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.

1.1 Acute myeloid leukemia

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

```
R> AMLw <- IPCweights(Surv(clinical$time, clinical$event))
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> 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> ctrl <- cforest_control(mincriterion = 0.1, mtry = 5,
        minsplit = 5, ntree = 250)
R> AMLrf <- cforest(I(log(time)) ~ ., data = AMLlearn,
        control = ctrl, weights = AMLw)
```

and L_2Boosting for censored data

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

Compute fitted values

```
R> AMLl2b <- AMLl2b[mstop(aic)]
R> cAML <- coef(AMLl2b)
R> cAML[abs(cAML) > 0]

     (Intercept)              Age                 WBC
      0.03094981       0.00854937         -0.00364371
       MLL.PTDyes    Tx.Group.AUTO         Tx.Group.IC
     -0.50709786       0.90185340          0.04037578
    Tx.Group.Ind riskintermediate      `IMAGE:145643`
     -1.86134842       0.11825619          0.19788355
`IMAGE:2542486`   `IMAGE:345601`      `IMAGE:377560`
      0.00442375       0.02935101          0.11000322
 `IMAGE:428782`  `IMAGE:2043415`     `IMAGE:1584563`
      0.01010658       0.05911671         -0.17883619
 `IMAGE:347035`   `IMAGE:262695`      `IMAGE:950479`
     -0.03307600       0.00080156          0.09049309
 `IMAGE:898305`  `IMAGE:1472689`      `IMAGE:150702`
      0.00523016       0.03498572          0.01367553
`IMAGE:1526826`    `IMAGE:66507`      `IMAGE:786302`
     -0.01805326       0.00399127          0.08941300
 `IMAGE:243614`   `IMAGE:417884`     `IMAGE:1592006`
     -0.05776062      -0.04890054         -0.02269622
`IMAGE:1917063`   `IMAGE:884333`      `IMAGE:133273`
```

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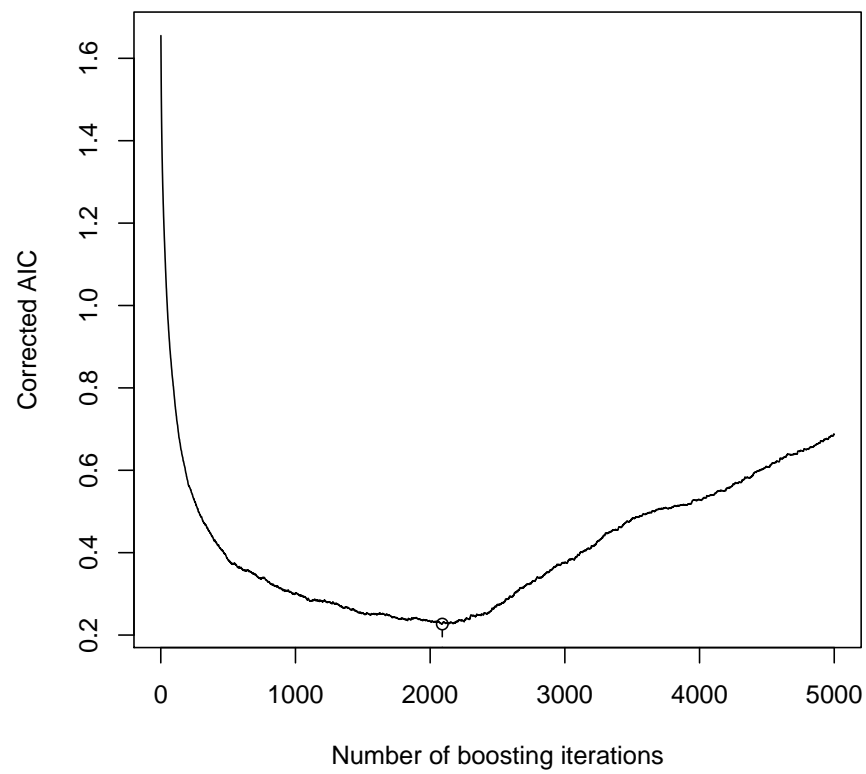

Figure 1: AIC criterion for AML data.

```
     -0.06536720        0.04189990        0.06594787
  `IMAGE:950888`     `IMAGE:809533`     `IMAGE:49389`
      0.02027810       -0.15986981        0.06352703
  `IMAGE:789357`     `IMAGE:142139`    `IMAGE:1558053`
     -0.01252187        0.00089307        0.07795515
  `IMAGE:856174`     `IMAGE:504421`     `IMAGE:435036`
      0.01115234        0.06861766        0.06094620
  `IMAGE:491751`     `IMAGE:782835`     `IMAGE:52930`
      0.04336285       -0.17924185       -0.03503330
 `IMAGE:2545705`     `IMAGE:756405`     `IMAGE:502664`
     -0.09886616        0.07713650        0.03620466
  `IMAGE:129032`    `IMAGE:1610168`     `IMAGE:327676`
     -0.31322459        0.01260374       -0.02117310
   `IMAGE:69002`     `IMAGE:121551`    `IMAGE:2019101`
     -0.41671336       -0.08107446       -0.06531175
 `IMAGE:1456160`     `IMAGE:430318`    `IMAGE:2566064`
     -0.10208684       -0.07297586        0.06126683
   `IMAGE:74537`    `IMAGE:1606557`     `IMAGE:306812`
      0.04523784        0.14243526        0.03504441
  `IMAGE:565083`     `IMAGE:843028`     `IMAGE:68794`
      0.29555347        0.05619983        0.23722775
  `IMAGE:488505`     `IMAGE:167205`     `IMAGE:291756`
      0.33464829        0.00217136        0.04973319
  `IMAGE:810801`    `IMAGE:1702742`     `IMAGE:380462`
      0.08725523       -0.04428190       -0.13182519
  `IMAGE:154472`     `IMAGE:302540`     `IMAGE:135221`
     -0.24723347        0.17175129       -0.01972168
 `IMAGE:1567220`     `IMAGE:594630`
      0.02473376       -0.07396882
```

```
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> data("GBSG2", package = "ipred")
R> GBSG2w <- IPCweights(Surv(GBSG2$time, GBSG2$cens))
R> GBSG2learn <- cbind(GBSG2[, -which(names(GBSG2) %in%
        c("time", "cens"))], ltime = log(GBSG2$time))
R> n <- nrow(GBSG2learn)
```

Model fitting

```
R> LMmod <- lm(ltime ~ ., data = GBSG2learn, weights = GBSG2w)
R> LMerisk <- sum((GBSG2learn$ltime - predict(LMmod))^2 *
        GBSG2w)/n
R> TRmod <- rpart(ltime ~ ., data = GBSG2learn, weights = GBSG2w)
R> TRerisk <- sum((GBSG2learn$ltime - predict(TRmod))^2 *
        GBSG2w)/n
R> ctrl <- cforest_control(mincriterion = qnorm(0.95),
```
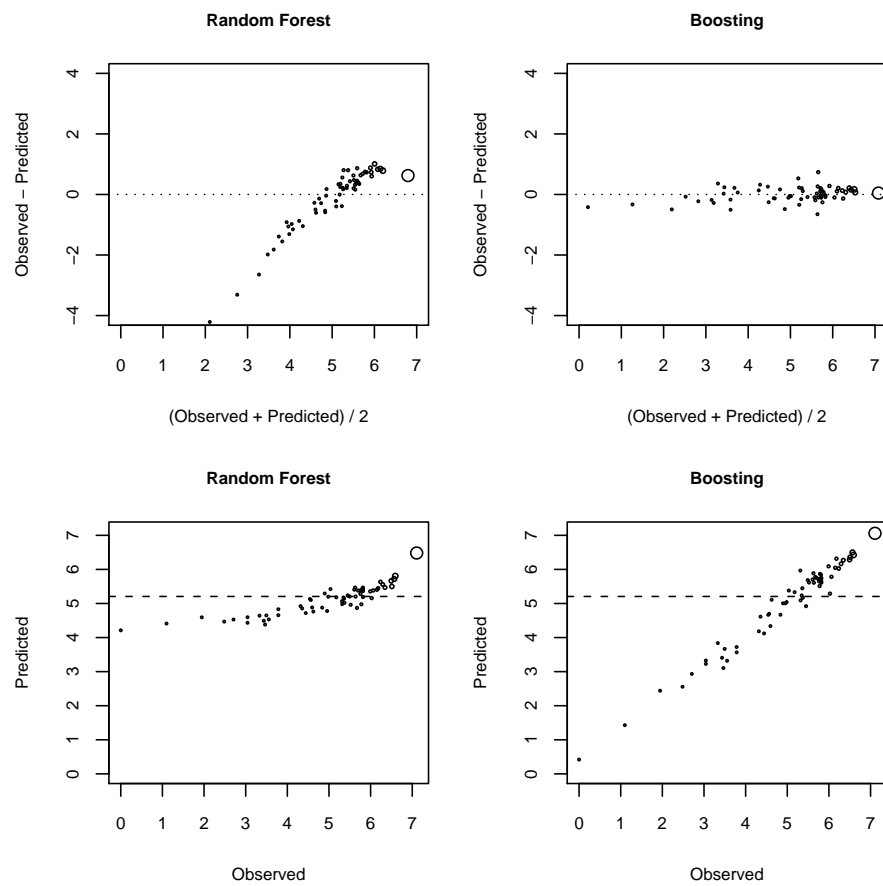
Figure 2: AML data: Reproduction of Figure 1.

```
              mtry = 5, minsplit = 5, ntree = 100)
R> RFmod <- cforest(ltime ~ ., data = GBSG2learn,
          weights = GBSG2w, control = ctrl)
R> L2Bmod <- glmboost(ltime ~ ., data = GBSG2learn,
          weights = GBSG2w, control = boost_control(mstop = 250))
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))
```
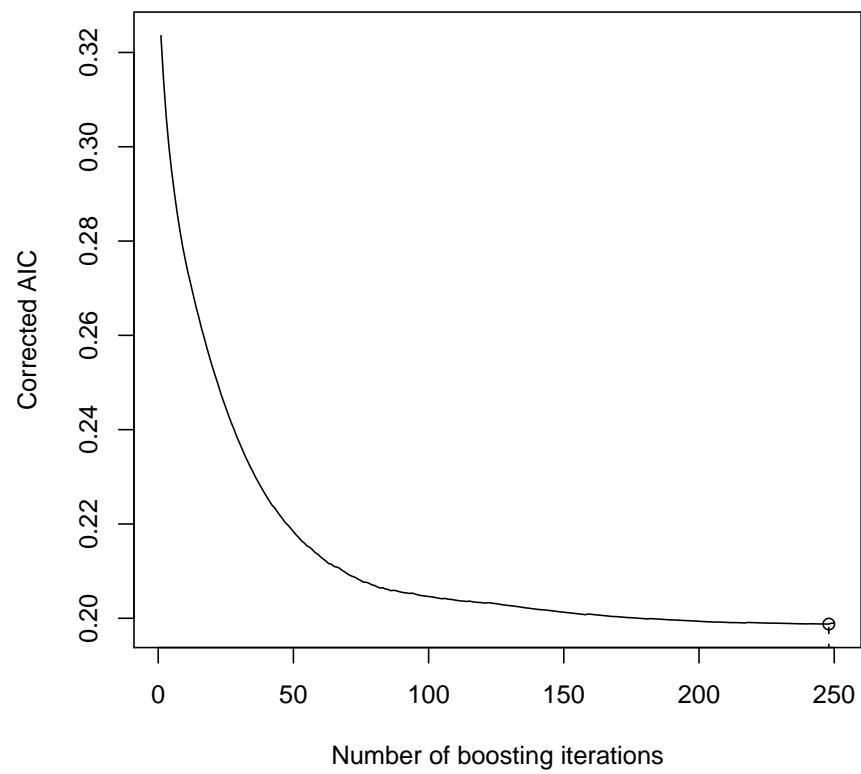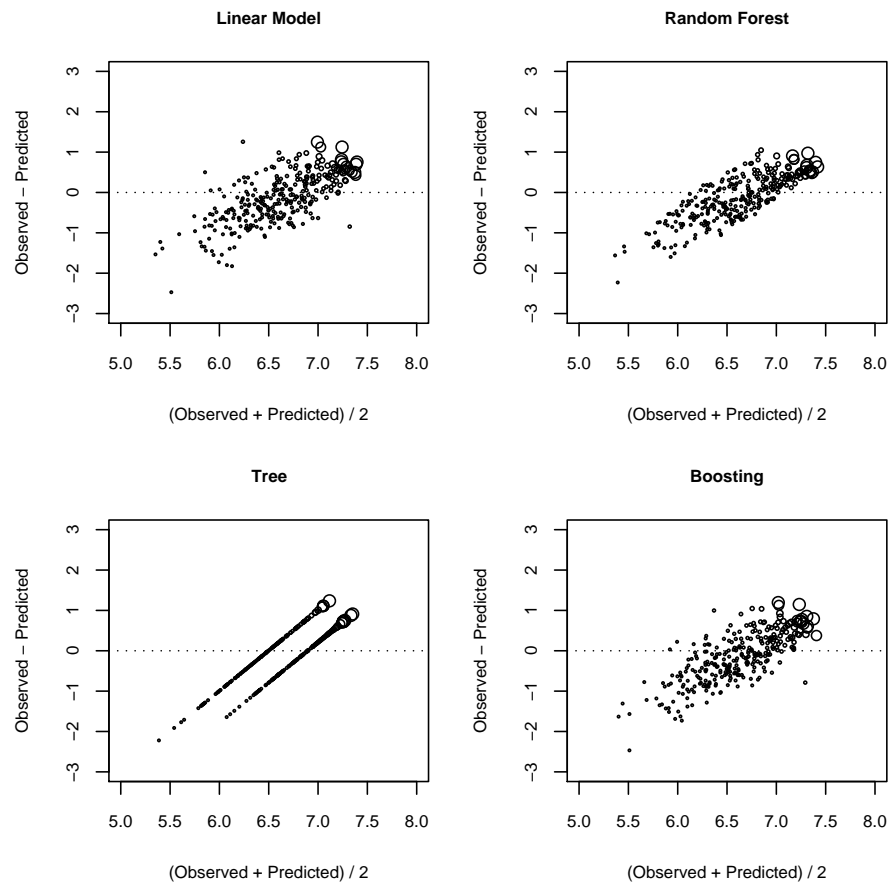

Figure 3: AIC criterion for GBSG2 data.
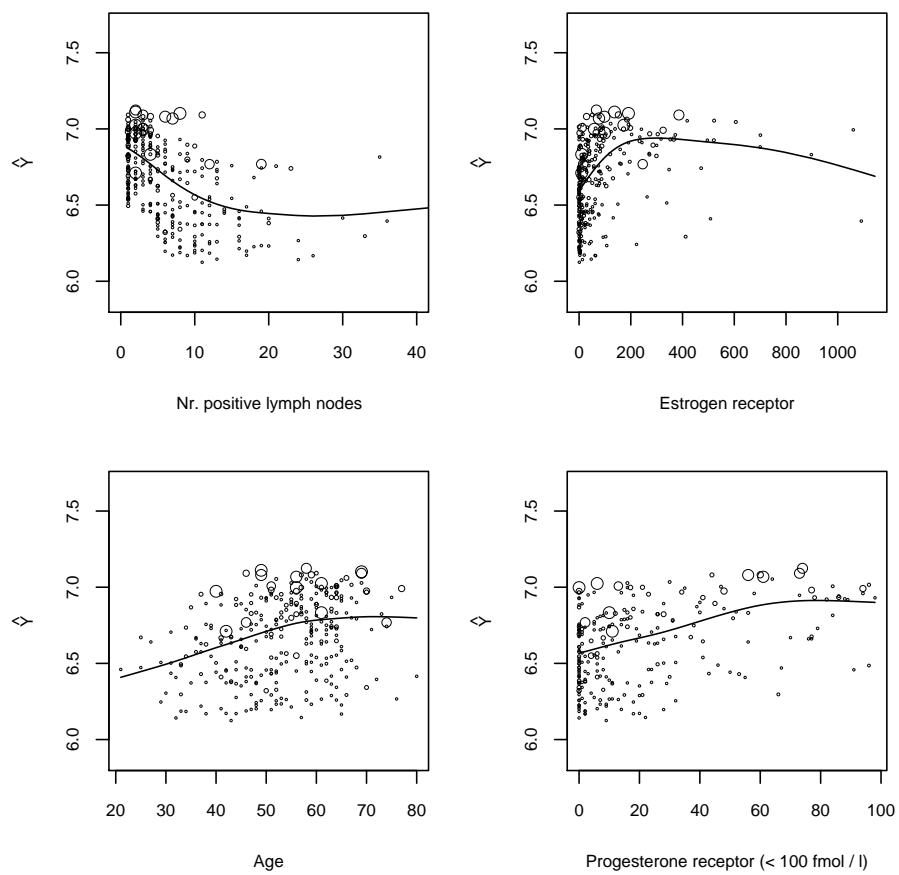
Figure 4: GBSG-2 data: Reproduction of Figure 3.
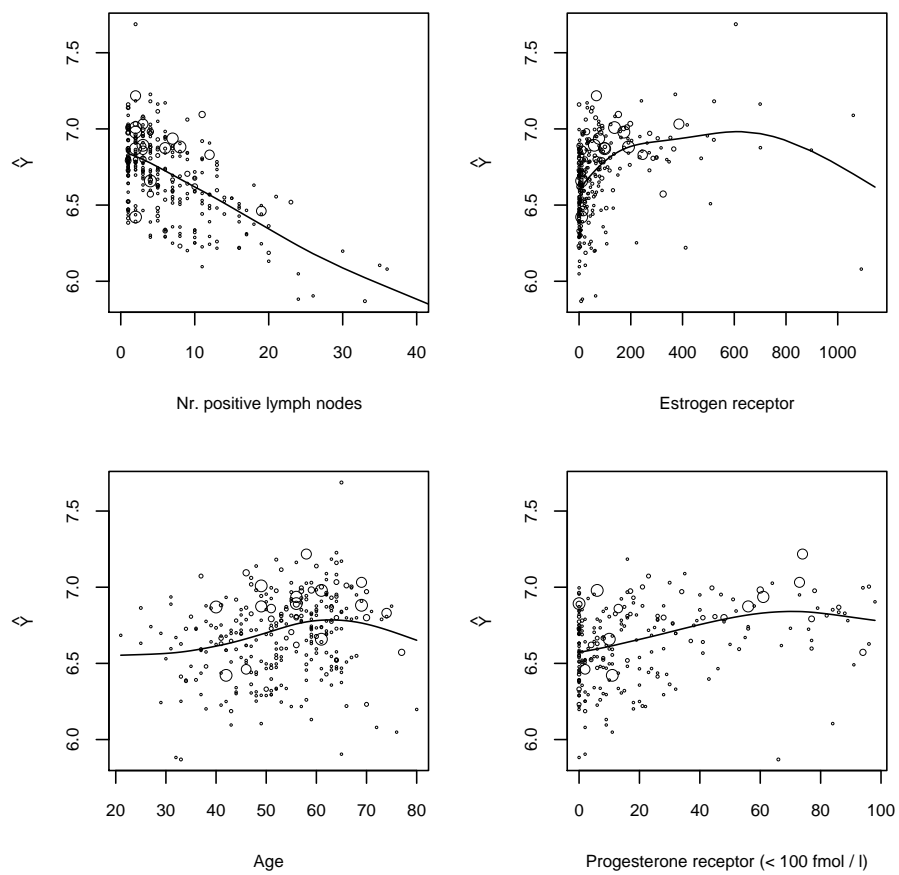
Figure 5: GBSG-2 data: Reproduction of Figure 5.
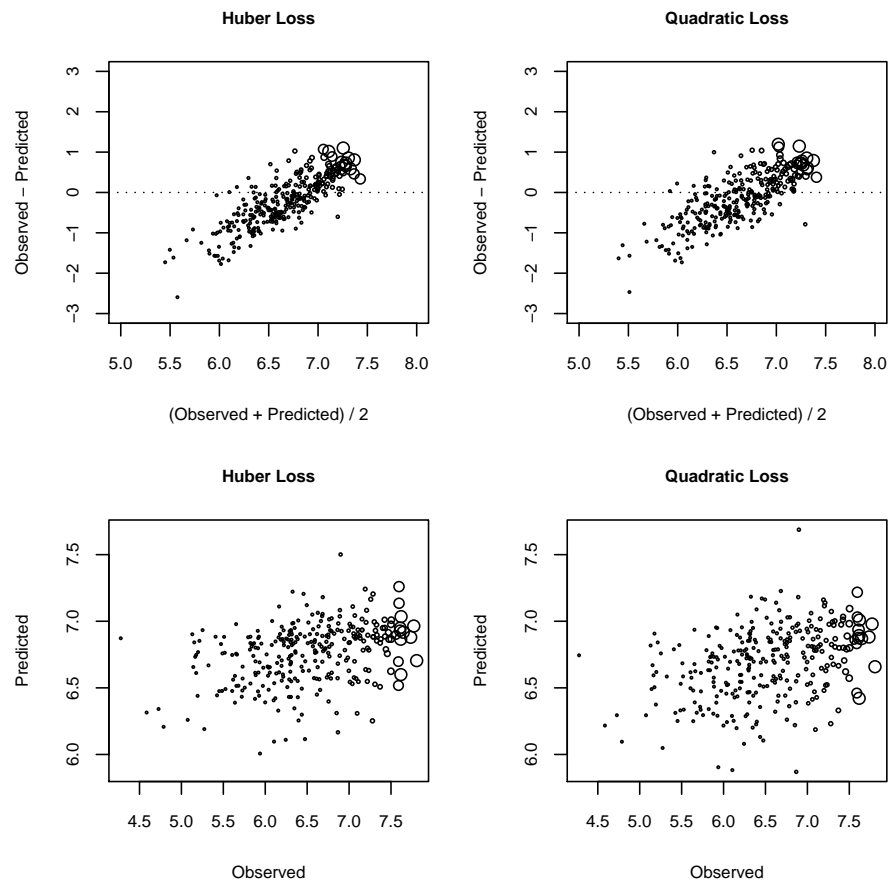
Figure 6: GBSG-2 data: Reproduction of Figure 6.

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

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References

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