Right Heart Catheterization Dataset

This dataset was used in Connors *et al*. (1996): The effectiveness of RHC in the initial care of critically ill patients. *J American Medical Association* 276:889-897. The dataset pertains to day 1 of hospitalization, i.e., the "treatment" variable `swang1` is whether or not a patient received a RHC (also called the Swan-Ganz catheter) on the first day in which the patient qualified for the SUPPORT study (see above). The dataset is suitable for use in papers submitted in response to the call for papers on causal inference, by the journal *Health Services and Outcomes Research Methodology*. The original analysis by Connors *et al*. used binary logistic model to develop a propensity score that was then used for matching RHC patients with non-RHC patients. A sensitivity analysis was also done. The results provided some evidence that patients receiving RHC had decreased survival time, and the sensitivity analysis indicated that any unmeasured confounder would have to be somewhat strong to explain away the results. See Lin DY, Psaty BM, Kronmal RA (1998): Assessing the sensitivity of regression results to unmeasured confounders in observational studies. *Biometrics* 54:948-963 for useful methods for sensitivity analysis, one of which was applied to the RHC results.

Here is a `.zip` containing the original SAS code used to do the published analyses, from Charles Thomas. A reverse chronological directory of the SAS code files is here.

The S-Plus dataset is easy to use if you have the Hmisc library in effect. If you don't, you need to define the following S-Plus functions.

```
ddmmmyy <- function(x)
{
        y <- month.day.year(trunc(oldUnclass(x)), attr(x,"origin"))
        yr <- y$year
        m <- c("Jan","Feb","Mar","Apr","May","Jun","Jul","Aug","Sep","Oct",
               "Nov","Dec")[y$month]
        ifelse(yr<1900 | yr>=2000, paste(y$day,m,yr,sep=""),
               paste(y$day,m,yr-1900,sep=""))
}

"[.labelled"<- function(x, ...) {
  lab <- attr(x, "label")
  x <- NextMethod("[")
  attr(x, "label") <- lab
  if(!inherits(x,'labelled'))
    attr(x,'class') <- c("labelled", attr(x,'class'))
  x
}

as.data.frame.labelled <- function(x, ...) {
  y <- x
  cy <- attr(y,'class')
  cy <- if(length(cy)>1) cy[cy!='labelled'] else NULL
  if(length(cy)==0) cy <- NULL  # handles wierd case e.g. class=rep('lab..',2)
  attr(y,'class') <- cy
  d <- data.class(y)
  methodname <- paste("as.data.frame", d, sep = '.')
  if(exists(methodname, mode = "function"))
            (get(methodname, mode = "function"))(x, ...)
  else {
        if(options()$check)
                warning(paste("no method for coercing",d,"to data.frame"))
        as.data.frame.AsIs(y, ...)
  }
}
```

If using S-Plus 5.x or 6.x, you don't need to define the last two functions. Instead you will need to run the data frame through a special function `cleanup.import` to remove old S-Plus classes.

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This documents the SAS transport data file and the S-Plus data file for The Study to Understand Prognoses and Preferences for Outcomes and Risks of Treatments (SUPPORT).

1. First unzip either of the two files
2. The SAS file may be transferred to another computing platform using SAS PROC CIMPORT.
3. The S-plus data file was created using S-plus function data.dump, so it may be restored by using function data.restore to put the data into your local _Data directory.
4. The variable descriptions are presented in the following table.

Table 1: SUPPORT Variable Description

Variable name	**Variable Definition**
Age	Age
Sex	Sex
Race	Race
Edu	Years of education
Income	Income
Ninsclas	Medical insurance
Cat1	Primary disease category
Cat2	Secondary disease category
Categories of admission diagnosis:	
Resp	Respiratory Diagnosis
Card	Cardiovascular Diagnosis
Neuro	Neurological Diagnosis
Gastr	Gastrointestinal Diagnosis
Renal	Renal Diagnosis
Meta	Metabolic Diagnosis

Hema	Hematologic Diagnosis
Seps	Sepsis Diagnosis
Trauma	Trauma Diagnosis
Ortho	Orthopedic Diagnosis
Adld3p	ADL
Das2d3pc	DASI (Duke Activity Status Index)
Dnr1	DNR status on day1
Ca	Cancer
Surv2md1	Support model estimate of the prob. of surviving 2 months
Aps1	APACHE score
Scoma1	Glasgow Coma Score
Wtkilo1	Weight
Temp1	Temperature
Meanbp1	Mean blood pressure
Resp1	Respiratory rate
Hrt1	Heart rate
Pafi1	PaO2/FIO2 ratio
Paco21	PaCo2
Ph1	PH
Wblc1	WBC
Hema1	Hematocrit
Sod1	Sodium
Pot1	Potassium
Crea1	Creatinine
Bili1	Bilirubin

Alb1	Albumin
Urin1	Urine output
Categories of comorbidities illness:	
Cardiohx	Acute MI, Peripheral Vascular Disease, Severe Cardiovascular Symptoms (NYHA-Class III), Very Severe Cardiovascular Symptoms (NYHA-Class IV)
Chfhx	Congestive Heart Failure
Dementhx	Dementia, Stroke or Cerebral Infarct, Parkinson's Disease
Psychhx	Psychiatric History, Active Psychosis or Severe Depression
Chrpulhx	Chronic Pulmonary Disease, Severe Pulmonary Disease, Very Severe Pulmonary Disease
Renalhx	Chronic Renal Disease, Chronic Hemodialysis or Peritoneal Dialysis
Liverhx	Cirrhosis, Hepatic Failure
Gibledhx	Upper GI Bleeding
Malighx	Solid Tumor, Metastatic Disease, Chronic Leukemia/Myeloma, Acute Leukemia, Lymphoma
Immunhx	Immunosupperssion, Organ Transplant, HIV Positivity, Diabetes Mellitus Without End Organ Damage, Diabetes Mellitus With End Organ Damage, Connective Tissue Disease
Transhx	Transfer (> 24 Hours) from Another Hospital
Amihx	Definite Myocardial Infarction
Swang1	Right Heart Catheterization (RHC)
Sadmdte	Study Admission Date
Dthdte	Date of Death
Lstctdte	Date of Last Contact
Dschdte	Hospital Discharge Date
Death	Death at any time up to 180 Days
Ptid	Patient ID

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