
Measurement, Statistical Consulting, and Computing Issues

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1. Measurement issues in chemometrics: What's wrong with ratios?
2. Assay / Microarray measurement issues
3. Problems with ratios in clinical lab data
4. Strategies for analyses that are "correct enough"
5. Applications of pharmacoeconomics to drug discovery
6. Bayesian methods in drug discovery and dose response assessment
7. Problems with discrete survival data
8. Competition from software, and statistical knowledge dissemination
9. Web-based computing as a statistician extender
10. Merck Drug Discovery StatServer
11. SAS vs. S-PLUS

1. Measurement Issues / Ratios

- Unlike differences or log ratios, ratios are asymmetric
- What to subtract from denominator? Most researchers assume zero.
- Ratios have strange distributions
- Kronmal (1993) [2] cited many problems with using ratios in statistical modeling
 - Spurious correlation in using ratio variables even if all component variables of ratios are uncorrelated
 - Division of only the dependent variable by an independent variable can result in regression coefficient estimates for the other independent variables that cause inappropriate conclusions
 - Use of a ratio as an independent variable can result in inadequate adjustment for component variables of the ratio

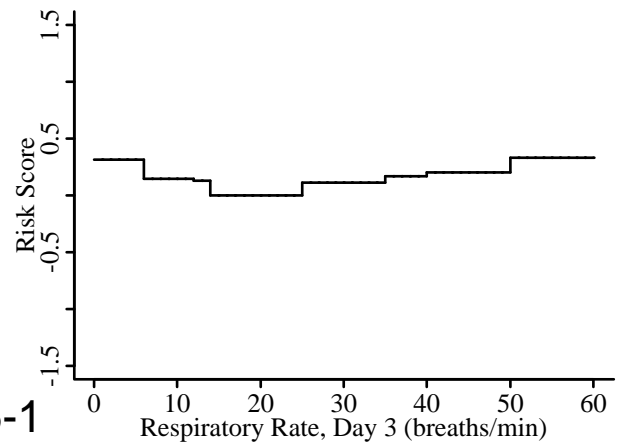
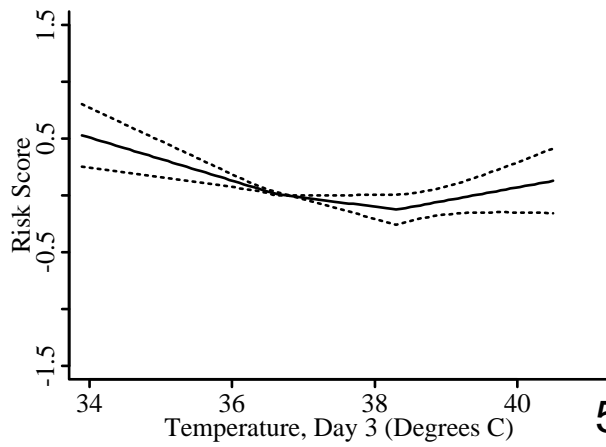
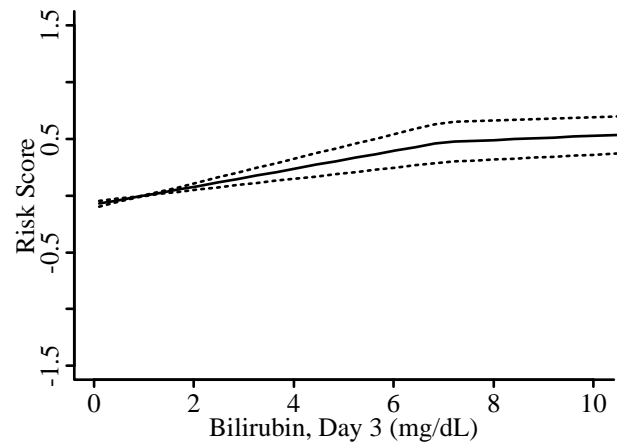
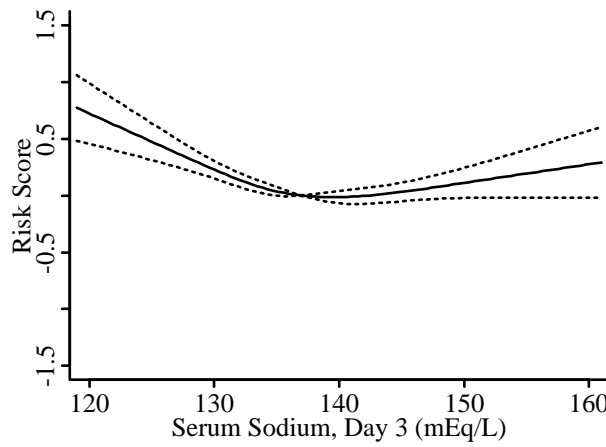
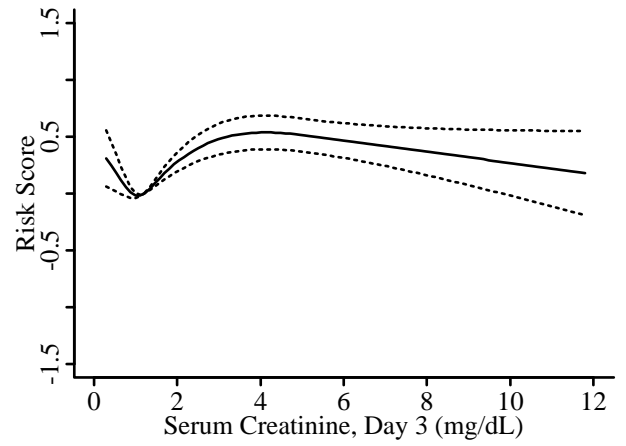
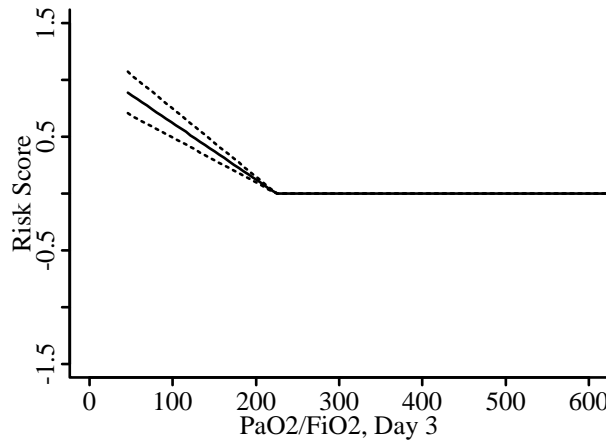
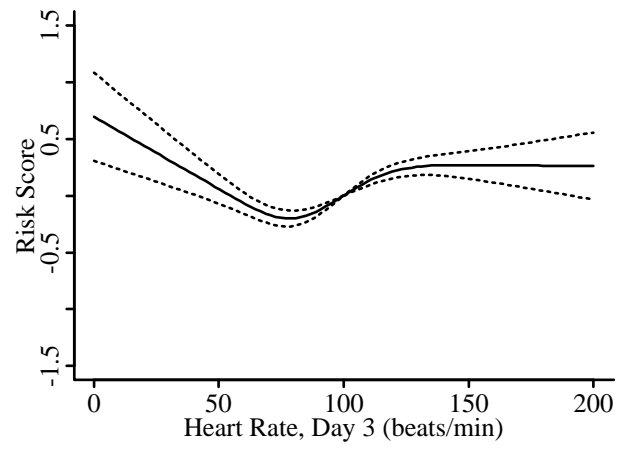
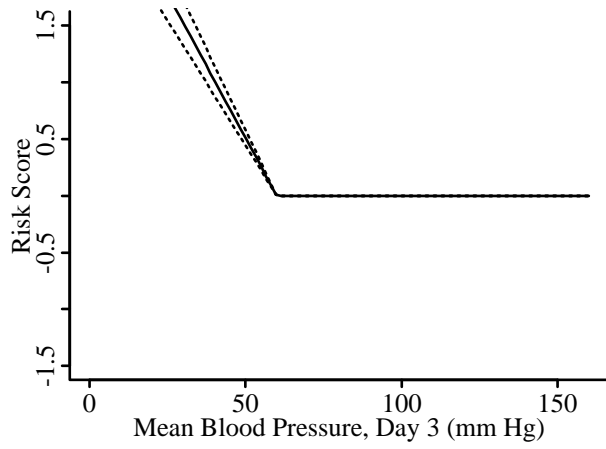
- Ratio variables should only be used in a full model containing all the component variables
- Results of regression analyses incorporating ratios are not readily comparable across studies with different distributions
- Kaiser (1989) [1] states that whatever effect measure is chosen (ratio, difference, etc.) should be demonstrated to be uncorrelated with the base value

2. Assay / Microarray Sequencing Issues

- What about values below the lower limit of detectability?
- Not appropriate to eliminate samples
- If using parametric analysis it may not be appropriate to treat values as zero
- Instead, treat them as left-censored
- For rank-based analyses zeros are usually OK
- Wikman *et al.* (2000) [8]: Affymetrix p53 Genechip's 1464 gene chip positions — need to regard “each chip position as a separate entity with its own noise and threshold characteristics”
- Account for row and column effects

3. Problems with Ratios in Clinical Lab Data

- It is common to report the proportion of patients with a lab value $> 3\times$ upper limit of normal
- Problematic: loses information from continuous variables, patients who were “almost abnormal” at baseline will have an easy time moving to the abnormal category
- Problem with non-monotonic risk relationships (e.g., normal range in the middle of the distribution)
- Need to treat lab values as continuous variables without allowing abnormally low values to cancel abnormally high values
- Advantageous to transform to a scale for which “abnormality points” can be added, e.g., log odds, log hazard, log survival time
- Example: scoring physiologic derangements



4. Strategies That are “Correct Enough”

- Example: can one ignore heteroscedasticity in a regression model? It depends.
- Rather than doing a weighted analysis, make the transformation of variables an integral part of the analysis
- Regression splines for independent variables
- Nonparametric smoothers in transform-both-sides generalized additive models, e.g. AVAS (Tibshirani [6]): transform Y to make variance of residuals independent of \hat{Y} .
- When only two variables are being analyzed at a time and only a P -value is needed, use rank test and rank correlation
- Use robust rank-based regression (Cox, proportional odds model) for multiple variables

5. Pharmacoeconomics in Drug Discovery

- Can't think of any applications except for Bayesian decision analysis incorporating costs (below)
- Are plenty of applications to drug *development*
- See Senn (1996) [5] for probabilistic decision analysis for portfolio management of compounds

6. Bayesian Methods in Drug Discovery and Dose Response Assessment

- In drug discovery type I error is of concern
- Bayesian prior distributions are usually a better way to deal with multiplicity
- Can incorporate prior distribution for the chances that a biomarker is an efficacy marker or for probability of monotonicity of dose-response
- Can do formal Bayesian decision analysis that incorporates costs of false positives and false negatives
- Bayesian methods have small-sample exactness without conditioning on only part of the data
- Opportunity for statisticians to be called on more by other researchers: “It takes time to be a Bayesian”

7. Discrete Survival Data

- May be best to use a method that is dedicated to heavily tied data, e.g. Prentice-Gloeckner [4]
- Investigate using Efron likelihood in Cox model
- Try randomly breaking ties and using ordinary Cox likelihood

8. Competition from Software / Statistical Knowledge Dissemination

- Not enough statisticians to go around
- Researchers are using statistical software and choosing the wrong software (e.g., Excel)
- Newsletter on choice of software
- Ongoing short course series (e.g., Statistical Thinking in Biomedical Research) emphasizing study design, bias, measurement, precision, power, graphics, demos (“what a statistician does with data”)
- Clients should know almost as much about statistics as we know about biology

9. Web-Based Computing as a Statistician Extender

- “Safe Statistics”: Pikounis, Gunter, Liaw, Pajni (2000) [3]
- Statistical strategies that
 - “Produce useful answers ‘most’ of the time
 - Indicate where answers may not be useful
 - Have ‘adequate’ performance
 - Handle missing values and other data problems
 - Are tuned to user skill level

- In practice this means
 - Graphics
 - Well designed user interface
 - Resistant methods
 - Fewest assumptions possible (nonparametric procedures)
 - Use of subject matter knowledge whenever possible”

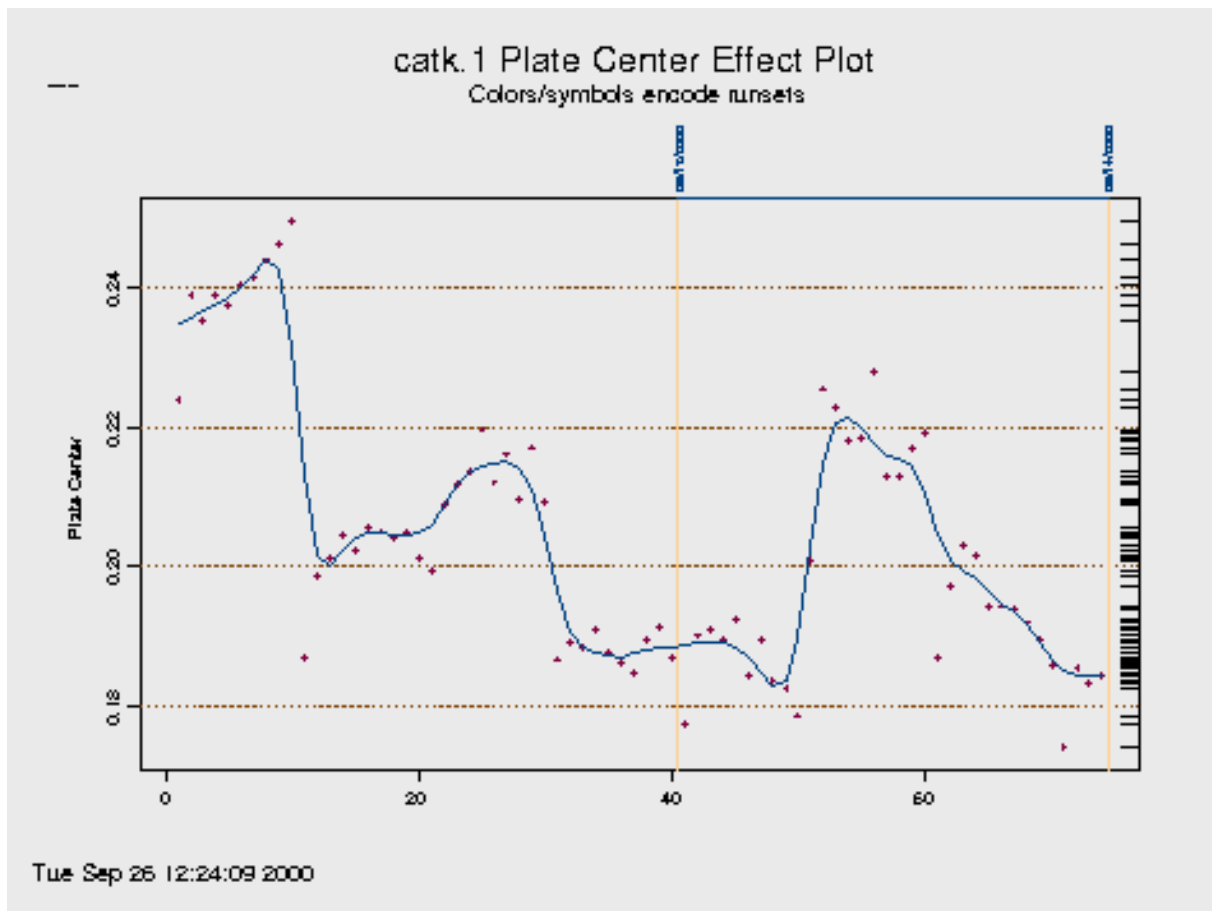
- Statisticians can control which methods are distributed or emphasized to non-statisticians

10. Merck S-PLUS HTS StatServer

- S-PLUS StatServer is web based, no special client software
- 96-3456 well plates for HTS assays in drug discovery
- Take into account positional effects within plates (esp. edge effects), changing background response and assay sensitivity, trends, cycles, shifts, missing values
- Used by 3000 scientists with little formal stat knowledge, fewer than 10 statisticians to support them
- Drilling down after potential problems seen (e.g., analysis by rows or by columns)
- Heavy on graphics and nonparametric trends
- Error messages to users are also E-mailed to statisticians

- Detailed usage accounting data

HTS QC Plots	HTS Image Plot
Index Of First Plate: <input type="text" value="1"/>	Index Of First Plate: <input type="text" value="1"/>
Index Of End Plate: <input type="text" value="74"/>	Index Of End Plate: <input type="text" value="20"/>
Plot Display: <input type="text" value="Color"/>	Layout: <input type="text" value="4 X 5"/>
Analysis Name: catk	Graph Type: <input type="text" value="Estimated Background"/>
<input type="button" value="Create QC Plots"/>	Analysis Name: catk
	<input type="button" value="Create Image Plot"/>



- SAS 8 has narrowed the gap to 5 years
- Major advantages of S-PLUS:
 1. No distinction between DATA and PROC steps
 2. No macro language; all commands are “live”.

Example:

```
if(is.category(x) |  
is.character(x) |  
length(unique(x)) < 20)  
table(x) else quantile(x)
```

3. Many more data types than SAS, users can add their own attributes to data (e.g., flag strange or imputed values)
4. Truly interactive
5. Graphics
6. S-PLUS 2000 comes with 2900 functions

7. Language is extendible and relatively simple to program; user-written functions are written in the same language used by the developers; statisticians world-wide are writing functions
8. Speed of implementation of modern methods (StatLib)
9. Methods for modeling, exploratory data analysis, missing data, graphics after model fitting, bootstrap, table making, much more [7]

10. No need for output delivery system:

- All entities are objects, allowing all functions to communicate directly

- Special methods for formatting output, e.g.:

```
# create LATEX table (alt: HTML)
latex(summary(marker ~ age+sex))
# logistic regression model with
# regression splines, interactions
f ← lrm(y ~ rcs(age,5)*sex +
        rcs(pressure,4))
f          # ordinary printout
plot(f)    # show fitted shapes
Function(f) # create S+ function
sascode(Function(f)) # SAS code

# typeset fit in algebraic form
w ← latex(f)
html(w)          # convert to HTML
# future: convert to XML with
# embedded MathML
xml(f)
```

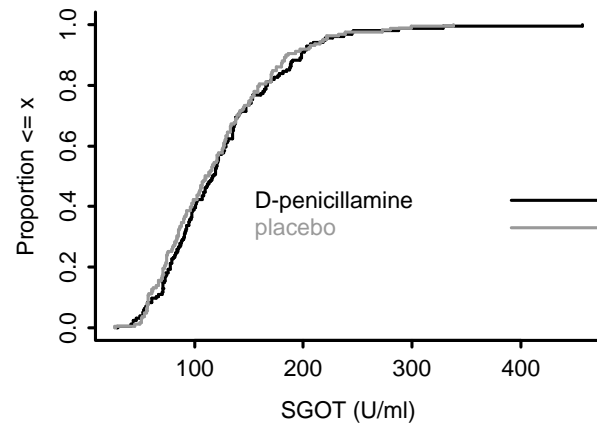
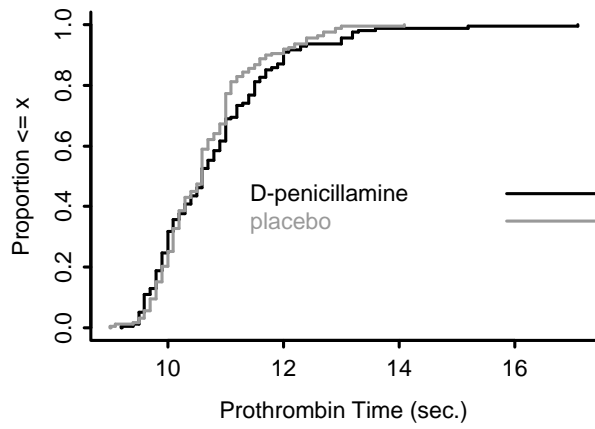
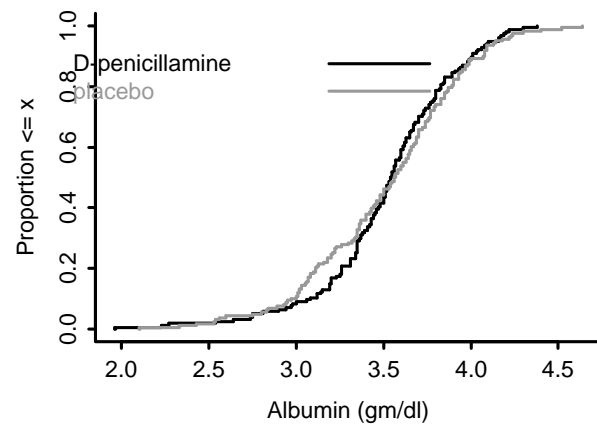
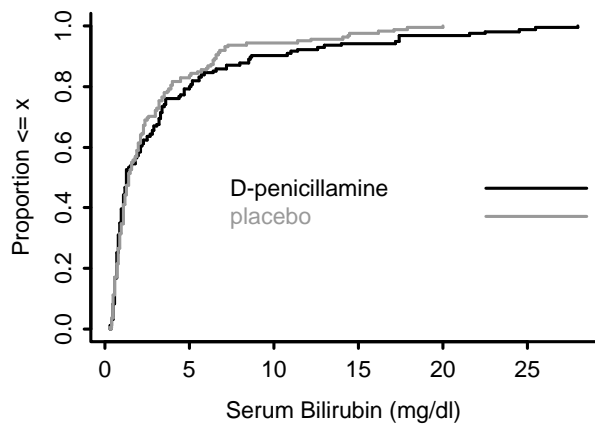
Table Making Example

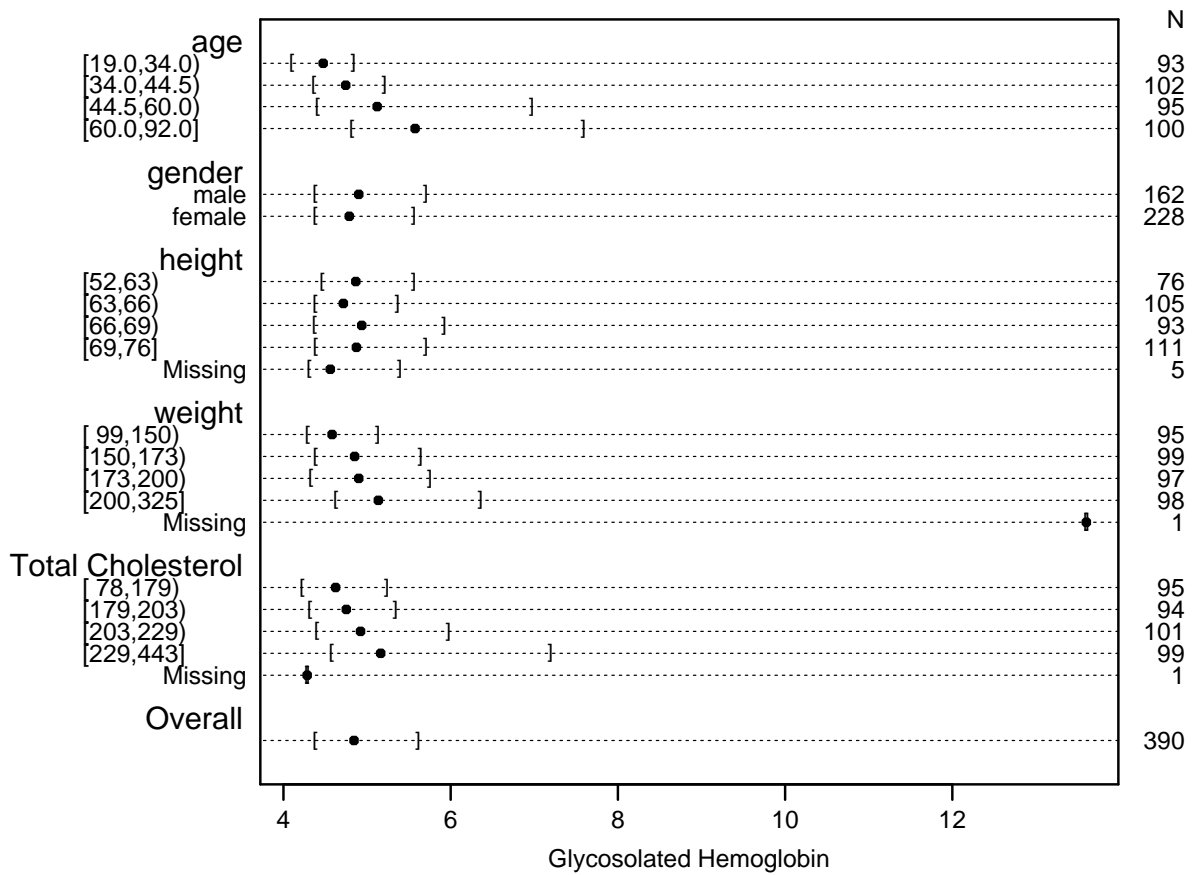
```
s ← summary(drug ~ bili + albumin +
            stage + protime + sex + age +
            spiders, method='reverse')
latex(s, npct='both')
```

	N	D-penicillamine ($N = 154$)	placebo ($N = 158$)
Serum Bilirubin (mg/dl)	418	0.725 1.300 3.600	0.800 1.400 3.200
Albumin (gm/dl)	418	3.34 3.54 3.78	3.21 3.56 3.83
Histologic Stage, Ludwig Criteria : 1	412	3% $\frac{4}{154}$	8% $\frac{12}{158}$
2		21% $\frac{32}{154}$	22% $\frac{35}{158}$
3		42% $\frac{64}{154}$	35% $\frac{56}{158}$
4		35% $\frac{54}{154}$	35% $\frac{55}{158}$
Prothrombin Time (sec.)	416	10.0 10.6 11.4	10.0 10.6 11.0
Sex : female	418	90% $\frac{139}{154}$	87% $\frac{137}{158}$
Age	418	41.4 48.1 55.8	43.0 51.9 58.9
Spiders	312	29% $\frac{45}{154}$	28% $\frac{45}{158}$

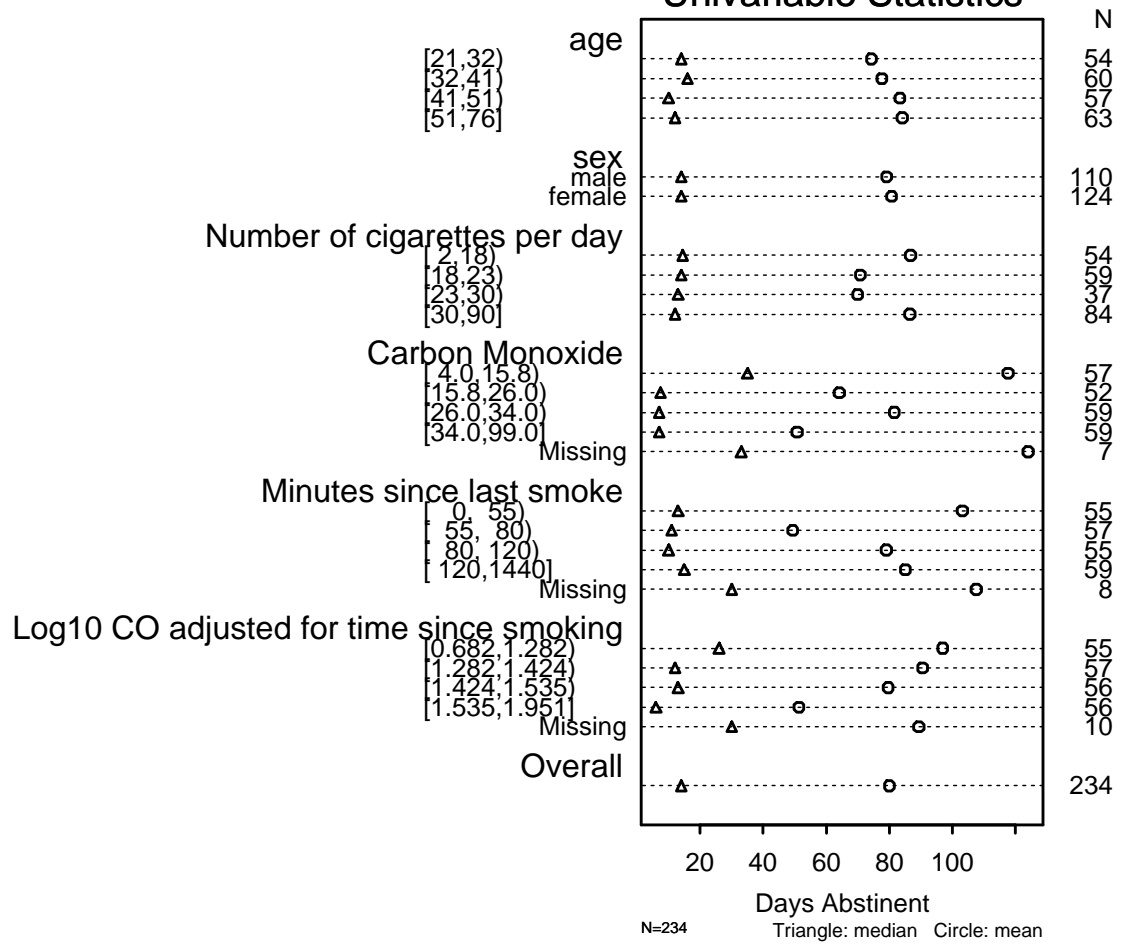
$a b c$ represent the lower quartile a , the median b , and the upper quartile c for continuous variables.

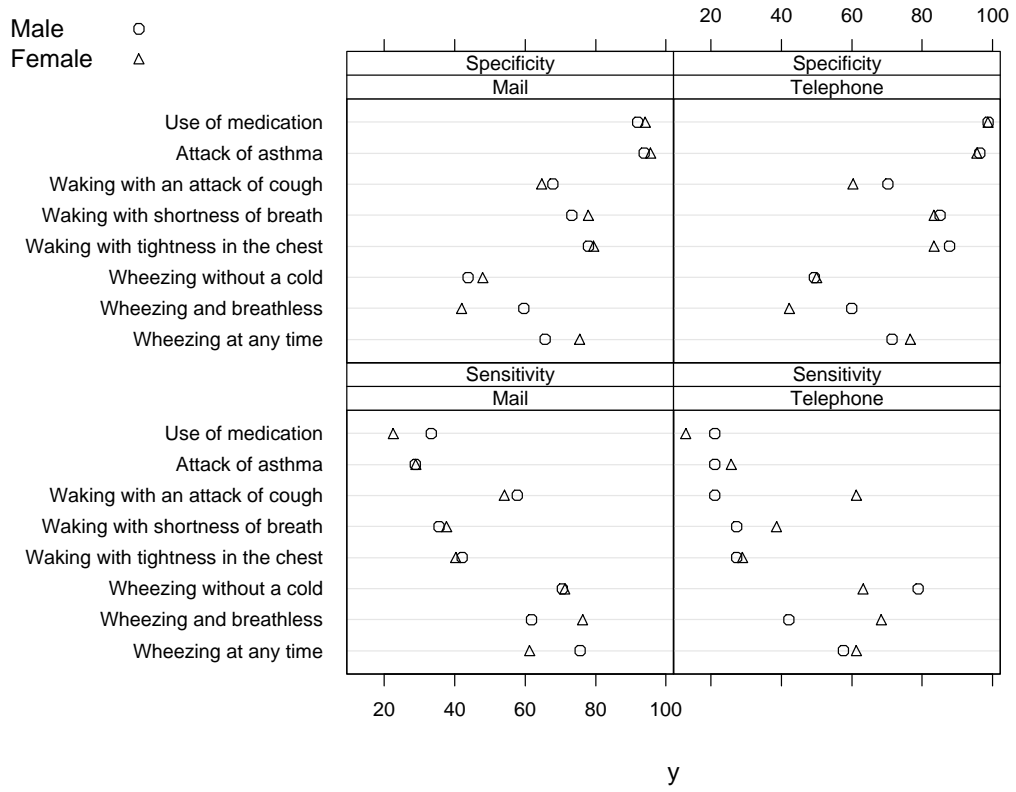
N is the number of non-missing values.

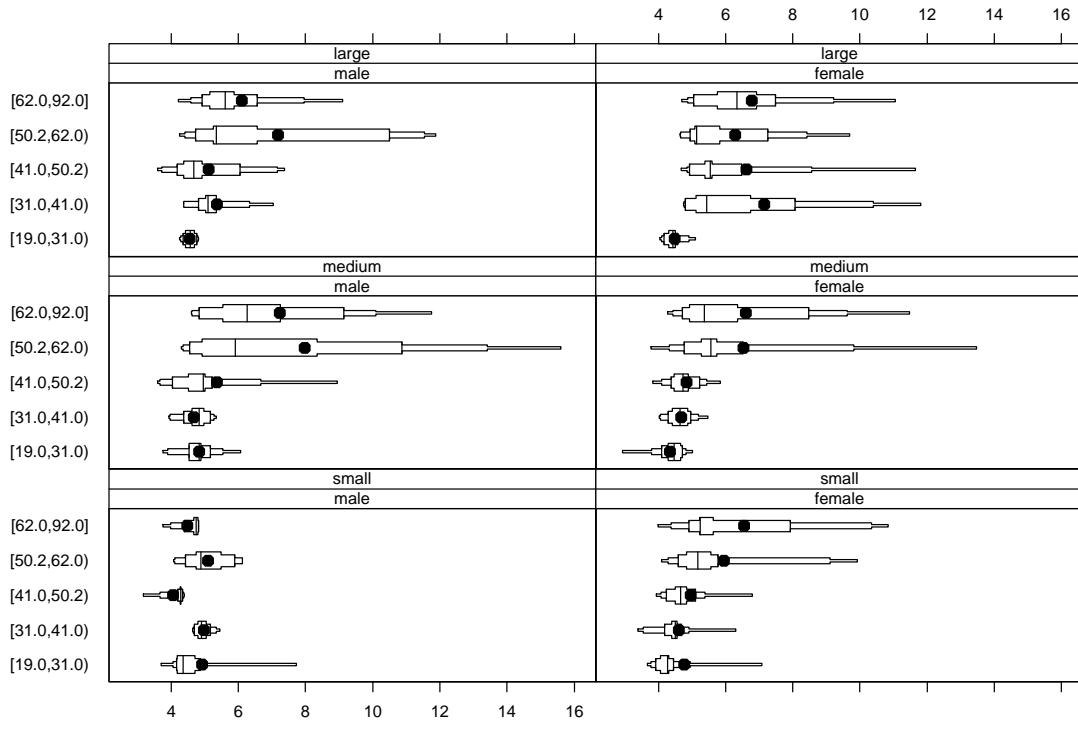




Duration of Abstinence Univariable Statistics



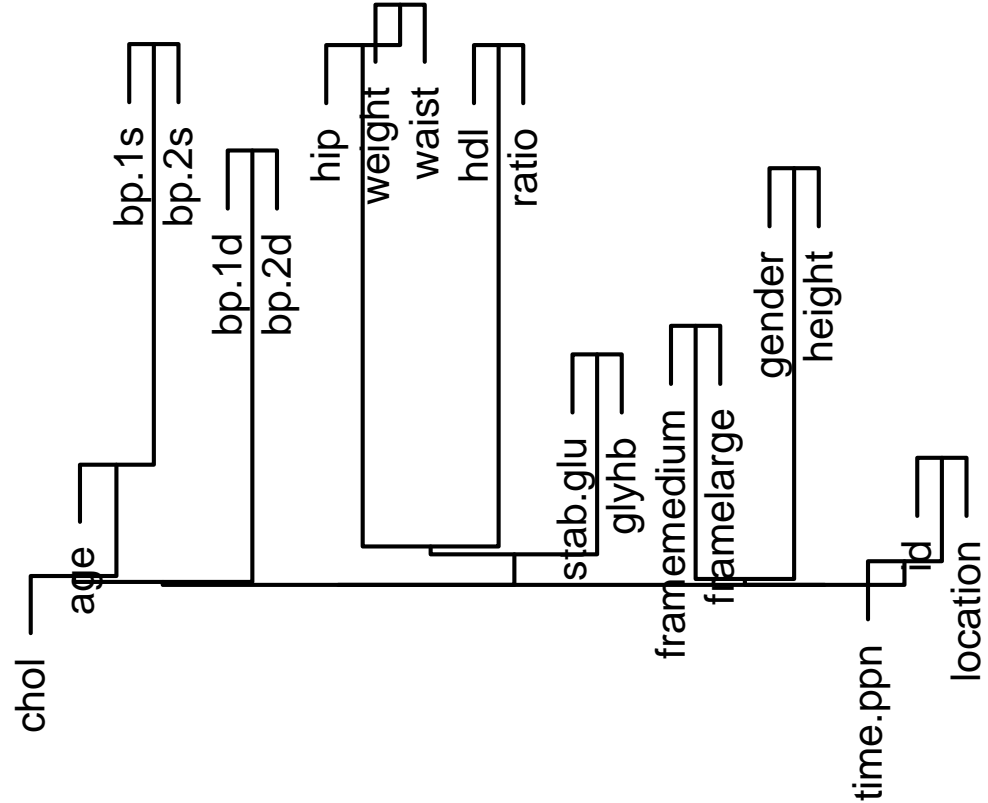


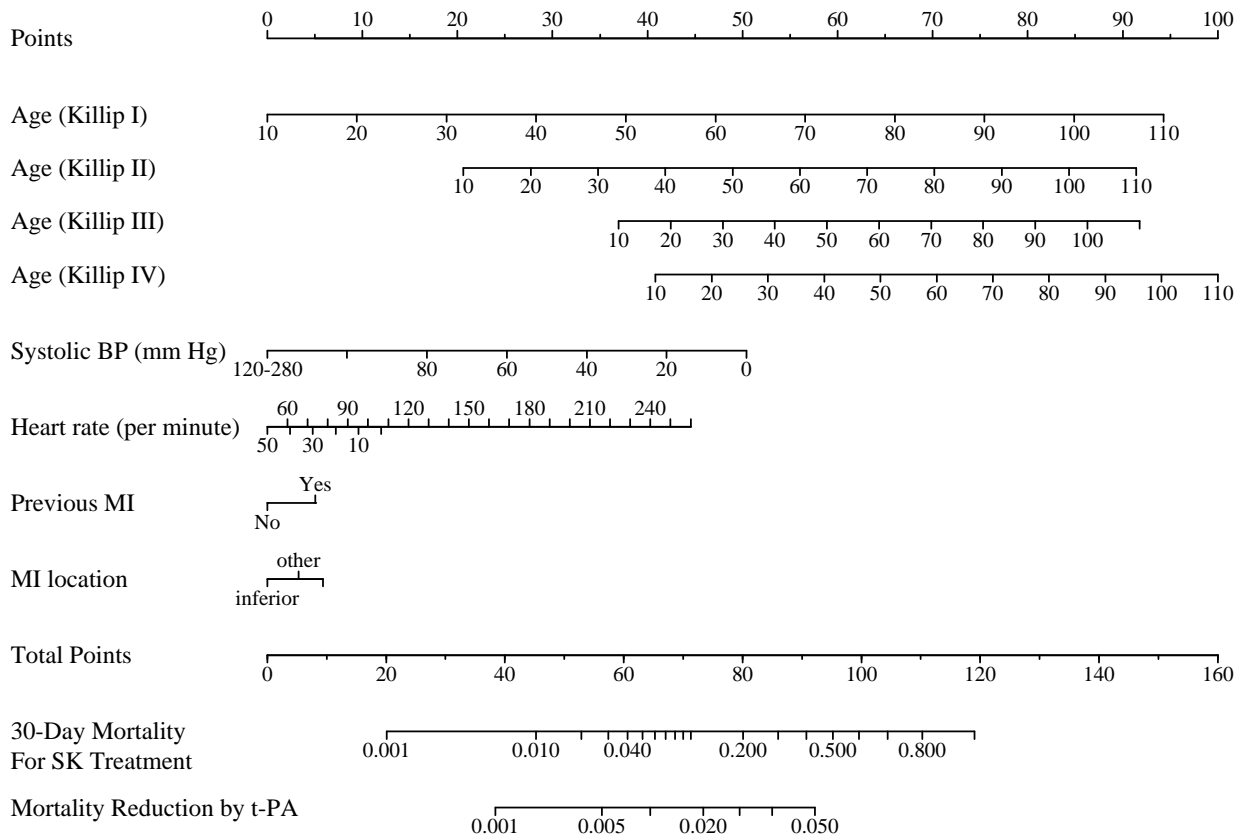


glyhb

Similarity (Spearman rho^2)

0.0 0.2 0.4 0.6





19 Variables pbc
418 Observations

bili : Serum Bilirubin (mg/dl)

n	missing	unique	Mean	.05	.10	.25	.50	.75	.90	.95
418	0	98	3.221	0.50	0.60	0.80	1.40	3.40	8.03	14.00

lowest : 0.3 0.4 0.5 0.6 0.7, highest: 21.6 22.5 24.5 25.5 28.0

albumin : Albumin (gm/dl)

n	missing	unique	Mean	.05	.10	.25	.50	.75	.90	.95
418	0	154	3.497	2.750	2.967	3.243	3.530	3.770	4.010	4.141

lowest : 1.96 2.10 2.23 2.27 2.31, highest: 4.30 4.38 4.40 4.52 4.64

stage : Histologic Stage, Ludwig Criteria

n	missing	unique	Mean
412	6	4	3.024

1 (21, 5%), 2 (92, 22%), 3 (155, 38%), 4 (144, 35%)

protime : Prothrombin Time (sec.)

n	missing	unique	Mean	.05	.10	.25	.50	.75	.90	.95
416	2	48	10.73	9.60	9.80	10.00	10.60	11.10	12.00	12.45

lowest : 9.0 9.1 9.2 9.3 9.4, highest: 13.8 14.1 15.2 17.1 18.0

sex : Sex

n	missing	unique
418	0	2

male (44, 11%), female (374, 89%)

fu.days : Time to Death or Liver Transplantation

n	missing	unique	Mean	.05	.10	.25	.50	.75	.90	.95
418	0	399	1918	245.1	606.8	1092.8	1730.0	2613.5	3524.2	4040.6

lowest : 41 43 51 71 77, highest: 4500 4509 4523 4556 4795

age : Age

n	missing	unique	Mean	.05	.10	.25	.50	.75	.90	.95
418	0	345	50.74	33.84	36.37	42.83	51.00	58.24	64.30	67.92

lowest : 26.28 28.88 29.56 30.28 30.57
highest: 74.52 75.00 75.01 76.71 78.44

spiders : Spiders

n	missing	unique
312	106	2

absent (222, 71%), present (90, 29%)

References

- [1] Lee Kaiser. Adjusting for baseline: Change or percentage change? *Statistics in Medicine*, 8:1183–1190, 1989.
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- [6] Robert Tibshirani. Estimating transformations for regression via additivity and variance stabilization. *Journal of the American Statistical Association*, 83:394–405, 1988.
- [7] William N. Venables and Brian D. Ripley. *Modern Applied Statistics with S-Plus*. Springer-Verlag, New York, third edition, 1999.
- [8] Friedrik P. Wilman, Ming-Lan Lu, Thomas Thykjaer, Sanne H. Olesen, Lars D. Andersen, Carlos Cordon-Cardo, and Torben F. Orntoft. Evaluation of the performance of a p53 sequencing microarray chip using 140 previously sequenced bladder tumor samples. *Clinical Chemistry*, 46:1555–1561, 2000.