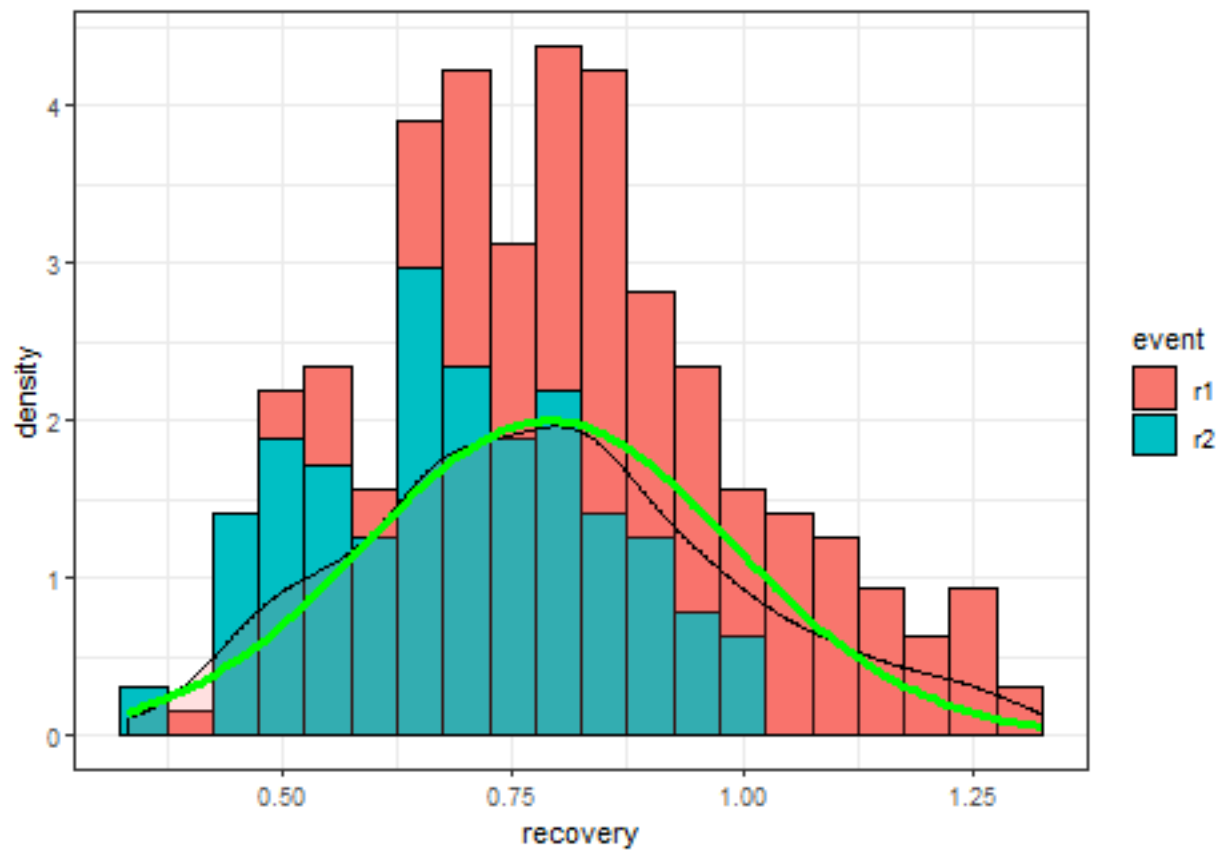


Recovery_Analysis

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```
##      mean      sd
## 0.789570071 0.202778505
## (0.012673657) (0.008961629)
```

```
## boundary (singular) fit: see ?isSingular
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```

```
rcv.mod.names <- c("recov.null","recov.spp", "recov.treat", "recov.phot", "recov.add", "recov.add2", "r")
rcv.mods <- list( )
```

```
for(i in 1:length(rcv.mod.names)) {
```

```

rcv.mods[[i]] <- get(rcv.mod.names[i]) }
print(aictab(cand.set = rcv.mods,
            modnames = rcv.mod.names))

##
## Model selection based on AICc:
##
##           K      AICc Delta_AICc AICcWt Cum.Wt Res.LL
## recov.spp  11 -248.65      0.00   0.98   0.98 135.87
## recov.add  12 -240.55      8.10   0.02   1.00 132.92
## recov.int  19 -217.65     31.00   0.00   1.00 129.43
## recov.null   4 -124.02    124.63   0.00   1.00  66.09
## recov.phot   5 -123.90    124.75   0.00   1.00  67.07
## recov.treat  5 -116.42    132.23   0.00   1.00  63.33
## recov.add2   6 -116.27    132.39   0.00   1.00  64.30
## recov.int2   7 -110.40    138.25   0.00   1.00  62.42

#Get parameter estimates averaged top models
rcv.mod.names.top <- c("recov.spp", "recov.add")
rcv.mods.top <- list( )
  for(i in 1:length(rcv.mod.names.top)) {
    rcv.mods.top[[i]] <- get(rcv.mod.names.top[i]) }

rcv.terms <- c("speciesAGCR", "speciesAGST", "speciesBODA", "speciesBOGR",
              "speciesCYDA", "speciesPAVI", "speciesSCAR",
              "speciesTHIN", "trtT" )
rcv.av.params <- as.data.frame(array(NA,c(length(rcv.terms),4)))
colnames(rcv.av.params)<-c("term","estimate","ciL","ciU")
for(i in 1:length(rcv.terms)) {
  rcv.av <- modavg(parm = paste(rcv.terms[i]),
                  cand.set = rcv.mods.top,
                  modnames = rcv.mod.names.top)
  rcv.av.params[i,1] <- rcv.terms[i]
  rcv.av.params[i,2] <- round(rcv.av$Mod.avg.beta, 2)
  rcv.av.params[i,3] <- round(rcv.av$Lower.CL, 3)
  rcv.av.params[i,4] <- round(rcv.av$Upper.CL, 3) }

rcv.av.params

##           term estimate      ciL      ciU
## 1 speciesAGCR      1.04   0.974  1.100
## 2 speciesAGST      0.84   0.777  0.903
## 3 speciesBODA      0.82   0.759  0.885
## 4 speciesBOGR      0.83   0.771  0.896
## 5 speciesCYDA      0.62   0.555  0.681
## 6 speciesPAVI      0.78   0.713  0.839
## 7 speciesSCAR      0.79   0.724  0.850
## 8 speciesTHIN      0.63   0.563  0.689
## 9          trtT      0.01  -0.017  0.042

rcv.av.params$term <- factor(rcv.av.params$term,
                             levels=c("speciesCYDA", "speciesPAVI",
                                       "speciesBODA", "speciesBOGR",
                                       "speciesTHIN", "speciesSCAR", "speciesAGST",

```

```

      "speciesAGCR", "trtT"),
    labels=c("Bermuda grass", "Switchgrass", "Buffalograss", "Blue grama",
             "Intermediate \n wheatgrass", "Tall fescue",
             "Creeping \n bentgrass",
             "Crested \n wheatgrass", "Dust"))

rcv.av.params <- rcv.av.params %>%
  mutate(photo=ifelse(term=="Crested \n wheatgrass"|term=="Creeping \n bentgrass"|
                      term=="Tall fescue"|term=="Intermediate \n wheatgrass", "C3","C4"))

```

