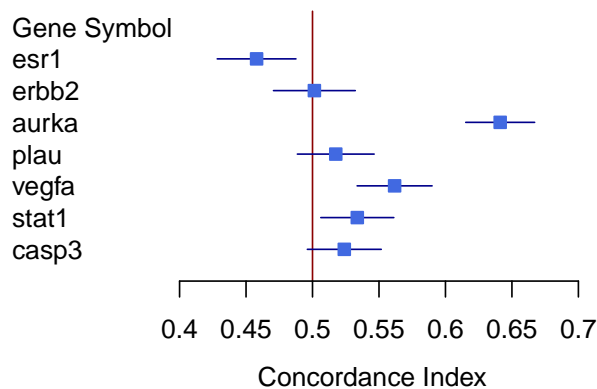
| | hratio | hratio.se | lower | upper |
|-------|--------|-----------|-------|-------|
| esr1 | -0.27 | -3.63 | -0.57 | -0.01 |
| erbb2 | 0.38 | -3.11 | 0.10 | 0.61 |
| aurka | 2.07 | -2.59 | 1.95 | 2.18 |
| plau | 0.84 | -2.34 | 0.50 | 1.13 |
| vegfa | 0.93 | -2.79 | 0.69 | 1.13 |
| stat1 | 0.48 | -2.68 | 0.12 | 0.76 |
| casp3 | 3.24 | -1.23 | 3.11 | 3.36 |

Table 5: Combined log2 hazard ratios of each gene for the six datasets.

2.4 The forestplot.surv

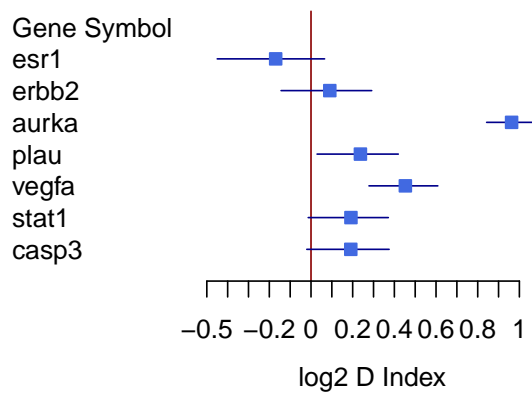
To display the combined concordance indices of each genes over all datasets, we use the `forestplot.surv()` function [7]. The resulting forestplot for all concordance indices is:

```
> labeltext <- cbind(c("Gene Symbol", gsList), c(rep(myspace, 8)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, ccindex$cindex)
> r.lower <- c(NA, ccindex$lower)
> r.upper <- c(NA, ccindex$upper)
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0.5, align = c("l"), graphwidth = unit(2,
+   "inches"), x.ticks = seq(0.4, 0.7, 0.05), xlab = paste("Concordance Index",
+   myspace, sep = ""), col = meta.colors(box = "royalblue",
+   line = "darkblue", zero = "darkred"), box.size = bs,
+   clip = c(0.4, 1))
```



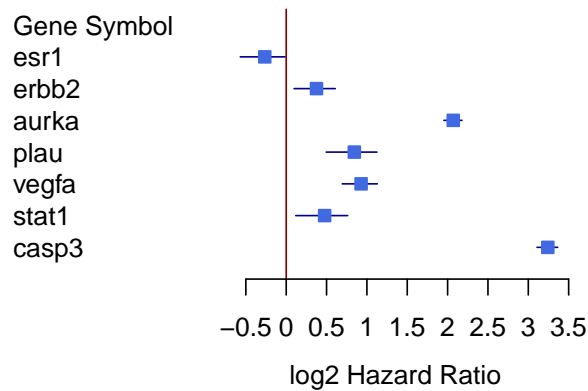
The resulting forestplot for all D indices is:

```
> labeltext <- cbind(c("Gene Symbol", gsList), c(rep(myspace, 8)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, log2(cdindex$dindex))
> r.lower <- c(NA, log2(cdindex$lower))
> r.upper <- c(NA, log2(cdindex$upper))
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0, align = c("l"), graphwidth = unit(2,
+   "inches"), x.ticks = seq(-0.5, 1, 0.1), xlab = paste("log2 D Index",
+   myspace, sep = ""), col = meta.colors(box = "royalblue",
+   line = "darkblue", zero = "darkred"), box.size = bs,
+   clip = c(-0.5, 1.25))
```

The resulting forestplot for all hazard ratios is:

```
> labeltext <- cbind(c("Gene Symbol", gsList), c(rep(mybigspace,
+      8)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, log2(chratio$hratio))
> r.lower <- c(NA, log2(chratio$lower))
> r.upper <- c(NA, log2(chratio$upper))
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0, align = c("l"), graphwidth = unit(2,
+     "inches"), x.ticks = seq(-0.5, 3.5, 0.5), xlab = paste("log2 Hazard Ratio",
+     myspace, sep = ""), col = meta.colors(box = "royalblue",
+     line = "darkblue", zero = "darkred"), box.size = bs,
+   clip = c(-0.75, 3.5))
```



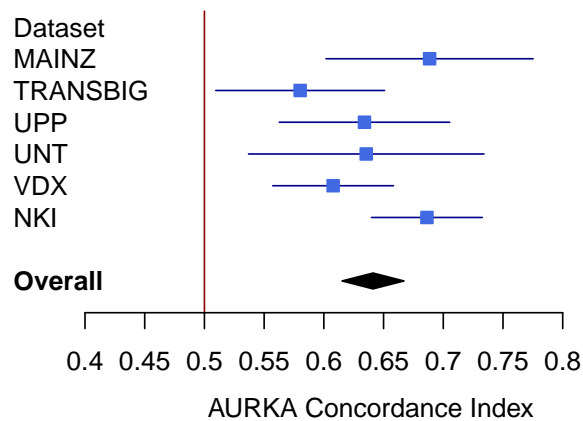
Taking a more specific look, e.g. at the genes AURKA and VEGF, we create the forestplot the same way as before, showing the concordance indices for both genes in each dataset and the combined estimation over all datasets.

```
> tt <- rbind(cindexall.mainz.small[3, ], cindexall.transbig.small[3,
+           ], cindexall.upp.small[3, ], cindexall.unt.small[3, ], cindexall.vdx.small[3,
+           ], cindexall.nki.small[3, ], NA, as.numeric(ccindex[3, ]))
> rownames(tt) <- datasetList
> tt <- as.data.frame(tt)
> labeltext <- cbind(c("Dataset", datasetList), c(rep(mybigspace,
+           length(datasetList) + 1)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, tt$cindex)
> r.lower <- c(NA, tt$lower)
> r.upper <- c(NA, tt$upper)
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+           upper = r.upper, zero = 0.5, align = c("l"), graphwidth = unit(2,
+           "inches"), x.ticks = seq(0.4, 0.8, 0.05), xlab = paste("AURKA Concordance I
```

```

+      myspace, sep = ""), col = meta.colors(box = "royalblue",
+      line = "darkblue", zero = "darkred"), box.size = bs,
+      clip = c(0.5, 1), is.summary = (c(rep(FALSE, 8), TRUE)))

```

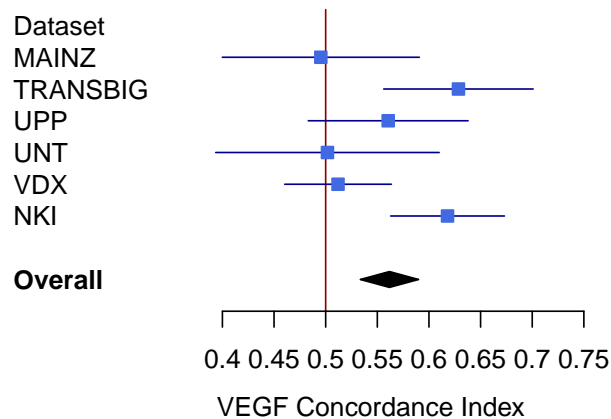


```

> tt <- rbind(cindexall.mainz.small[5, ], cindexall.transbig.small[5,
+   ], cindexall.upp.small[5, ], cindexall.unt.small[5, ], cindexall.vdx.small[5,
+   ], cindexall.nki.small[5, ], NA, as.numeric(ccindex[5, ]))
> rownames(tt) <- datasetList
> tt <- as.data.frame(tt)
> labeltext <- cbind(c("Dataset", datasetList), c(rep(mybigspace,
+   length(datasetList) + 1)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, tt$cindex)
> r.lower <- c(NA, tt$lower)
> r.upper <- c(NA, tt$upper)
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0.5, align = c("l"), graphwidth = unit(2,

```

```
+      "inches"), x.ticks = seq(0.4, 0.75, 0.05), xlab = paste("VEGF Concordance I
+      myspace, sep = ""), col = meta.colors(box = "royalblue",
+      line = "darkblue", zero = "darkred"), box.size = bs,
+      clip = c(0.3, 0.75), is.summary = (c(rep(FALSE, 8), TRUE)))
```



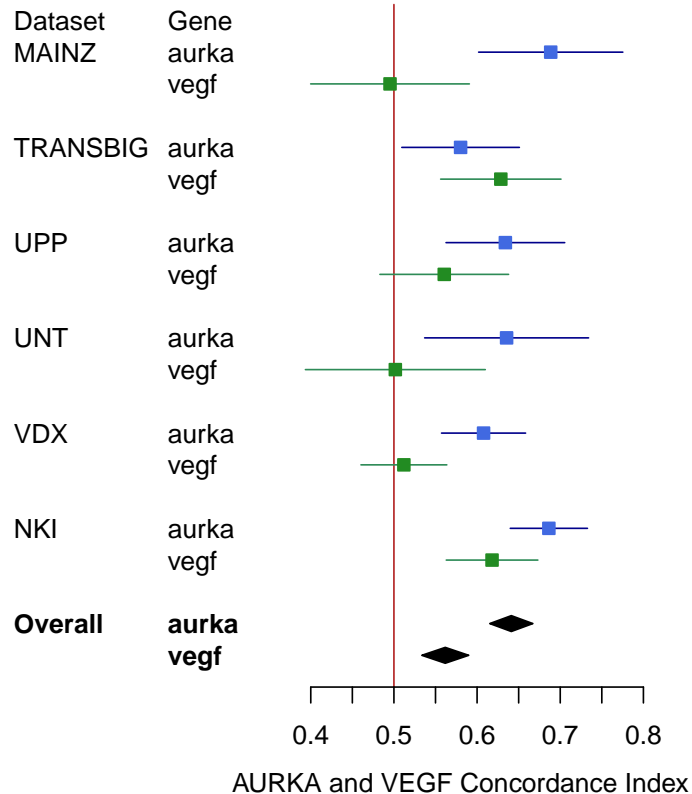
More advanced displaying of the genes AURKA and VEGF in a single forestplot with different colors and labels is possible:

```
> tt <- rbind(cindexall.mainz.small[3, ], cindexall.mainz.small[5,
+ ], NA, cindexall.transbig.small[3, ], cindexall.transbig.small[5,
+ ], NA, cindexall.upp.small[3, ], cindexall.upp.small[5, ],
+ NA, cindexall.unt.small[3, ], cindexall.unt.small[5, ], NA,
+ cindexall.vdx.small[3, ], cindexall.vdx.small[5, ], NA, cindexall.nki.small[3,
+ ], cindexall.nki.small[5, ], NA, as.numeric(ccindex[3,
+ ], as.numeric(ccindex[5, ]))
> rownames(tt) <- c("MAINZa", "MAINZv", "a", "TRANSBIGa", "TRANSBIGv",
+ "b", "UPPa", "UPPv", "c", "UNTa", "UNTv", "d", "VDXa", "VDXv",
+ "e", "NKIa", "NKIv", "f", "ALLa", "ALLv")
```

```

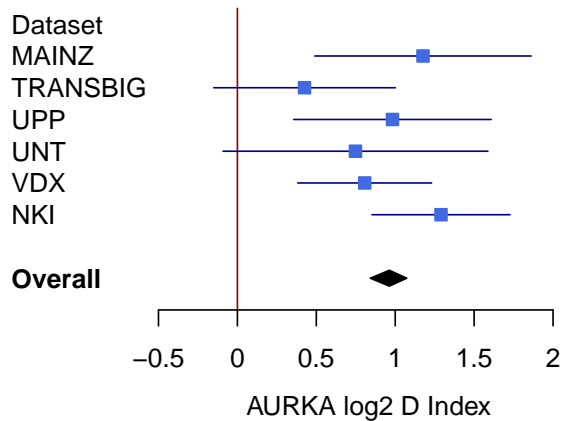
> tt <- as.data.frame(tt)
> labeltext <- cbind(c("Dataset", "MAINZ", NA, NA, "TRANSBIG",
+   NA, NA, "UPP", NA, NA, "UNT", NA, NA, "VDX", NA, NA, "NKI",
+   NA, NA, "Overall", NA), c("Gene", rep(c("aurka", "vegf",
+   NA), length(datasetList) - 2), c("aurka", "vegf")), c(rep(mybigspace,
+   21)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, tt$cindex)
> r.lower <- c(NA, tt$lower)
> r.upper <- c(NA, tt$upper)
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0.5, align = c("l"), graphwidth = unit(2,
+   "inches"), x.ticks = seq(0.4, 0.8, 0.05), xlab = paste("AURKA and VEGF Conc
+   myspace, sep = ""), col = meta.colors(line = c(rep(c(NA,
+   "darkblue", "seagreen"), 7)), zero = "firebrick", box = c(rep(c(NA,
+   "royalblue", "forestgreen"), 7))), box.size = bs, clip = c(0.3,
+   1), is.summary = (c(rep(FALSE, 19), TRUE, TRUE)))

```



We display the D indices for both genes in each dataset and the combined estimation over all datasets in the same way.

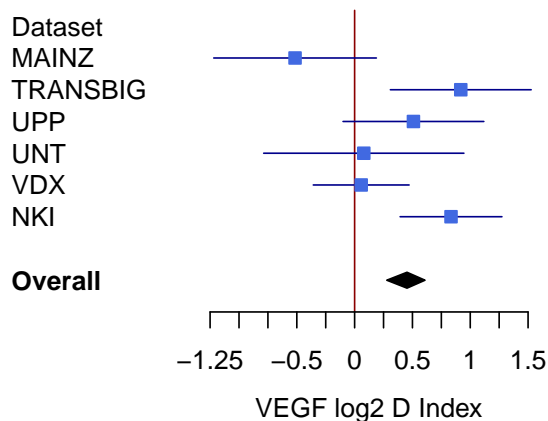
```
> tt <- rbind(dindexall.mainz.small[3, ], dindexall.transbig.small[3,
+ ], dindexall.upp.small[3, ], dindexall.unt.small[3, ], dindexall.vdx.small[3,
+ ], dindexall.nki.small[3, ], NA, as.numeric(cdindex[3, ]))
> rownames(tt) <- datasetList
> tt <- as.data.frame(tt)
> labeltext <- cbind(c("Dataset", datasetList), c(rep(mybigspace,
+   length(datasetList) + 1)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, log2(tt$dindex))
> r.lower <- c(NA, log2(tt$lower))
> r.upper <- c(NA, log2(tt$upper))
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0, align = c("l"), graphwidth = unit(2,
+     "inches"), x.ticks = seq(-0.5, 2, 0.5), xlab = paste("AURKA log2 D Index",
+     myspace, sep = ""), col = meta.colors(box = "royalblue",
+     line = "darkblue", zero = "darkred"), box.size = bs,
+   clip = c(-0.25, 2), is.summary = (c(rep(FALSE, 8), TRUE)))
```



```

> tt <- rbind(dindexall.mainz.small[5, ], dindexall.transbig.small[5,
+   ], dindexall.upp.small[5, ], dindexall.unt.small[5, ], dindexall.vdx.small[5,
+   ], dindexall.nki.small[5, ], NA, as.numeric(cdindex[5, ]))
> rownames(tt) <- datasetList
> tt <- as.data.frame(tt)
> labeltext <- cbind(c("Dataset", datasetList), c(rep(mybigspace,
+   length(datasetList) + 1)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, log2(tt$dindex))
> r.lower <- c(NA, log2(tt$lower))
> r.upper <- c(NA, log2(tt$upper))
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+   upper = r.upper, zero = 0, align = c("l"), graphwidth = unit(2,
+   "inches"), x.ticks = seq(-1.25, 1.5, 0.25), xlab = paste("VEGF log2 D Index",
+   myspace, sep = ""), col = meta.colors(box = "royalblue",
+   line = "darkblue", zero = "darkred"), box.size = bs,
+   clip = c(-1.5, 1.75), is.summary = (c(rep(FALSE, 8), TRUE)))

```

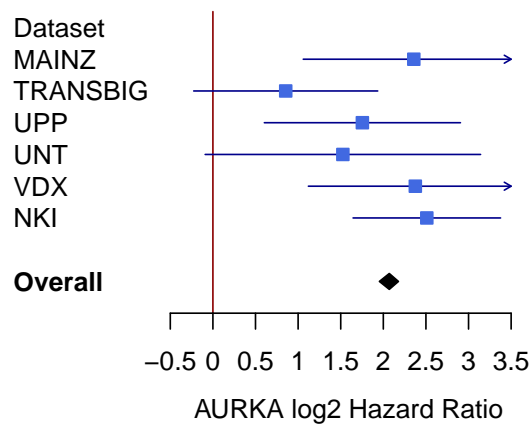


And at last the hazard ratio for the gene AURKA in each dataset and the combined estimation over all datasets.

```
> tt <- rbind(hratio.mainz.small[3, ], hratio.transbig.small[3,
+ ], hratio.upp.small[3, ], hratio.unt.small[3, ], hratio.vdx.small[3,
+ ], hratio.nki.small[3, ], NA, as.numeric(chratio[3, ]))
> rownames(tt) <- datasetList
> tt <- as.data.frame(tt)
> labeltext <- cbind(c("Dataset", datasetList), c(rep(myspace,
+ length(datasetList) + 1)))
> bs <- rep(0.5, nrow(labeltext))
> r.mean <- c(NA, log2(tt$hratio))
> r.lower <- c(NA, log2(tt$lower))
> r.upper <- c(NA, log2(tt$upper))
> forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+ upper = r.upper, zero = 0, align = c("l"), graphwidth = unit(2,
+ "inches"), x.ticks = seq(-0.5, 3.5, 0.5), xlab = paste("AURKA log2 Hazard R
+ myspace, sep = ""), col = meta.colors(box = "royalblue",
```



```
+      line = "darkblue", zero = "darkred"), box.size = bs,
+      clip = c(-0.5, 3.5), is.summary = (c(rep(FALSE, 8), TRUE)))
```



The following small loop shows an easy way for creating several forestplots showing the concordance indices for a single gene for all datasets and the combined estimation over all datasets. The same can be done for the D indices and hazard ratios. Since it is not yet possible to combine several forestplots in one figure (e.g. with `par(mfrow=c(2,2))`), we don't display the results of the following loop.

```
> for (i in 1:length(gsList)) {
+   tt <- rbind(cindexall.mainz.small[i, ], cindexall.transbig.small[i,
+     ], cindexall.upp.small[i, ], cindexall.unt.small[i, ],
+     cindexall.vdx.small[i, ], cindexall.nki.small[i, ], NA,
+     as.numeric(ccindex[i, ]))
+   rownames(tt) <- datasetList
+   tt <- as.data.frame(tt)
+   labeltext <- cbind(c("Dataset", datasetList), c(rep(myspace,
+     length(datasetList) + 1)))
```

```

+   bs <- rep(0.5, nrow(labeltext))
+   r.mean <- c(NA, tt$cindex)
+   r.lower <- c(NA, tt$lower)
+   r.upper <- c(NA, tt$upper)
+   x.ticks.lower <- (floor((min(r.mean, na.rm = TRUE) - 0.1) *
+     10)/10)
+   x.ticks.upper <- (floor((max(r.mean, na.rm = TRUE) + 0.2) *
+     10)/10)
+   forestplot.surv(labeltext = labeltext, mean = r.mean, lower = r.lower,
+     upper = r.upper, zero = 0.5, align = c("l"), graphwidth = unit(2,
+     "inches"), x.ticks = seq(x.ticks.lower, x.ticks.upper,
+     0.05), xlab = paste(gsList[i], " Concordance Index",
+     mspace, sep = ""), col = meta.colors(box = "royalblue",
+     line = "darkblue", zero = "darkred"), box.size = bs,
+     clip = c(0.3, 0.8), is.summary = (c(rep(FALSE, 8), TRUE)))
+ }

```

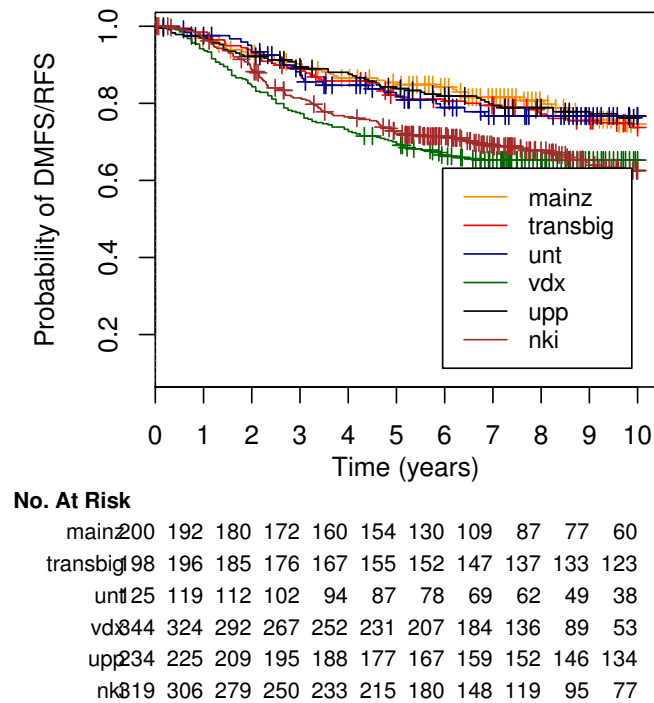
2.5 Kaplan Meier survival curves

To display a Kaplan Meier curve [8] for all datasets you can use:

```

> surv.data <- censor.time(surv.time = c(pData(mainz7g)[, "t.dmfs"],
+   pData(transbig7g)[, "t.dmfs"], pData(unt7g)[, "t.dmfs"],
+   pData(vdx7g)[, "t.dmfs"], pData(upp7g)[, "t.rfs"], pData(nki7g)[,
+   "t.dmfs"])/365, surv.event = c(pData(mainz7g)[, "e.dmfs"],
+   pData(transbig7g)[, "e.dmfs"], pData(unt7g)[, "e.dmfs"],
+   pData(vdx7g)[, "e.dmfs"], pData(upp7g)[, "e.rfs"], pData(nki7g)[,
+   "e.dmfs"])), time.cens = tc/365)
> gg <- factor(c(rep("mainz", nrow(pData(mainz7g))), rep("transbig",
+   nrow(pData(transbig7g))), rep("unt", nrow(pData(unt7g))),
+   rep("vdx", nrow(pData(vdx7g))), rep("upp", nrow(pData(upp7g))),
+   rep("nki", nrow(pData(nki7g)))), levels = c("mainz", "transbig",
+   "unt", "vdx", "upp", "nki"))
> dd <- data.frame(time = surv.data[[1]], event = surv.data[[2]],
+   group = gg)
> km.coxph.plot(formula.s = formula(Surv(time, event) ~ group),
+   data.s = dd, sub.s = "all", x.label = "Time (years)", y.label = "Probability of
+   main.title = "", sub.title = "", leg.pos = "bottomright",
+   leg.inset = 0.05, o.text = FALSE, v.line = FALSE, h.line = FALSE,
+   .lty = rep(1, length(levels(gg))), show.n.risk = TRUE, n.risk.step = 1,
+   n.risk.cex = 0.85, .col = c("darkorange", "red", "darkblue",
+   "darkgreen", "black", "brown"), leg.text = paste(levels(gg),
+   mspace, sep = ""), verbose = FALSE, ylim = c(0.1, 1))

```



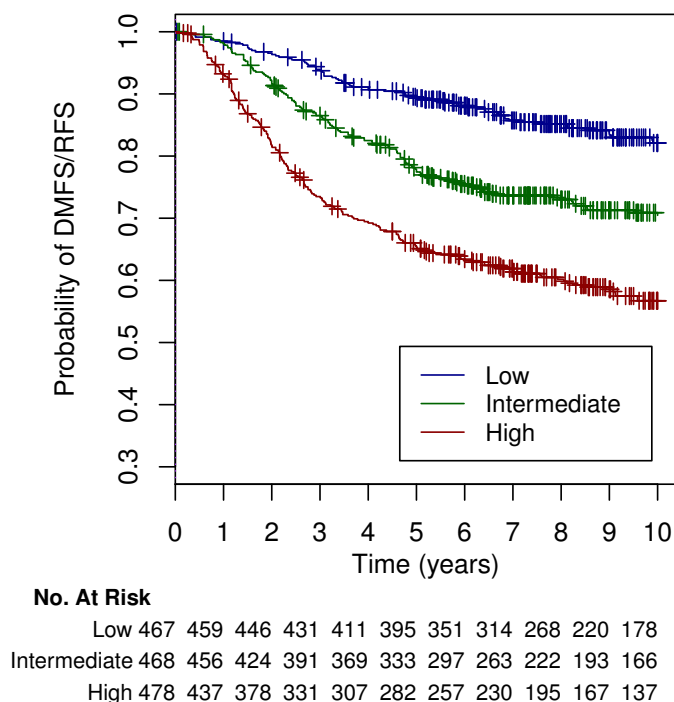
If you want to display the survival curve for a single gene using the data of all six datasets, we have to concatenate the survival and expression data of all datasets (see `surv.time.all`, `surv.event.all` and `aurka.exprs` below). After that we split the patients in each dataset into three parts according to their gene expression. We use the function `quantile()` for that. In the end we have three groups, representing the low gene expression group (lowest 33% of the gene expression), intermediate gene expression group (gene expression between 33% and 66%) and high gene expression group (over 66%).

```
> aurkaGs <- "AURKA"
> aurkaGid <- 6790
> aurkaPaf <- "208079_s_at"
> aurkaPagi <- "NM_003600"
> surv.time.all <- c(pData(mainz7g)[, "t.dmfs"], pData(transbig7g)[,
+   "t.dmfs"], pData(unt7g)[, "t.dmfs"], pData(upp7g)[, "t.rfs"],
+   pData(vdx7g)[, "t.dmfs"], pData(nki7g)[, "t.dmfs"])
> surv.event.all <- c(pData(mainz7g)[, "e.dmfs"], pData(transbig7g)[,
+   "e.dmfs"], pData(unt7g)[, "e.dmfs"], pData(upp7g)[, "e.rfs"],
+   pData(vdx7g)[, "e.dmfs"], pData(nki7g)[, "e.dmfs"])
```

```

> aurka.exprs <- c(exprs(mainz7g)[aurkaPaf, ], exprs(transbig7g)[aurkaPaf,
+ ], exprs(unt7g)[aurkaPaf, ], exprs(upp7g)[aurkaPaf, ], exprs(vdx7g)[aurkaPaf,
+ ], exprs(nki7g)[aurkaPagi, ])
> aurka.exprs.length <- c(length(exprs(mainz7g)[aurkaPaf, ]), length(exprs(transbig7g
+ ]), length(exprs(unt7g)[aurkaPaf, ]), length(exprs(upp7g)[aurkaPaf,
+ ]), length(exprs(vdx7g)[aurkaPaf, ]), length(exprs(nki7g)[aurkaPagi,
+ ]))
> pos <- 0
> mygroup <- NULL
> for (i in aurka.exprs.length) {
+   qq <- aurka.exprs[(pos + 1):(pos + i)]
+   myq <- quantile(qq, probs = c(0.33, 0.66), na.rm = TRUE)
+   qq[aurka.exprs[(pos + 1):(pos + i)] < myq[1]] <- 1
+   qq[aurka.exprs[(pos + 1):(pos + i)] >= myq[1] & aurka.exprs[(pos +
+ 1):(pos + i)] < myq[2]] <- 2
+   qq[aurka.exprs[(pos + 1):(pos + i)] > myq[2]] <- 3
+   qq <- factor(x = qq, levels = 1:3)
+   mygroup <- c(mygroup, qq)
+   pos <- pos + i
+ }
> surv.data <- censor.time(surv.time = surv.time.all/365, surv.event = surv.event.all
+ time.cens = tc/365)
> dd <- data.frame(time = surv.data[[1]], event = surv.data[[2]],
+   gg = mygroup)
> gg <- factor(c(rep("mainz", nrow(pData(mainz7g))), rep("transbig",
+   nrow(pData(transbig7g))), rep("unt", nrow(pData(unt7g))),
+   rep("upp", nrow(pData(upp7g))), rep("vdx", nrow(pData(vdx7g))),
+   rep("nki", nrow(pData(nki7g)))), levels = c("mainz", "transbig",
+   "unt", "upp", "vdx", "nki"))
> km.coxph.plot(formula.s = formula(Surv(time, event) ~ gg), data.s = dd,
+   sub.s = "all", x.label = "Time (years)", y.label = "Probability of DMFS/RFS",
+   main.title = "", sub.title = "", leg.text = c("Low ", "Intermediate ",
+   "High "), leg.pos = "bottomright", leg.inset = 0.05,
+   o.text = FALSE, v.line = FALSE, h.line = FALSE, .col = c("darkblue",
+   "darkgreen", "darkred"), .lty = 1, show.n.risk = TRUE,
+   n.risk.step = 1, n.risk.cex = 0.85, verbose = FALSE, ylim = c(0.3,
+   1))

```



2.6 Meta analysis of estimation values

The *SurvComp* package integrates functions for meta-analysis of risk-prediction models, e.g. for the concordance index or the D index. The following example shows the `cindex.comp.meta()` function [9]. Table 6 shows the p-values representing the difference between the cindices of two genes using the cindices of all six datasets. For example, the cindex of the gene AURKA is with a p-value of 0.00001 significantly different from the cindex of the gene VEGF using the six datasets.

```
> cindexMetaMainz <- t(apply(X = exprs(mainz7g), MARGIN = 1, function(x,
+   y, z) {
+   tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+     method = "noether", na.rm = TRUE)
+   return(tt)
+ }, y = pData(mainz7g)[, "t.dmfs"], z = pData(mainz7g)[, "e.dmfs"]))
> cindexMetaTransbig <- t(apply(X = exprs(transbig7g), MARGIN = 1,
+   function(x, y, z) {
```

```

+         tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+             method = "noether", na.rm = TRUE)
+         return(tt)
+     }, y = pData(transbig7g)[, "t.dmf5"], z = pData(transbig7g)[,
+         "e.dmf5"])))
> cindexMetaUpp <- t(apply(X = exprs(upp7g), MARGIN = 1, function(x,
+     y, z) {
+         tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+             method = "noether", na.rm = TRUE)
+         return(tt)
+     }, y = pData(upp7g)[, "t.rfs"], z = pData(upp7g)[, "e.rfs"])))
> cindexMetaUnt <- t(apply(X = exprs(unt7g), MARGIN = 1, function(x,
+     y, z) {
+         tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+             method = "noether", na.rm = TRUE)
+         return(tt)
+     }, y = pData(unt7g)[, "t.dmf5"], z = pData(unt7g)[, "e.dmf5"])))
> cindexMetaVdx <- t(apply(X = exprs(vdx7g), MARGIN = 1, function(x,
+     y, z) {
+         tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+             method = "noether", na.rm = TRUE)
+         return(tt)
+     }, y = pData(vdx7g)[, "t.dmf5"], z = pData(vdx7g)[, "e.dmf5"])))
> ccNki <- complete.cases(exprs(nki7g)[1, ], exprs(nki7g)[2, ],
+     exprs(nki7g)[3, ], exprs(nki7g)[4, ], exprs(nki7g)[5, ],
+     exprs(nki7g)[6, ], exprs(nki7g)[7, ], pData(nki7g)[, "e.dmf5"],
+     pData(nki7g)[, "e.dmf5"])
> cindexMetaNki <- t(apply(X = exprs(nki7g)[, ccNki], MARGIN = 1,
+     function(x, y, z) {
+         tt <- concordance.index(x = x, surv.time = y, surv.event = z,
+             method = "noether", na.rm = TRUE)
+         return(tt)
+     }, y = pData(nki7g)[ccNki, "t.dmf5"], z = pData(nki7g)[ccNki,
+         "e.dmf5"])))
> ccmData <- tt <- rr <- NULL
> for (i in 1:7) {
+     tt <- NULL
+     listOne <- list(mainz = cindexMetaMainz[[i]], transbig = cindexMetaTransbig[[i]]
+         upp = cindexMetaUpp[[i]], unt = cindexMetaUnt[[i]], vdx = cindexMetaVdx[[i]]
+         nki = cindexMetaNki[[i]])
+     for (j in 1:7) {
+         listTwo <- list(mainz = cindexMetaMainz[[j]], transbig = cindexMetaTransbig

```

| | esr1 | erbb2 | aurka | plau | vegfa | stat1 | casp3 |
|-------|---------|---------|---------|---------|---------|---------|---------|
| esr1 | 1.00000 | 0.96698 | 1.00000 | 0.99489 | 1.00000 | 0.99967 | 0.99860 |
| erbb2 | 0.03302 | 1.00000 | 1.00000 | 0.79944 | 0.99855 | 0.94848 | 0.87718 |
| aurka | 0.00000 | 0.00000 | 1.00000 | 0.00000 | 0.00001 | 0.00000 | 0.00000 |
| plau | 0.00511 | 0.20056 | 1.00000 | 1.00000 | 0.98988 | 0.80287 | 0.62407 |
| vegfa | 0.00000 | 0.00145 | 0.99999 | 0.01012 | 1.00000 | 0.07944 | 0.02743 |
| stat1 | 0.00033 | 0.05152 | 1.00000 | 0.19713 | 0.92056 | 1.00000 | 0.28393 |
| casp3 | 0.00140 | 0.12282 | 1.00000 | 0.37593 | 0.97257 | 0.71607 | 1.00000 |

Table 6: `cindex.comp.meta()` results showing the significance of the difference between concordance indices.

```

+           upp = cindexMetaUpp[[j]], unt = cindexMetaUnt[[j]],
+           vdx = cindexMetaVdx[[j]], nki = cindexMetaNki[[j]])
+   rr <- cindex.comp.meta(list.cindex1 = listOne, list.cindex2 = listTwo)
+   tt <- cbind(tt, rr$p.value)
+ }
+   ccmData <- rbind(ccmData, tt)
+ }
> ccmData <- as.data.frame(ccmData)
> colnames(ccmData) <- gsList
> rownames(ccmData) <- gsList

```

3 Session Info

- R version 2.12.1 (2010-12-16), i686-pc-linux-gnu
- Locale: LC_CTYPE=en_US.utf8, LC_NUMERIC=C, LC_TIME=en_US.utf8, LC_COLLATE=C, LC_MONETARY=C, LC_MESSAGES=en_US.utf8, LC_PAPER=en_US.utf8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.utf8, LC_IDENTIFICATION=C
- Base packages: base, datasets, grDevices, graphics, grid, methods, splines, stats, utils
- Other packages: Biobase 2.10.0, KernSmooth 2.23-4, MASS 7.3-7, SuppDists 1.1-8, bootstrap 1.0-22, class 7.3-2, ipred 0.8-11, mlbench 2.1-0, nnet 7.3-1, prodlim 1.1.3, rmeta 2.16, rpart 3.1-48, survcomp 1.1.8, survival 2.36-5, survivalROC 1.0.0, xtable 1.5-6
- Loaded via a namespace (and not attached): tools 2.12.1

4 Functions within SurvComp

For references to the following functions, please see [2]-[21].

| Function | Description |
|--------------------|--|
| D.index | Function to compute the D index |
| breastCancerData | Sample data containing six datasets for gene expression, annotations and clinical data |
| sensor.time | Function to artificially censor survival data |
| cindex.comp | Function to compare two concordance indices |
| cindex.comp.meta | Function to compare two concordance indices |
| combine.est | Function to combine estimates |
| combine.test | Function to combine probabilities |
| concordance.index | Function to compute the concordance index for survival or binary class prediction |
| cvpl | Function to compute the CVPL |
| dindex.comp | Function to compare two D indices |
| dindex.comp.meta | Function to compare two D indices |
| fisherz | Function to compute Fisher z transformation |
| forestplot.surv | Forest plots enables to display performance estimates of survival models |
| getsurv2 | Function to retrieve the survival probabilities at a specific point in time |
| hazard.ratio | Function to estimate the hazard ratio through Cox regression |
| hr.comp | Function to statistically compare two hazard ratios |
| hr.comp.meta | Function to compare two concordance indices |
| hr.comp2 | Function to statistically compare two hazard ratios (alternative interface) |
| iauc.comp | Function to compare two IAUCs through time-dependent ROC curves |
| ibsc.comp | Function to compare two IBSCs |
| km.coxph.plot | Function to plot several Kaplan-Meier survival curves |
| logpl | Function to compute the log partial likelihood of a Cox model |
| no.at.risk | Function to compute the number of individuals at risk |
| sbrier.score2proba | Function to compute the BSCs from a risk score, for all the times of event occurrence |
| score2proba | Function to compute the survival probabilities from a risk score |
| survcomp-package | Performance Assessment and Comparison for Survival Analysis |
| td.sens.spec | Function to compute sensitivity and specificity for a binary classification of survival data |
| tdrocc | Function to compute time-dependent ROC curves |
| test.hetero.est | Function to test the heterogeneity of set of probabilities |
| test.hetero.test | Function to test the heterogeneity of set of probabilities |

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