# Survival Ensembles

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## 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 <- ctree_control(testtype = "Teststatistic",
                         teststat = "maximum", mincriterion = .1, minsplit = 5)
R> ### was: cforest_control(mincriterion = 0.1, mtry = 5, minsplit = 5, ntree = 250)
R>
R> ### fit random forest for censored data (warnings are OK here)
R> AMLrf <- cforest(log(time) ~ ., data = AMLlearn, control = ctrl,
                    weights = AMLw, mtry = 5, ntree = 250,
                    perturb = list(replace = TRUE, fraction = 0.632))
```

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]
```

```
    (Intercept)             Age             WBC
        0.56429         0.00598        -0.00562
     MLL.PTDyes   Tx.Group.AUTO    Tx.Group.Ind
       -0.31539         0.45430        -2.12161
 `IMAGE:145643`  `IMAGE:345601`  `IMAGE:377560`
        0.10626         0.00430         0.02757
`IMAGE:2043415` `IMAGE:1584563`  `IMAGE:347035`
        0.05509        -0.00259        -0.00848
 `IMAGE:262695`   `IMAGE:26418`  `IMAGE:950479`
        0.02696         0.00802         0.03717
```

```
R> ### AIC criterion
R> plot(aic <- AIC(AMLl2b))
```

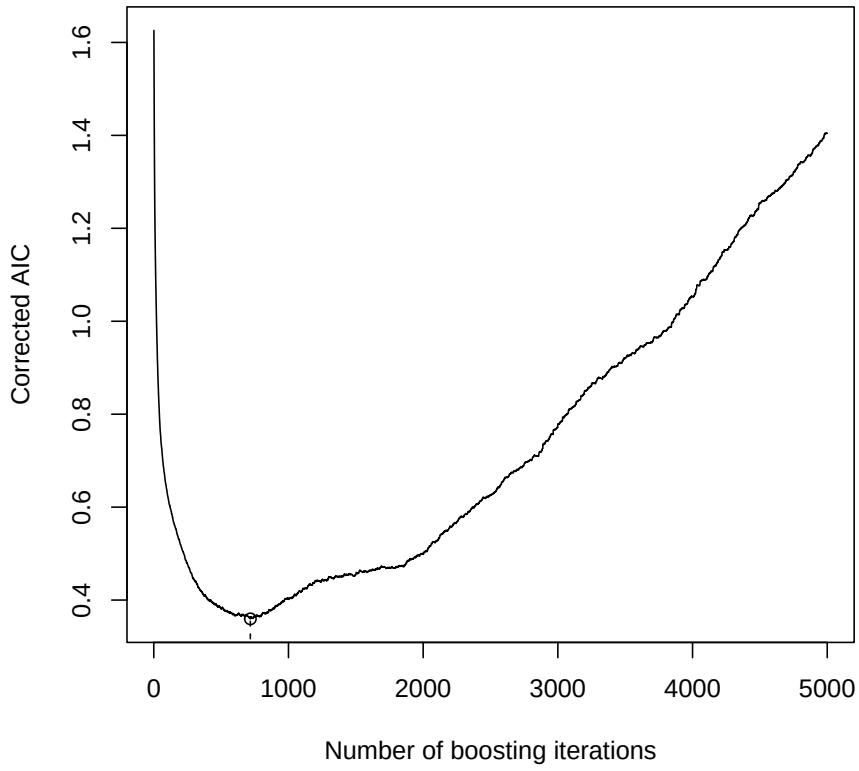


Figure 1: AIC criterion for AML data.

```
`IMAGE:1534700` `IMAGE:1472689` `IMAGE:1526826`
        0.02836         0.02256        -0.02784
 `IMAGE:786302`  `IMAGE:243614`  `IMAGE:417884`
        0.04493        -0.05667        -0.02489
`IMAGE:1592006`  `IMAGE:884333`  `IMAGE:133273`
       -0.03551         0.01281         0.02579
 `IMAGE:950888`  `IMAGE:809533`   `IMAGE:49389`
        0.03485        -0.05835         0.12105
 `IMAGE:856174`  `IMAGE:435036`  `IMAGE:491751`
        0.02054         0.06202         0.11555
 `IMAGE:782835`   `IMAGE:52930` `IMAGE:2545705`
       -0.11085        -0.02452        -0.07884
 `IMAGE:756405`  `IMAGE:129032` `IMAGE:1610168`
        0.00853        -0.11582         0.01380
  `IMAGE:69002` `IMAGE:2019101` `IMAGE:1456160`
       -0.27933        -0.09666        -0.10415
`IMAGE:2566064`  `IMAGE:565083`  `IMAGE:843028`
        0.01547         0.18756         0.06983
  `IMAGE:68794`  `IMAGE:488505`  `IMAGE:291756`
        0.07614         0.27846         0.09949
 `IMAGE:810801` `IMAGE:1702742`  `IMAGE:380462`
        0.04659        -0.01045        -0.09573
 `IMAGE:154472`  `IMAGE:302540`  `IMAGE:135221`
       -0.14547         0.01888        -0.03668
`IMAGE:1567220`
        0.04851
```

```
R> ### fitted values
R> AMLprf <- predict(AMLrf, 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 = "TH.data")
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
```

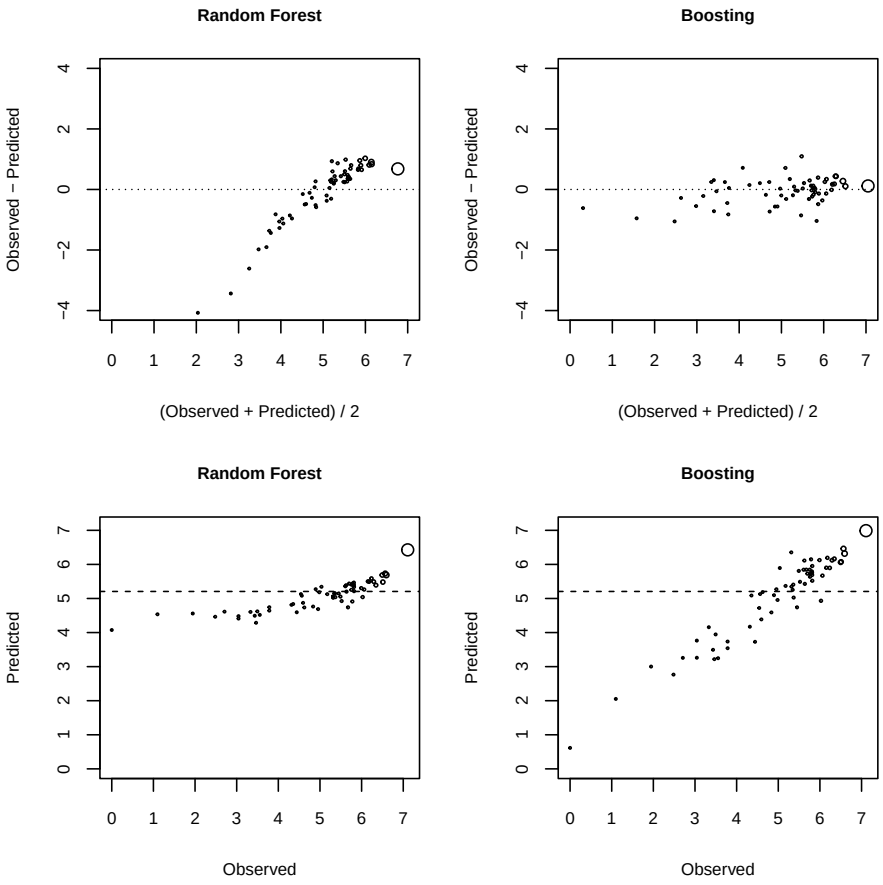


Figure 2: AML data: Reproduction of Figure 1.

```
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
R> ctrl <- ctree_control(testtype = "Teststatistic",
                         teststat = "maximum", mincriterion = qnorm(.95),
                         minsplit = 5)
R> ### was: cforest_control(mincriterion = qnorm(0.95), mtry = 5,
R> ###                     minsplit = 5, ntree = 100)
R>
R>
R> ### fit random forest for censored data (warnings are OK here)
R> RFmod <- cforest(ltime ~ . , data = GBSG2learn, weights = GBSG2w,
                    control = ctrl, mtry = 5, ntree = 100,
                    perturb = list(replace = TRUE,
                        fraction = 0.632 * sum(GBSG2w > 0)))
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))
```

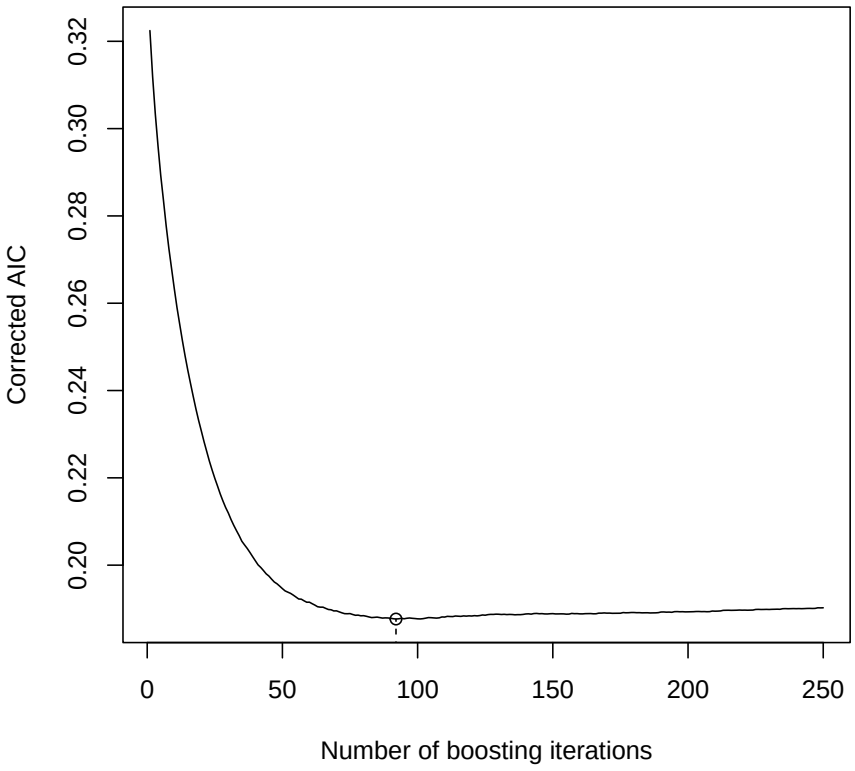


Figure 3: AIC criterion for GBSG2 data.

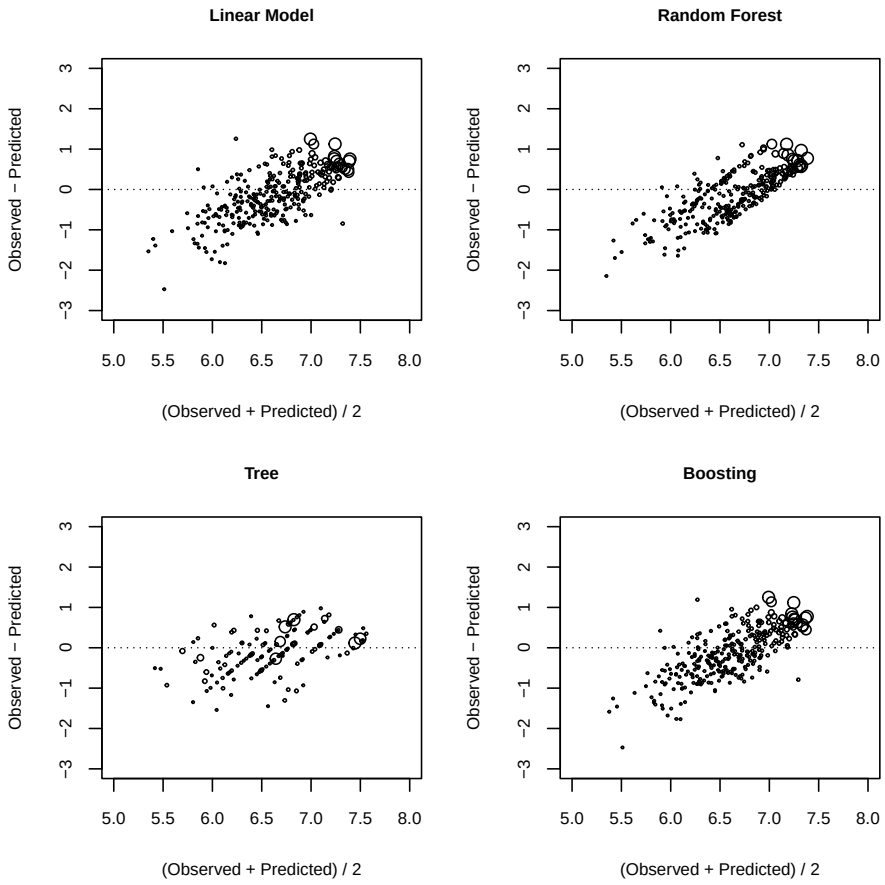


Figure 4: GBSG-2 data: Reproduction of Figure 3.

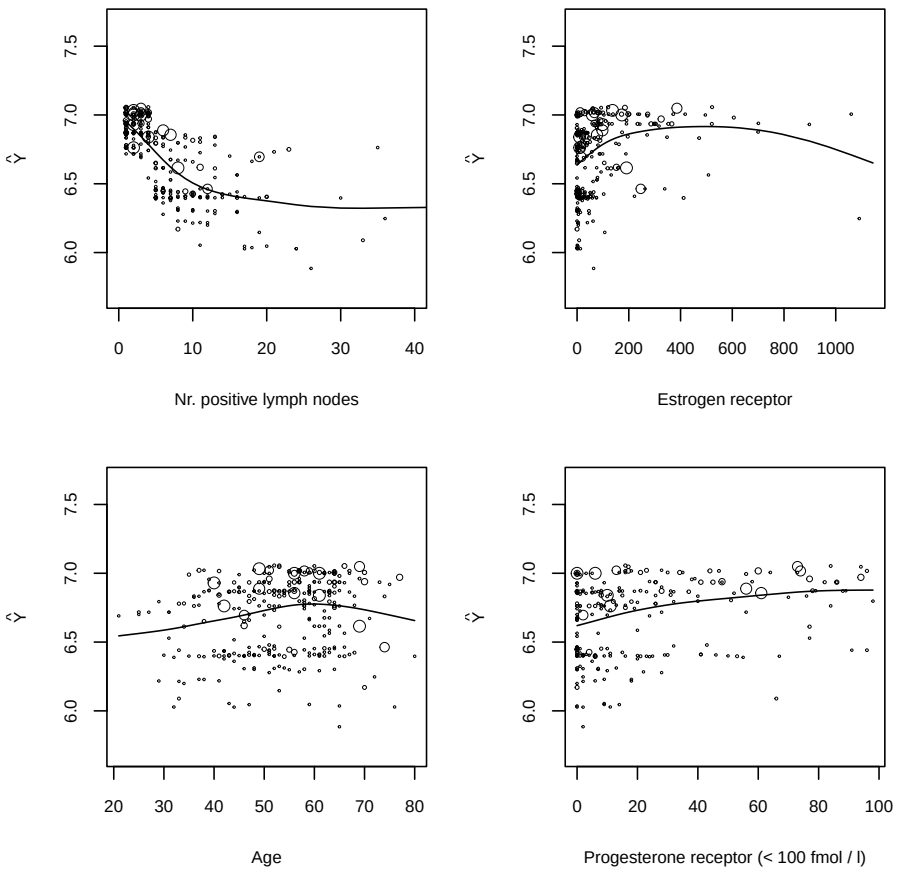


Figure 5: GBSG-2 data: Reproduction of Figure 5.

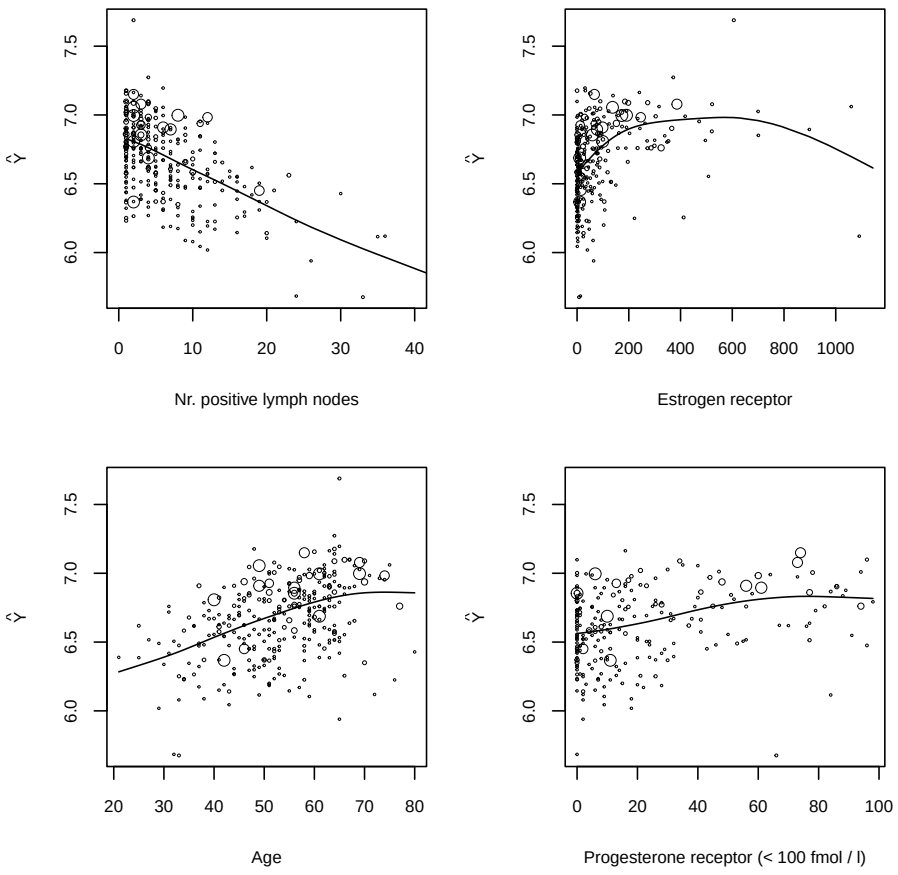


Figure 6: GBSG-2 data: Reproduction of Figure 6.

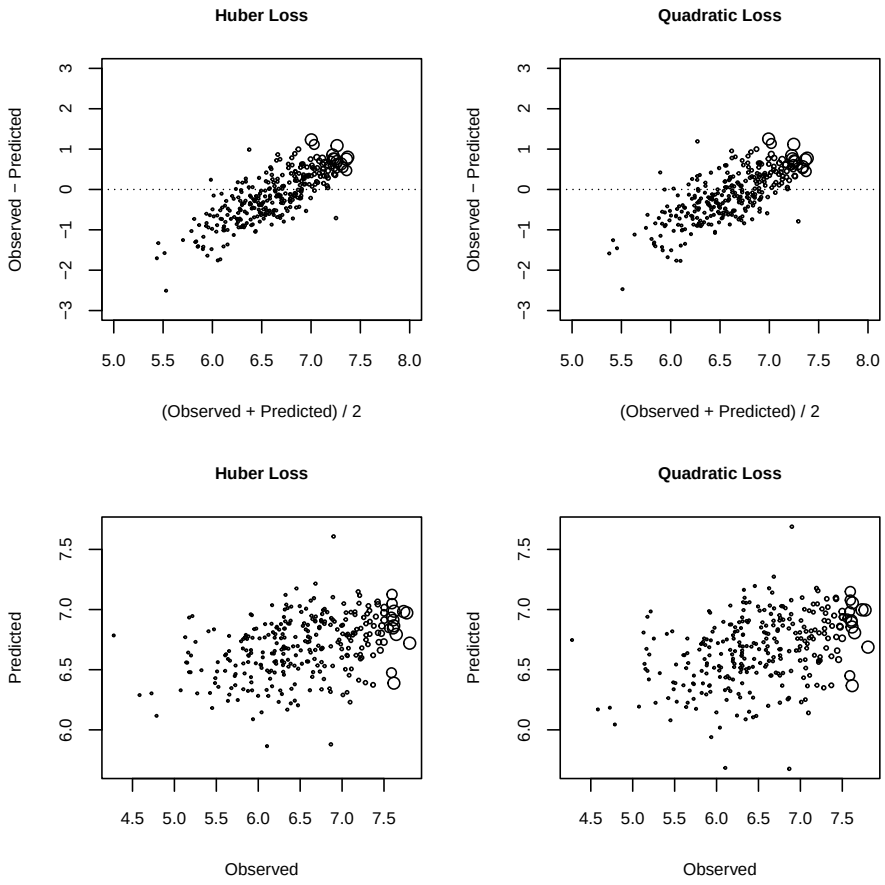


Figure 7: GBSG-2 data: Reproduction of Figure 7.

# References

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