CO_sgs_code_forMS

```
Load packages
```

```
require(cowplot)
require(effects)
require(lattice)
require(latticeExtra)
require(gridExtra)
require(grid)
require(ggpubr)
require(lme4)
require(ggeffects)
require(tidyverse)
```

Load model output data

```
#### set wd ####
setwd("/Users/Alice/Dropbox/Grad School/Research/Trait Project/CO_sgs Analysis")
#get model result data into the environment
load("./SCRIPTS/models_11232020.RData") #change the file name to the most current version of model runs
```

Make a figure of model results for LDMC, RDMC, and TLP for forb and gram survival

```
#make figure for graminoid survival
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI_G <- mean(CO_grams$SPEI_s)</pre>
sdSPEI_G <- sd(CO_grams$SPEI_s)</pre>
#get 97.5 quantile of the distribution
SPEI_97_5_G <- qnorm(.975, meanSPEI_G, sdSPEI_G)</pre>
SPEI_2_5_G <- qnorm(.025, meanSPEI_G, sdSPEI_G)</pre>
spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)</pre>
#for TLP s
TLP_vals <- seq(min(CO_grams$TLP_s, na.rm = TRUE), max(CO_grams$TLP_s, na.rm = TRUE), length.out = 20)
TLP_G_dat <- ggpredict(m1_grams, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed", bac
#for LDMC_s
LDMC_vals <- seq(min(CO_grams$LDMC_s, na.rm = TRUE), max(CO_grams$LDMC_s, na.rm = TRUE), length.out = 2
LDMC_G_dat <- ggpredict(m2_grams, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed",
#for RDMC_s
RDMC_vals <- seq(min(CO_grams$RDMC_s, na.rm = TRUE), max(CO_grams$RDMC_s, na.rm = TRUE), length.out = 2
RDMC_G_dat <- ggpredict(m9, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.t
```

RDiam_vals <- seq(min(CO_grams\$RDiam_s, na.rm = TRUE), max(CO_grams\$RDiam_s, na.rm = TRUE), length.out

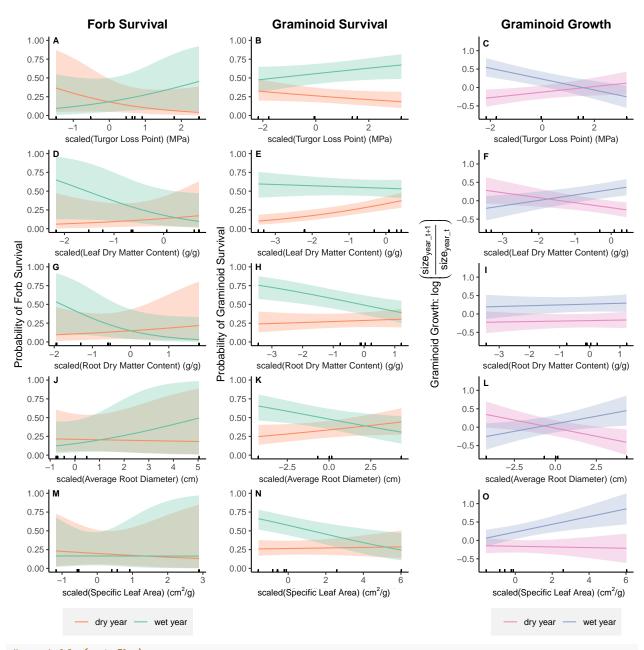
```
RDiam_G_dat <- ggpredict(m14, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed", ba
# for SLA
SLA_vals <- seq(min(CO_grams$SLA_s), max(CO_grams$SLA_s), length.out = 20)
SLA_G_dat <- ggpredict(m5, terms = c("SLA_s[SLA_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tran
#make a data.frame to contain all of the values for each trait
GramDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_G_dat$x, GramSurv = TLP_G_d
GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_G_dat
GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Root Dry Matter Content) (g/g)"), x = RDMC_G_dat
GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Average Root Diameter) (cm)"), x = RDiam_G_dat$x</pre>
GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Specific Leaf Area) (g/cm2)"), x = SLA_G_dat$x,
\#levels(GramDat\$trait) <- c("scaled(Turgor~Loss~Point)~(MPa)", "scaled(Leaf~Dry~Matter~Content)~(g/g)", The scaled(Leaf~Dry~Matter~Content)~(g/g)", The scaled(Leaf~Dry~Matter~Content)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g/g)~(g
#make data for rug plot
RugDat_G <- data.frame(rug = CO_grams$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")</pre>
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$LDMC_s, trait = "scaled(Leaf Dry Matter Content)</pre>
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$RDMC_s, trait = "scaled(Root Dry Matter Content)</pre>
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$RDiam_s, trait = "scaled(Average Root Diameter) (</pre>
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$SLA_s, trait = "scaled(Specific Leaf Area) (g/cm2</pre>
\#levels(RugDat\_G\$trait) < -c("scaled(Turgor\sim Loss\sim Point)\sim (MPa)", "scaled(Leaf\sim Dry\sim Matter\sim Content)\sim (g/g)",
#text for labels
dat_text <- data.frame(</pre>
  label = c("B", "E", "H", "K", "N"),
  trait = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dr
           = c(min(TLP_G_dat$x),min(LDMC_G_dat$x),min(RDMC_G_dat$x), min(RDiam_G_dat$x), min(SLA_G_dat$x)),
\#levels(dat\_text\$trait) \leftarrow c("scaled(Turgor\sim Loss\sim Point)\sim (MPa)", "scaled(Leaf\sim Dry\sim Matter\sim Content)\sim (g/g)"
#make a multipanel figure that shows only the graminoid survival probs for 3 traits
gramSurvFigure <- ggplot(data = GramDat) +</pre>
   geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
   geom_line(aes(x=x, GramSurv, col = SPEI)) +
   geom_rug(aes(x = rug), data = RugDat_G) +
   labs(title = "Graminoid Survival") +
   xlab(NULL) +
   ylab("Probability of Graminoid Survival") +
   scale_y_continuous(limits = c(0,1)) +
   scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62", "#66c2a5"), guide = FALSE
   scale_fill_manual(values = c("#fc8d62","#66c2a5"), guide = FALSE) +
   facet_wrap(~trait, scales = "free_x", strip.position = "bottom", ncol =1) +
   theme_classic()+
   theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fi
   geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold")
```

```
make figure for forb survival
```

```
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI_F <- mean(CO_point_all$SPEI_s)</pre>
sdSPEI_F <- sd(CO_point_all$SPEI_s)</pre>
#get 97.5 quantile of the distribution
SPEI_97_5_F <- qnorm(.975, meanSPEI_F, sdSPEI_F)</pre>
SPEI_2_5_G <- qnorm(.025, meanSPEI_F, sdSPEI_F)</pre>
spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)</pre>
#for TLP_s
TLP_vals <- seq(min(CO_point_all$TLP_s, na.rm = TRUE), max(CO_point_all$TLP_s, na.rm = TRUE), length.ou
TLP_F_dat <- ggpredict(m3, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tran
#for LDMC_s
LDMC_vals <- seq(min(CO_point_all$LDMC_s, na.rm = TRUE), max(CO_point_all$LDMC_s, na.rm = TRUE), length
LDMC_F_dat <- ggpredict(m4, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.t.
#for RDMC s
RDMC_vals <- seq(min(CO_point_all$RDMC_s, na.rm = TRUE), max(CO_point_all$RDMC_s, na.rm = TRUE), length
RDMC_F_dat <- ggpredict(m11, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back."
#for RDiam_s
RDiam_vals <- seq(min(CO_point_all$RDiam_s, na.rm = TRUE), max(CO_point_all$RDiam_s, na.rm = TRUE), len
RDiam_F_dat <- ggpredict(m16, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed", ba
#for SLA
SLA_vals <- seq(min(CO_point_SLA$SLA_s, na.rm = TRUE), max(CO_point_SLA$SLA_s, na.rm = TRUE), length.ou
SLA_F_dat <- ggpredict(m6, terms = c("SLA_s[SLA_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tran
#make a data.frame to contain all of the values for each trait
ForbDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_F_dat$x, ForbSurv = TLP_F_d
ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_F_dat
ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Root Dry Matter Content) (g/g)"), x = RDMC_F_dat
ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Average Root Diameter) (cm)"), x = RDiam_F_dat$x
ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Specific Leaf Area) (g/cm2)"), x = SLA_F_dat$x,
#make data for rug plot
RugDat_F <- data.frame(rug = CO_point_all$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")</pre>
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$LDMC_s, trait = "scaled(Leaf Dry Matter Conte
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$RDMC_s, trait = "scaled(Root Dry Matter Conte
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$RDiam_s, trait = "scaled(Average Root Diameter</pre>
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$SLA_s, trait = "scaled(Specific Leaf Area) (g
#text for labels
dat_text <- data.frame(</pre>
label = c("A", "D", "G", "J", "M"),
```

```
trait = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dr
           = c(min(TLP_F_dat\$x),min(LDMC_F_dat\$x),min(RDMC_F_dat\$x), min(RDiam_F_dat\$x), min(SLA_F_dat\$x)),
              = c(1,1,1,1,1)
   У
)
#make a multipanel figure that shows only the graminoid survival probs for 3 traits
forbSurvFigure <- ggplot(data = ForbDat) +</pre>
   geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
   geom_line(aes(x=x, ForbSurv, col = SPEI)) +
   geom_rug(aes(x = rug), data = RugDat_F) +
   labs(title = "Forb Survival") +
   xlab(NULL) +
   ylab("Probability of Forb Survival") +
   scale_y_continuous(limits = c(0,1)) +
   scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62","#66c2a5")) +
   geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold") +
   scale_fill_manual(values = c("#fc8d62","#66c2a5"), guide = FALSE) +
   facet_wrap(~trait, scales = "free_x", strip.position = "bottom", ncol = 1) +
   theme_classic()+
   theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fi
Make figure for graminoid growth models
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI <- mean(CO grow TLP$SPEI s)</pre>
sdSPEI <- sd(CO_grow_TLP$SPEI_s)</pre>
#get 97.5 quantile of the distribution
SPEI_97_5 <- qnorm(.975, meanSPEI, sdSPEI)</pre>
SPEI_2_5 <- qnorm(.025, meanSPEI, sdSPEI)</pre>
spei_vals <- c(SPEI_2_5, SPEI_97_5)</pre>
#for TLP_s
TLP_vals <- seq(min(CO_grow_TLP$TLP_s, na.rm = TRUE), max(CO_grow_TLP$TLP_s, na.rm = TRUE), length.out
TLP_grow_dat <- ggpredict(mGrowTLP, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed")
#for LDMC_s
LDMC_vals <- seq(min(CO_grow_LDMC$LDMC_s, na.rm = TRUE), max(CO_grow_LDMC$LDMC_s, na.rm = TRUE), length
LDMC_grow_dat <- ggpredict(mGrowLDMC, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed type = "f
#for RDMC s
RDMC_vals <- seq(min(CO_grow_RDMC$RDMC_s, na.rm = TRUE), max(CO_grow_RDMC$RDMC_s, na.rm = TRUE), length
RDMC_grow_dat <- ggpredict(mGrowRDMC, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixe-
#for RDiam_s
RDiam_vals <- seq(min(CO_grow_RDiam$RDiam_s, na.rm = TRUE), max(CO_grow_RDiam$RDiam_s, na.rm = TRUE), 1
RDiam_grow_dat <- ggpredict(mGrowRDiam, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = ".
#for SLA_s
SLA_vals <- seq(min(CO_grow_SLA$SLA_s, na.rm = TRUE), max(CO_grow_SLA$SLA_s, na.rm = TRUE), length.out
SLA_grow_dat <- ggpredict(mGrowSLA, terms = c("SLA_s[SLA_vals]", "SPEI_s[spei_vals]"), type = "fixed")
```

```
#make a data.frame to contain all of the values for each trait
GrowthDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_grow_dat$x, Growth = TLP_
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_g
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Root Dry Matter Content) (g/g)"), x = RDMC_
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Average Root Diameter) (cm)"), x = RDiam_gro
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Specific Leaf Area) (g/cm2)"), x = SLA_grow_
#make a data.frame with data for the rug plot
RugDat <- data.frame(rug = CO grow TLP$TLP s, trait = "scaled(Turgor Loss Point) (MPa)")</pre>
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_LDMC$LDMC_s, trait = "scaled(Leaf Dry Matter Content)</pre>
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_RDMC$RDMC_s, trait = "scaled(Root Dry Matter Content)
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_RDiam_$RDiam_s, trait = "scaled(Average Root Diameter)
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_SLA$SLA_s, trait = "scaled(Specific Leaf Area) (g/cm2)
#text for labels
dat_text <- data.frame(</pre>
 label = c("C", "F", "I", "L", "O"),
 trait = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dr
      = c(min(TLP_grow_dat$x), min(LDMC_grow_dat$x), min(RDMC_grow_dat$x), min(RDiam_grow_dat$x), min(
        = c(1.2,1.2,1.2,1.2,1.2)
#make a multipanel figure
GrowthExtraFig <- ggplot(data = GrowthDat) +</pre>
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, Growth, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat) +
  labs(title = "Graminoid Growth") +
  xlab(NULL) +
  ylab(expression("Graminoid Growth: log" ~ bgroup("(",frac(size[year_t+1],size[year_t]),")"))) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#e78ac3", "#8da0cb")) +
  scale_fill_manual(values = c("#e78ac3", "#8da0cb"), guide = FALSE) +
  geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold") +
   facet_wrap(vars(trait), scales = "free_x", strip.position = "bottom", ncol = 1) +
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fi
Combine into one figure
mainObs <- plot grid(forbSurvFigure, gramSurvFigure, GrowthExtraFig, ncol = 3, align = "h", axis = "tb"
  ggdraw() + draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white")) ,hjust = 0, vjust
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Specific Leaf Area) (c"*m^2*"/g)"),x = .5, y =
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Specific Leaf Area) (c"*m^2*"/g)"),x = .19, y
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Specific Leaf Area) (c"*m^2*"/g)"),x = .873,
mainObs
```



#as_gtable(mainObs)

#add_sub(as_gtable(mainObs), label = bquote("scaled(Specific Leaf Area) (g/c"* m^2 *")"),x = .5, y = 3, s #add_sub(label = bquote("scaled(Specific Leaf Area) (g/c"* m^2 *")"),x = .19, y = 4, $size = 9) %>% #add_sub(label = bquote("scaled(Specific Leaf Area) (<math>g/c$ "* m^2 *")"),x = .873, y = 5, size = 9) %>% #qqdraw()

Make climate variability figure for use in the conceptual diagram (fig. 1)

source("/Users/Alice/Dropbox/Grad School/Research/Trait Project/Data/Climate Data/CrossSiteClimateCompa

```
#figure of annual precip variability at CO site
CO_precip <- ggplot(data = CO[!is.na(CO$Ann.Sum.Precip),])+
geom_line(aes(x = Year, y = Ann.Sum.Precip), col = "gray25") +</pre>
```

```
ylab(expression("MAP (mm)" %->% "")) +
   scale_x_continuous(labels = NULL, breaks = NULL) +
   scale_y_continuous(labels = NULL, breaks = NULL) +
   theme_classic()
setwd("/Users/Alice/Dropbox/Grad School/Research/Trait Project/CO sgs Analysis")
pdf("./Manuscript/Figures/CO_MAP.pdf", width = 3, height = 3)
CO precip
dev.off()
## pdf
##
Make a plot of random effects of individual plant size on survival for LDMC model (best model for graminoid
survival)
#get random effect data
#refit model w/ factors instead of logical values
m2_fac <- glmer(as.factor(survives_tplus1) ~ SPEI_s * LDMC_s + area_s + neighbors_10_s + as.factor(nea
sppAreaPreds_s <- ggpredict(m2_fac, terms = c("area_s[all]", "species"), type = "random")</pre>
sppAreaPreds_s <- data.frame("x" = sppAreaPreds_s\(^x\), "preds" = sppAreaPreds_s\(^x\)predicted, "spp" = sppArea
globPreds_a_s <- ggpredict(m2_fac, terms = c("area_s[all]"), type = "random")</pre>
globPreds_a_s <- data.frame("x" = globPreds_a_s\$x, "preds" = globPreds_a_s\$predicted, "spp" = as.factor
AreaEffectSurv <- ggplot() +</pre>
   geom_line(data = sppAreaPreds_s, aes(x = x, y = preds, col = spp), alpha = .8)+
   geom_line(data = globPreds_a_s, aes(x = x, y = preds), lwd = 1.25) +
   \#geom\_line(aes(x = globPreds\_a\_s\$x, y = globPreds\_a\_s\$CI\_low)) +
   geom_polygon(aes(x = c(globPreds_a_s\$x,rev(globPreds_a_s\$x)), y = c( globPreds_a_s\$CI_low, rev(globPr
   theme classic() +
   ylim(c(0,1))+
   xlab(c(expression(size[year_t] ))) +
   ylab("P(Graminoid Survival)") +
   scale_color_manual(values = c("grey60", "grey60", "
   theme(axis.ticks.x.bottom = element_blank(),
              axis.text.x.bottom = element_blank(),
              legend.position = "none")
Make plot of fixed effect of neighborhood density for effect of LDMC*SPEI on graminoid survival
sppNeighPreds_s <- ggpredict(m2_fac, terms = c("neighbors_10_s[all]", "species"), type = "random")</pre>
sppNeighPreds_s <- data.frame("x" = sppNeighPreds_s\$x, "preds" = sppNeighPreds_s\$predicted, "spp" = sppN
globPreds_n_s <- ggpredict(m2_fac, terms = c("neighbors_10_s[all]"), type = "fixed")</pre>
globPreds_n_s <- data.frame("x" = globPreds_n_s\$x, "preds" = globPreds_n_s\$predicted, "spp" = as.factor
NeighEffectSurv <- ggplot() +</pre>
   geom_line(data = sppNeighPreds_s, aes(x = x, y = preds, col = spp), alpha = .8)+
   geom_line(data = globPreds_n_s, aes(x = x, y = preds), lwd = 1.25) +
   geom_polygon(aes(x = c(globPreds_n_s$x,rev(globPreds_n_s$x)), y = c( globPreds_n_s$CI_low, rev(globPr
   theme classic() +
   ylim(c(0,1))+
```

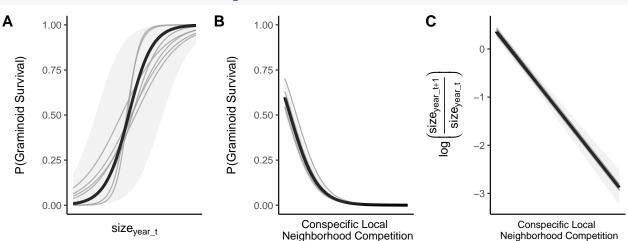
xlab("Conspecific Local \n Neighborhood Competition") +

```
ylab("P(Graminoid Survival)") +
scale_color_manual(values = c("grey60", "grey60", "grey60",
```

Make plot of fixed effect of neighborhood by species on growth for TLP model

```
mGrowTLP_fac<- lme4::lmer(logDiffArea ~ neighbors_10_s + TLP_s + SPEI_s * TLP_s + as.factor(nearEdge_t
sppNeighPreds g <- ggpredict(mGrowTLP fac, terms = c("neighbors 10 s[all]", "species"), type = "random"</pre>
sppNeighPreds_g <- data.frame("x" = sppNeighPreds_g$x, "preds" = sppNeighPreds_g$predicted, "spp" = sppN
globPreds_n_g <- ggpredict(mGrowTLP_fac, terms = c("neighbors_10_s[all]"), type = "fixed")</pre>
globPreds_n_g <- data.frame("x" = globPreds_n_g$x, "preds" = globPreds_n_g$predicted, "spp" = as.factor
NeighEffectGrowth <- ggplot() +</pre>
     geom_line(data = sppNeighPreds_g, aes(x = x, y = preds, col = spp), alpha = .8)+
     geom_line(data = globPreds_n_g, aes(x = x, y = preds), lwd = 1.25) +
     geom_polygon(aes(x = c(globPreds_n_g$x,rev(globPreds_n_g$x)), y = c( globPreds_n_g$CI_low, rev(globPr
     theme_classic() +
     xlab(c("Conspecific Local \n Neighborhood Competition")) +
     ylab(expression("log" ~ bgroup("(",frac(size[year_t+1],size[year_t]),")"))) +
     scale_color_manual(values = c("grey60", "grey60", "
     theme(axis.ticks.x =element_blank(),
                    axis.text.x = element_blank(),
                    legend.position = "none",
                    axis.title.x = element text(size = 9),
                    axis.title.y = element_text(margin = margin(r = 0)))
```

Make figure 3 (combination of figures for effect of size and local neighborhood on LDMC*SPEI effect of graminoid survival)



Make a figure of model results for forb survival and gram growth and survival for other traits

```
#make figure for graminoid survival
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI_G <- mean(CO_grams$SPEI_s)</pre>
sdSPEI_G <- sd(CO_grams$SPEI_s)</pre>
#get 97.5 quantile of the distribution
SPEI_97_5_G <- qnorm(.975, meanSPEI_G, sdSPEI_G)</pre>
SPEI_2_5_G <- qnorm(.025, meanSPEI_G, sdSPEI_G)</pre>
spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)</pre>
#for RTD_s
RTD_vals <- seq(min(CO_grams$RTD_s, na.rm = TRUE), max(CO_grams$RTD_s, na.rm = TRUE), length.out = 20)
RTD_G_dat <- ggpredict(m10, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tra
#for SRL_s
SRL_vals <- seq(min(CO_grams$SRL_s, na.rm = TRUE), max(CO_grams$SRL_s, na.rm = TRUE), length.out = 20)
SRL_G_dat <- ggpredict(m13, terms = c("SRL_s[SRL_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tra</pre>
#make a data.frame to contain all of the values for each trait
GramDat <- data.frame(trait = c("scaled(Root Tissue Density) (g/cm3)"), x = RTD_G_dat$x, GramSurv = RTD
GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_G_dat$x,
\#levels(GramDat\$trait) <- c(\#scaled(Turgor\sim Loss\sim Point)\sim (MPa)\#, \#scaled(Leaf\sim Dry\sim Matter\sim Content)\sim (q/q)\#,
#make data for rug plot
RugDat_G <- data.frame(rug = CO_grams$RTD_s, trait = "scaled(Root Tissue Density) (g/cm3)")</pre>
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams\$SRL_s, trait = "scaled(Specific Root Length) (m/g
\#levels(RugDat\_G\$trait) <-c("scaled(Turgor~Loss~Point)~(MPa)", "scaled(Leaf~Dry~Matter~Content)~(g/g)",
#text for labels
dat_text <- data.frame(</pre>
 label = c("B", "E"),
 trait = c("scaled(Root Tissue Density) (g/cm3)", "scaled(Specific Root Length) (m/g)"),
      = c(min(RTD_G_dat\$x),min(SRL_G_dat\$x)),
        = c(1,1)
 у
\#levels(dat\_text\$trait) <- c("scaled(Turgor~Loss~Point)~(MPa)", "scaled(Leaf~Dry~Matter~Content)~(g/g)"
#make a multipanel figure that shows only the graminoid survival probs for 3 traits
gramSurvFigure <- ggplot(data = GramDat) +</pre>
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, GramSurv, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat_G) +
  labs(title = "Graminoid Survival") +
  xlab(NULL) +
 ylab("Probability of Graminoid Survival") +
  scale_y_continuous(limits = c(0,1)) +
```

```
scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62", "#66c2a5"), guide = FALSE
  scale_fill_manual(values = c("#fc8d62","#66c2a5"), guide = FALSE) +
  facet_wrap(~trait, scales = "free_x", strip.position = "bottom", ncol =1) +
  theme classic()+
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fi
  geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold")
make figure for forb survival
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI_F <- mean(CO_point_all$SPEI_s)</pre>
sdSPEI_F <- sd(CO_point_all$SPEI_s)</pre>
#get 97.5 quantile of the distribution
SPEI_97_5_F <- qnorm(.975, meanSPEI_F, sdSPEI_F)</pre>
SPEI_2_5_G <- qnorm(.025, meanSPEI_F, sdSPEI_F)</pre>
spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)</pre>
#for RTD
RTD_vals <- seq(min(CO_point_all$RTD_s, na.rm = TRUE), max(CO_point_all$RTD_s, na.rm = TRUE), length.ou
RTD_F_dat <- ggpredict(m12, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tra
#for SRL
SRL_vals <- seq(min(CO_point_all$SRL_s, na.rm = TRUE), max(CO_point_all$SRL_s, na.rm = TRUE), length.ou
SRL_F_dat <- ggpredict(m15, terms = c("SRL_s[SRL_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.tra
#make a data.frame to contain all of the values for each trait
ForbDat <- data.frame(trait = c("scaled(Root Tissue Density) (g/cm3)"), x = RTD F dat$x, ForbSurv = RTD
ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_F_dat$x,
#make data for rug plot
RugDat_F <- data.frame(rug = CO_point_all$RTD_s, trait = "scaled(Root Tissue Density) (g/cm3)")</pre>
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$SRL_s, trait = "scaled(Specific Root Length)</pre>
#text for labels
dat_text <- data.frame(</pre>
 label = c("A", "D"),
 trait = c("scaled(Root Tissue Density) (g/cm3)", "scaled(Specific Root Length) (m/g)"),
      = c(min(RTD_F_dat$x),min(SRL_F_dat$x)),
        = c(1,1)
 У
#make a multipanel figure that shows only the graminoid survival probs for 3 traits
forbSurvFigure <- ggplot(data = ForbDat) +</pre>
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, ForbSurv, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat_F) +
 labs(title = "Forb Survival") +
 xlab(NULL) +
  ylab("Probability of Forb Survival") +
```

```
scale_y_continuous(limits = c(0,1)) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62","#66c2a5")) +
  geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold") +
  scale_fill_manual(values = c("#fc8d62","#66c2a5"), guide = FALSE) +
  facet_wrap(~trait, scales = "free_x", strip.position = "bottom", ncol = 1) +
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fi
Make figure for graminoid growth models
#qet 2.5 and 97.5 percentiles of the distribution
meanSPEI <- mean(CO grow TLP$SPEI s)</pre>
sdSPEI <- sd(CO_grow_TLP$SPEI_s)</pre>
#get 97.5 quantile of the distribution
SPEI_97_5 <- qnorm(.975, meanSPEI, sdSPEI)</pre>
SPEI_2_5 <- qnorm(.025, meanSPEI, sdSPEI)</pre>
spei_vals <- c(SPEI_2_5, SPEI_97_5)</pre>
#for RTD_s
RTD_vals <- seq(min(CO_grow_RTD$RTD_s, na.rm = TRUE), max(CO_grow_RTD$RTD_s, na.rm = TRUE), length.out
RTD_grow_dat <- ggpredict(mGrowRTD, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed")
#for SRL s
SRL_vals <- seq(min(CO_grow_SRL$SRL_s, na.rm = TRUE), max(CO_grow_SRL$SRL_s, na.rm = TRUE), length.out
SRL grow dat <- ggpredict(mGrowSRL, terms = c("SRL s[SRL vals]", "SPEI s[spei vals]"), type = "fixed")
#make a data.frame to contain all of the values for each trait
GrowthDat <- data.frame(trait = c("scaled(Root Tissue Density) (g/cm3)"), x = RTD_grow_dat$x, Growth = 1
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_grow_
#make a data.frame with data for the rug plot
RugDat <- data.frame(rug = CO_grow_RTD$RTD_s, trait = "scaled(Root Tissue Density) (g/cm3)")</pre>
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_SRL$SRL_s, trait = "scaled(Specific Root Length) (m/g)</pre>
#text for labels
dat_text <- data.frame(</pre>
 label = c("C", "F"),
 trait = c("scaled(Root Tissue Density) (g/cm3)", "scaled(Specific Root Length) (m/g)"),
      = c(min(RTD_grow_dat$x), min(SRL_grow_dat$x)),
        = c(1.2,1.2)
 У
#make a multipanel figure
GrowthExtraFig <- ggplot(data = GrowthDat) +</pre>
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, Growth, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat) +
  labs(title = "Graminoid Growth") +
  xlab(NULL) +
  ylab(expression("Graminoid Growth: log" ~ bgroup("(",frac(size[year_t+1],size[year_t]),")"))) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#e78ac3", "#8da0cb")) +
```

```
scale_fill_manual(values = c("#e78ac3", "#8da0cb"), guide = FALSE) +
geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold") +
  facet_wrap(vars(trait), scales = "free_x", strip.position = "bottom", ncol = 1) +
theme_classic()+
theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fi
```

Combine into one figure

