

# Survival Ensembles

Torsten Hothorn<sup>1,\*</sup>, Peter Bühlmann<sup>2</sup>, Sandrine Dudoit<sup>3</sup>,  
Annette Molinaro<sup>4</sup> and Mark J. van der Laan<sup>3</sup>

<sup>1</sup>Institut für Statistik  
Ludwig-Maximilians-Universität München  
Ludwigstraße 33, D-80539 München, Germany  
Tel: ++49-9131-8522707  
Fax: ++49-9131-8525740  
`Torsten.Hothorn@R-project.org`

<sup>2</sup>Seminar für Statistik, ETH Zürich, CH-8032 Zürich, Switzerland  
`buehlmann@stat.math.ethz.ch`

<sup>3</sup>Division of Biostatistics, University of California, Berkeley  
140 Earl Warren Hall, #7360, Berkeley, CA 94720-7360, USA  
`sandrine@stat.Berkeley.EDU`  
`laan@stat.Berkeley.EDU`

<sup>4</sup>Division of Biostatistics, Epidemiology and Public Health  
Yale University School of Medicine, 206 LEPH  
60 College Street PO Box 208034, New Haven CT 06520-8034  
`annette.molinaro@yale.edu`

## 1 Illustrations and Applications

This document reproduces the data analyses presented in [Hothorn et al. \(2006\)](#). For a description of the theory behind applications shown here we refer to the original manuscript. The results differ slightly due to technical changes or bug-fixes in **mboost** that have been implemented after the paper was printed.

### 1.1 Acute myeloid leukemia

**Data preprocessing** Compute IPC weights, define risk score and set up learning sample:

```
R> ### compute IPC weights
R> AMLw <- IPCweights(Surv(clinical$time, clinical$event))
```

```

R> ### risk score
R> risk <- rep(0, nrow(clinical))
R> rlev <- levels(clinical[, "Cytogenetic.group"])
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[c(7,8,4)]] <- "low"
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[c(5, 9)]] <- "intermediate"
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[-c(4,5, 7,8,9)]] <- "high"
R> risk <- as.factor(risk)
R> ### set-up learning sample
R> AMLlearn <- cbind(clinical[, c("time", "Sex", "Age", "LDH", "WBC",
                                "FLT3.aberration.", "MLL.PTD", "Tx.Group.")],
                    risk = risk,
                    iexpressions[, colnames(iexpressions) %in% selgenes[["Clone.ID"]]])
R> cc <- complete.cases(AMLlearn)
R> AMLlearn <- AMLlearn[AMLw > 0 & cc,]
R> AMLw <- AMLw[AMLw > 0 & cc]

```

**Model fitting** Fit random forest for censored data

```

R> ### controls for tree growing
R> ctrl <- cforest_control(mincriterion = 0.1, mtry = 5, minsplit = 5, ntree = 250)
R> ### fit random forest for censored data (warnings are OK here)
R> AMLrf <- cforest(I(log(time)) ~ ., data = AMLlearn, control = ctrl,
                    weights = AMLw)

```

and  $L_2$ Boosting for censored data

```

R> AMLl2b <- glmboost(I(log(time)) ~ ., data = AMLlearn, weights = AMLw,
                      control = boost_control(mstop = 5000))

```

Compute fitted values

```

R> ### restrict number of boosting iterations and inspect selected variables
R> AMLl2b <- AMLl2b[mstop(aic)]
R> cAML <- coef(AMLl2b)
R> cAML[abs(cAML) > 0]

```

<i>(Intercept)</i>	<i>Age</i>	<i>WBC</i>
0.5642932	0.0059785	-0.0056200
<i>MLL.PTDyes</i>	<i>Tx.Group.AUTO</i>	<i>Tx.Group.Ind</i>
-0.3153912	0.4542954	-2.1216104
`IMAGE:145643`	`IMAGE:345601`	`IMAGE:377560`
0.1062577	0.0043043	0.0275653
`IMAGE:2043415`	`IMAGE:1584563`	`IMAGE:347035`
0.0550938	-0.0025929	-0.0084766
`IMAGE:262695`	`IMAGE:26418`	`IMAGE:950479`
0.0269555	0.0080214	0.0371741
`IMAGE:1534700`	`IMAGE:1472689`	`IMAGE:1526826`
0.0283645	0.0225640	-0.0278373
`IMAGE:786302`	`IMAGE:243614`	`IMAGE:417884`
0.0449326	-0.0566722	-0.0248869
`IMAGE:1592006`	`IMAGE:884333`	`IMAGE:133273`

```
R> ### AIC criterion  
R> plot(aic <- AIC(AML12b))
```

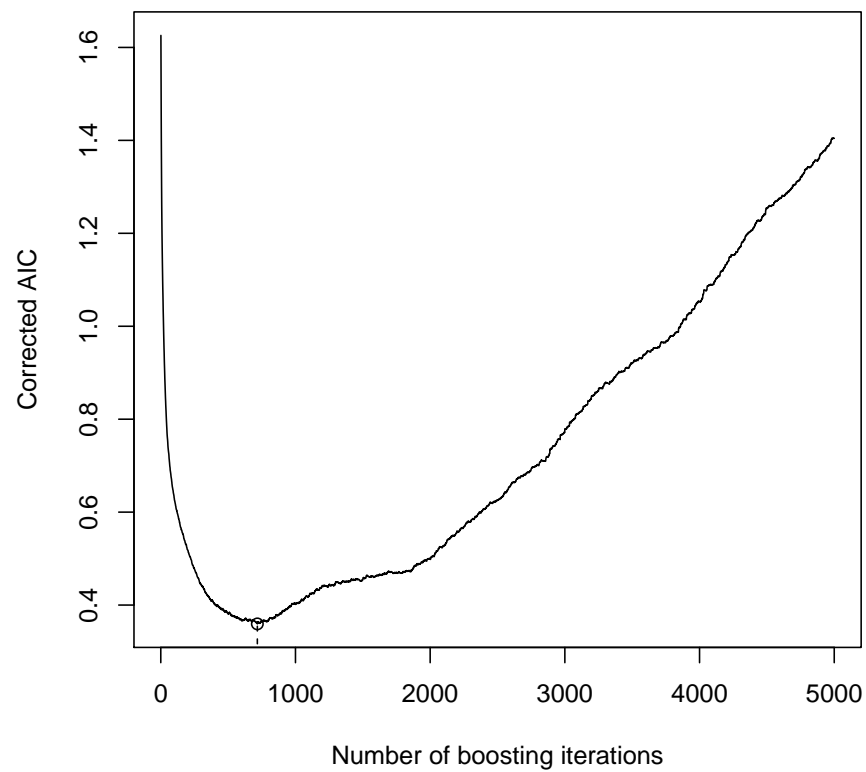


Figure 1: AIC criterion for AML data.

```

-0.0355121      0.0128054      0.0257924
`IMAGE:950888` `IMAGE:809533` `IMAGE:49389`
  0.0348510      -0.0583489      0.1210483
`IMAGE:856174` `IMAGE:435036` `IMAGE:491751`
  0.0205370      0.0620215      0.1155506
`IMAGE:782835` `IMAGE:52930` `IMAGE:2545705`
 -0.1108508      -0.0245246      -0.0788422
`IMAGE:756405` `IMAGE:129032` `IMAGE:1610168`
  0.0085293      -0.1158217      0.0137998
`IMAGE:69002` `IMAGE:2019101` `IMAGE:1456160`
 -0.2793326      -0.0966590      -0.1041466
`IMAGE:2566064` `IMAGE:565083` `IMAGE:843028`
  0.0154665      0.1875592      0.0698328
`IMAGE:68794` `IMAGE:488505` `IMAGE:291756`
  0.0761390      0.2784632      0.0994879
`IMAGE:810801` `IMAGE:1702742` `IMAGE:380462`
  0.0465851      -0.0104549      -0.0957299
`IMAGE:154472` `IMAGE:302540` `IMAGE:135221`
 -0.1454724      0.0188789      -0.0366827
`IMAGE:1567220`
  0.0485058

```

```

R> ### fitted values
R> AMLprf <- predict(AMLrfr, newdata = AMLlearn)
R> AMLpb <- predict(AMLl2b, newdata = AMLlearn)

```

## 1.2 Node-positive breast cancer

**Data preprocessing** Compute IPC weights and set up learning sample:

```

R> ### attach data
R> data("GBSG2", package = "ipred")
R> ### IPC weights
R> GBSG2w <- IPCweights(Surv(GBSG2$time, GBSG2$cens))
R> ### set-up learning sample
R> GBSG2learn <- cbind(GBSG2[,which(names(GBSG2) %in% c("time", "cens"))],
  ltime = log(GBSG2$time))
R> n <- nrow(GBSG2learn)

```

### Model fitting

```

R> ### linear model
R> LMmod <- lm(ltime ~ ., data = GBSG2learn, weights = GBSG2w)
R> LMerisk <- sum((GBSG2learn$ltime - predict(LMmod))^2*GBSG2w) / n
R> ### regression tree
R> pos <- GBSG2w > 0
R> TRmod <- rpart(ltime ~ ., data = GBSG2learn, weights = GBSG2w,
  subset = pos)
R> TRerisk <- sum((GBSG2learn$ltime[pos] - predict(TRmod))^2*GBSG2w[pos]) / n
R> ### tree controls

```

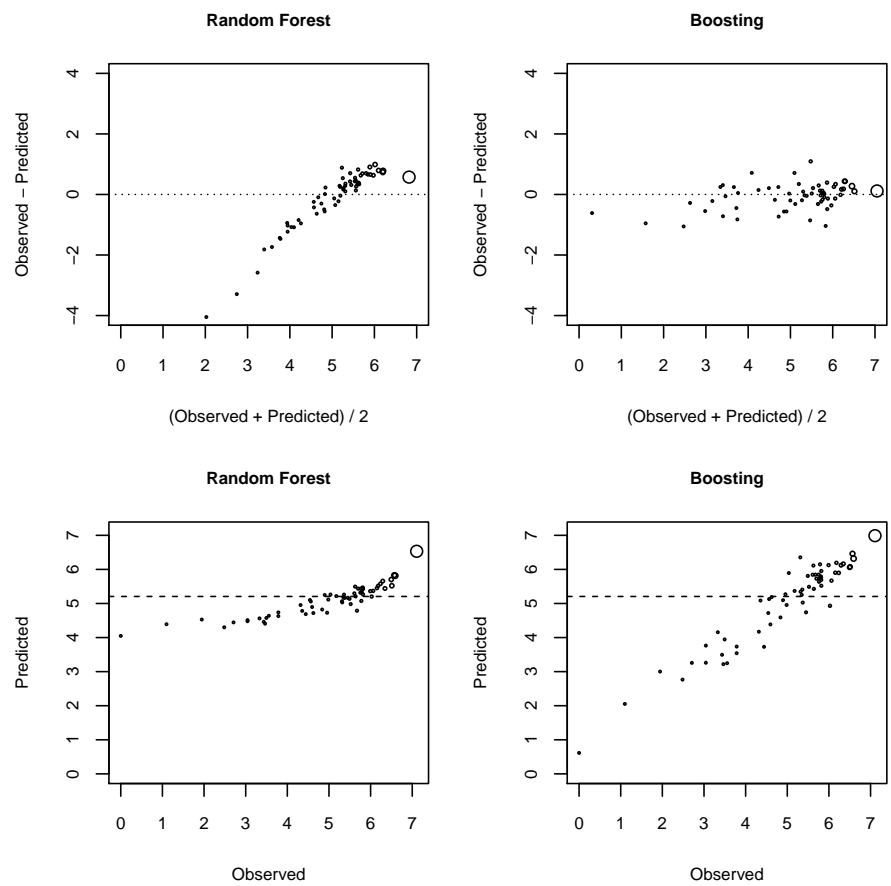


Figure 2: AML data: Reproduction of Figure 1.

```

R> ctrl <- cforest_control(mincriterion = qnorm(0.95), mtry = 5,
                           minsplit = 5, ntree = 100)
R> ### fit random forest for censored data (warnings are OK here)
R> RFmod <- cforest(ltime ~ ., data = GBSG2learn, weights = GBSG2w,
                   control = ctrl)
R> ### fit L2 boosting for censored data
R> L2Bmod <- glmboost(ltime ~ ., data = GBSG2learn, weights = GBSG2w,
                    control = boost_control(mstop = 250))
R> ### with Huber loss function
R> L2BHubermod <- glmboost(ltime ~ ., data = GBSG2learn, weights = GBSG2w,
                          family = Huber(d = log(2)))

```

Compute fitted values:

```

R> GBSG2Hp <- predict(L2BHubermod, newdata = GBSG2learn)
R> L2Berisk <- sum((GBSG2learn$ltime - predict(L2Bmod, newdata = GBSG2learn))^2*GBSG2w) / n
R> RFerisk <- sum((GBSG2learn$ltime - predict(RFmod, newdata = GBSG2learn))^2*GBSG2w) / n

```

```
R> plot(aic <- AIC(L2Bmod))
```

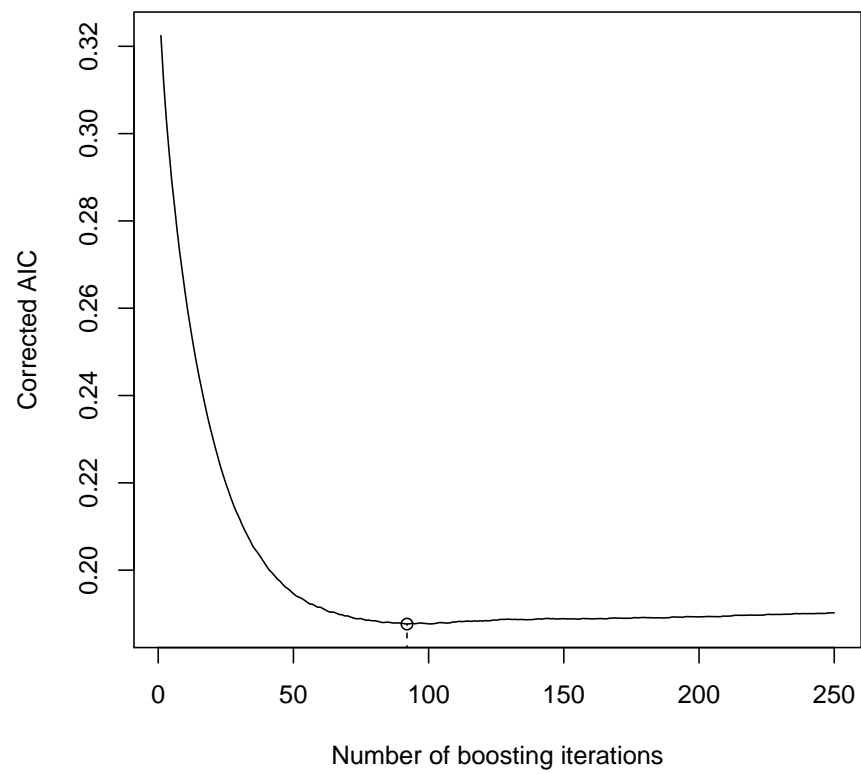


Figure 3: AIC criterion for GBSG2 data.

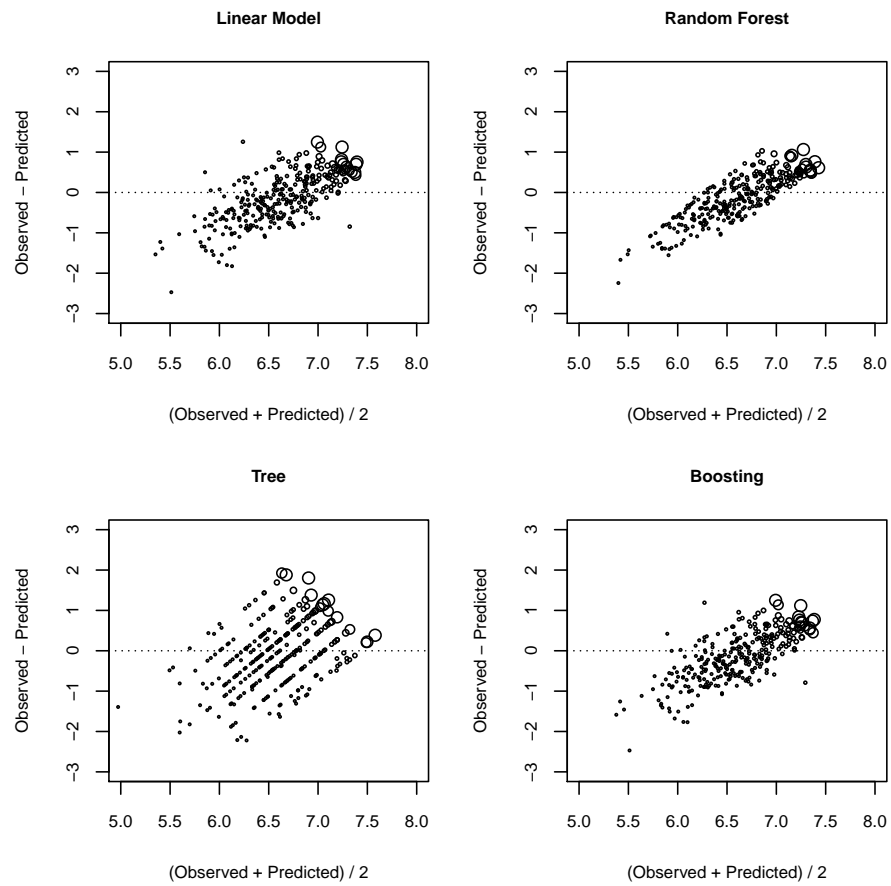


Figure 4: GBSG-2 data: Reproduction of Figure 3.



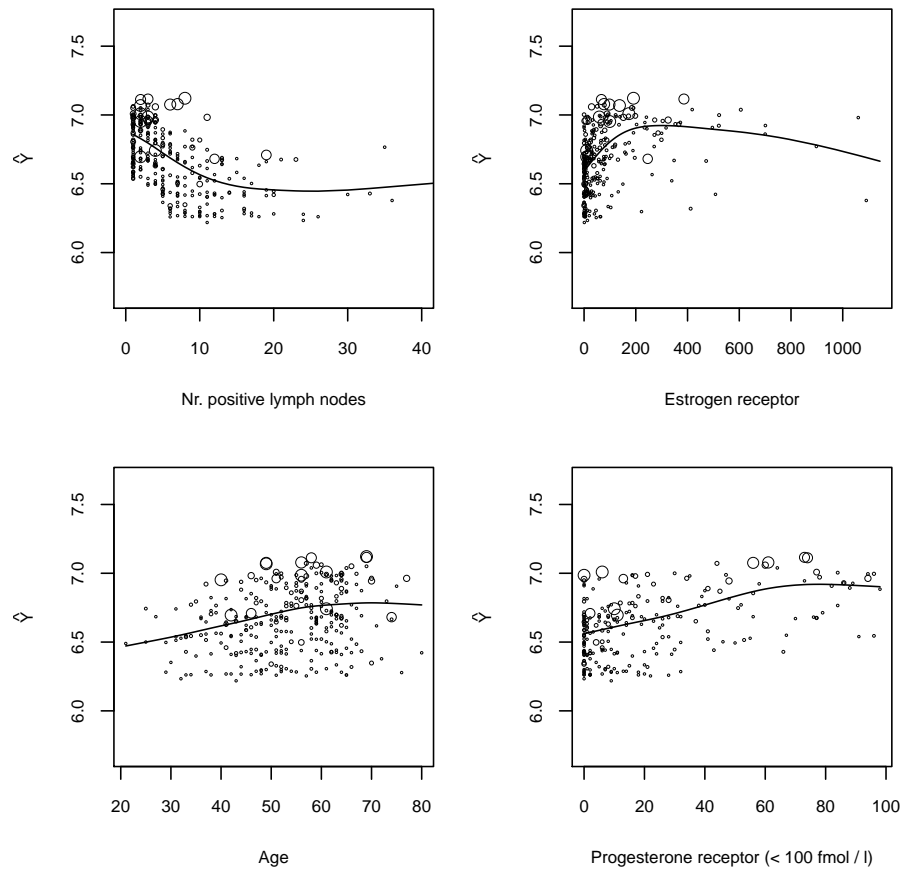


Figure 5: GBSG-2 data: Reproduction of Figure 5.

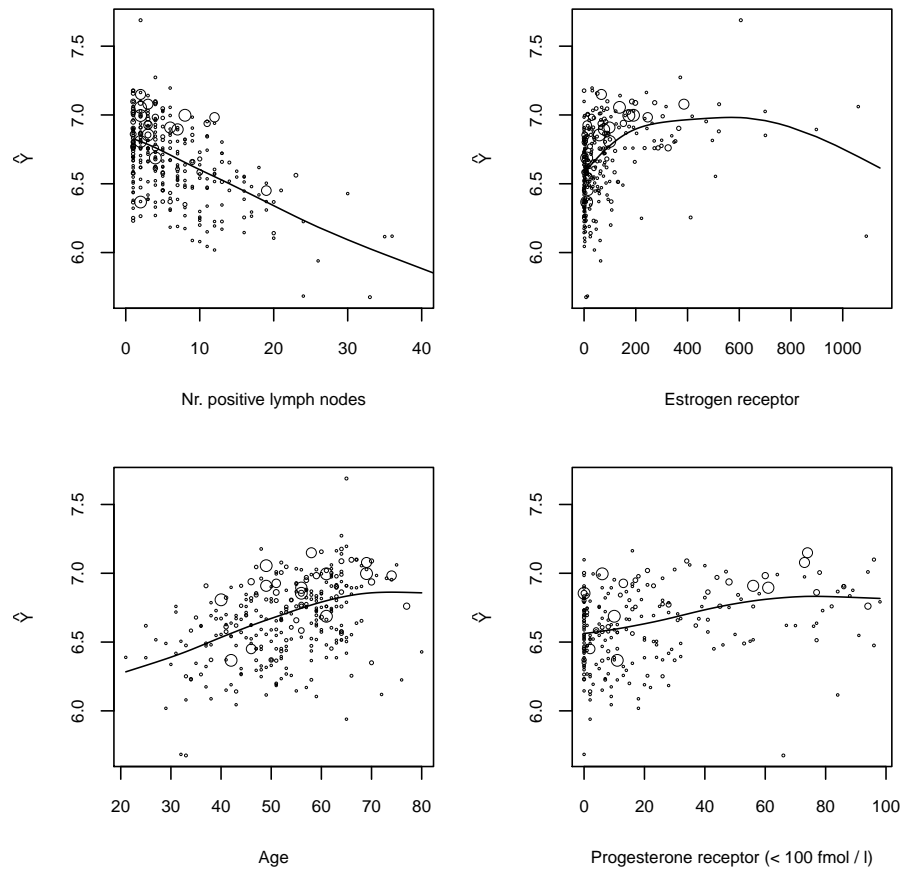


Figure 6: GBSG-2 data: Reproduction of Figure 6.

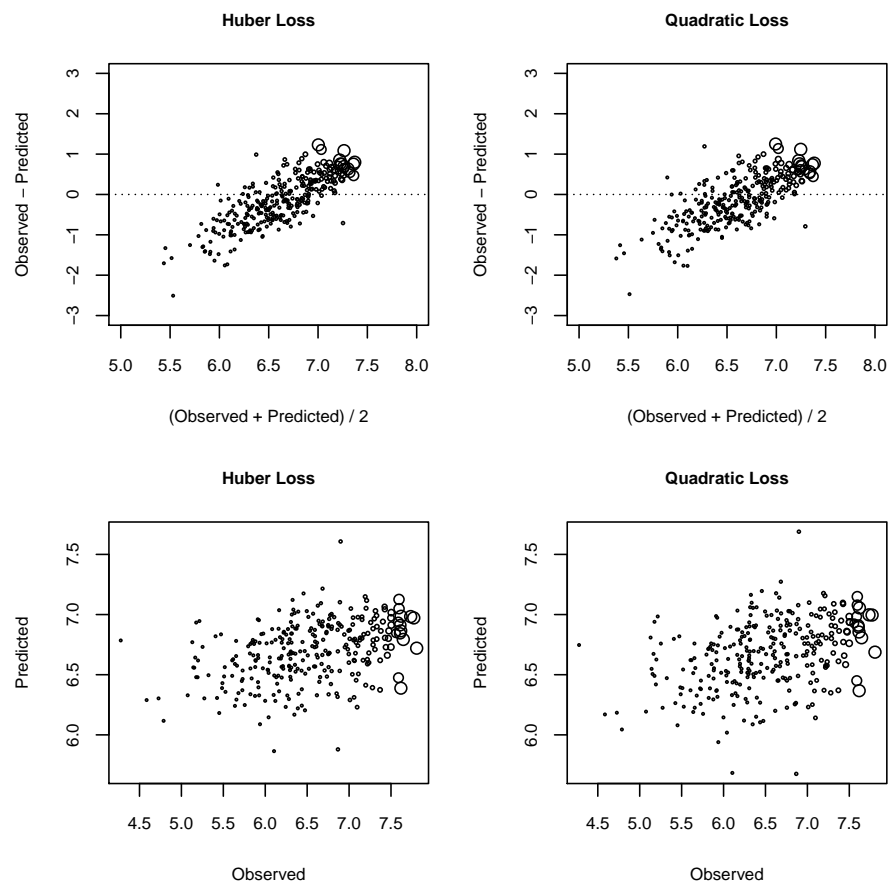


Figure 7: GBSG-2 data: Reproduction of Figure 7.

## References

- T.~Hothorn, P.~Bühlmann, S.~Dudoit, A.~Molinaro, and M.~van~der~Laan.  
Survival ensembles. *Biostatistics*, 7:355–373, 2006.