

CO_sgs_code_forMS

Load packages

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

Load model output data

```
#### set wd ####
#set the path to the name of the file containing the 'scripts' folder
path <- "/Users/Alice/Dropbox/Grad School/Research/Trait Project/CO_sgs Analysis/CO-Sgs-paper"
setwd(path)
#get model result data into the environment
load("./scripts/script4_output.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

```
## make figure for graminoid survival

#get 2.5 and 97.5 percentiles of the distribution
meanSPEI_G <- mean(CO_grams$SPEI_s, na.rm = TRUE)
sdSPEI_G <- sd(CO_grams$SPEI_s, na.rm = TRUE)
#get 97.5 quantile of the distribution
SPEI_97_5_G <- qnorm(.975, meanSPEI_G, sdSPEI_G)
SPEI_2_5_G <- qnorm(.025, meanSPEI_G, sdSPEI_G)

spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)

#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(mSurvTLP_grams, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed")
#the ggpredict() function uses mean values for each of the fixed effects that aren't specified, and p

#for LDMC_s
LDMC_vals <- seq(min(CO_grams$LDMC_s, na.rm = TRUE), max(CO_grams$LDMC_s, na.rm = TRUE), length.out = 20)
LDMC_G_dat <- ggpredict(mSurvLDMC_grams, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "f

#for RDMC_s
RDMC_vals <- seq(min(CO_grams$RDMC_s, na.rm = TRUE), max(CO_grams$RDMC_s, na.rm = TRUE), length.out = 20)
RDMC_G_dat <- ggpredict(mSurvRDMC_grams, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "f
```

```

# for RDiam
RDiam_vals <- seq(min(CO_grams$RDiam_s, na.rm = TRUE), max(CO_grams$RDiam_s, na.rm = TRUE), length.out = 20)
RDiam_G_dat <- ggpredict(mSurvRDiam_grams, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed")

# for SLA
SLA_vals <- seq(min(CO_grams$SLA_s, na.rm = TRUE), max(CO_grams$SLA_s, na.rm = TRUE), length.out = 20)
SLA_G_dat <- ggpredict(mSurvSLA_grams, 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
GramDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_G_dat$x, GramSurv = TLP_G_dat$y)

GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_G_dat$x, GramSurv = LDMC_G_dat$y))

GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Root Dry Matter Content) (g/g)"), x = RDMC_G_dat$x, GramSurv = RDMC_G_dat$y))

GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Average Root Diameter) (cm)"), x = RDiam_G_dat$x, GramSurv = RDiam_G_dat$y))

GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Specific Leaf Area) (g/cm2)"), x = SLA_G_dat$x, GramSurv = SLA_G_dat$y))

#make data for rug plot
RugDat_G <- data.frame(rug = CO_grams$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$LDMC_s, trait = "scaled(Leaf Dry Matter Content) (g/g)"))
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$RDMC_s, trait = "scaled(Root Dry Matter Content) (g/g)"))
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$RDiam_s, trait = "scaled(Average Root Diameter) (cm)"))
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$SLA_s, trait = "scaled(Specific Leaf Area) (g/cm2)"))

#text for labels
dat_text <- data.frame(
  label = c("A", "D", "G", "J", "M"),
  sig = c("*,S", "*,S", "*,S", "*,S", "*,S"),
  trait = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dry Matter Content) (g/g)", "scaled(Average Root Diameter) (cm)", "scaled(Specific Leaf Area) (g/cm2)"),
  x = 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$x)),
  y = c(1, 1, 1, 1, 1),
  x1 = c(max(TLP_G_dat$x), max(LDMC_G_dat$x), max(RDMC_G_dat$x), max(RDiam_G_dat$x), max(SLA_G_dat$x)),
  y1 = c(1, 1, 1, 1, 1)
)

#make a multipanel figure that shows only the graminoid survival probs for 3 traits
gramSurvFigure <- ggplot(data = GramDat) +
  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 Survival") +
  scale_y_continuous(limits = c(0,1)) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62", "#66c2a5")) +
  scale_fill_manual(values = c("#fc8d62", "#66c2a5"), guide = FALSE) +
  facet_wrap(.~factor(trait, levels = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dry Matter Content) (g/g)", "scaled(Average Root Diameter) (cm)", "scaled(Specific Leaf Area) (g/cm2)"))) +
  theme_classic() +
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fill = "white", stroke = "black", strokeWidth = 1))

```

```
geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold") +
geom_text(data= dat_text, mapping = aes(x = x1, y = y1, label = sig), size = 3.5, fontface = "bold")
```

Make a figure for forb survival

```
##make figure for forb survival
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI_F <- mean(CO_point_all$SPEI_s)
sdSPEI_F <- sd(CO_point_all$SPEI_s)
#get 97.5 quantile of the distribution
SPEI_97_5_F <- qnorm(.975, meanSPEI_F, sdSPEI_F)
SPEI_2_5_G <- qnorm(.025, meanSPEI_F, sdSPEI_F)

spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)

#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.out = 100)
TLP_F_dat <- ggpredict(mSurvTLP_forbs, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#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.out = 100)
LDMC_F_dat <- ggpredict(mSurvLDMC_forbs, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#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.out = 100)
RDMC_F_dat <- ggpredict(mSurvRDMC_forbs, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#for RDiam_s
RDiam_vals <- seq(min(CO_point_all$RDiam_s, na.rm = TRUE), max(CO_point_all$RDiam_s, na.rm = TRUE), length.out = 100)
RDiam_F_dat <- ggpredict(mSurvRDiam_forbs, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#for SLA
SLA_vals <- seq(min(CO_point_all$SLA_s, na.rm = TRUE), max(CO_point_all$SLA_s, na.rm = TRUE), length.out = 100)
SLA_F_dat <- ggpredict(mSurvSLA_forbs, 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
ForbDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_F_dat$x, ForbSurv = TLP_F_dat$y)

ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_F_dat$x, ForbSurv = LDMC_F_dat$y))

ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Root Dry Matter Content) (g/g)"), x = RDMC_F_dat$x, ForbSurv = RDMC_F_dat$y))

ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Average Root Diameter) (cm)"), x = RDiam_F_dat$x, ForbSurv = RDiam_F_dat$y))

ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Specific Leaf Area) (g/cm2)"), x = SLA_F_dat$x, ForbSurv = SLA_F_dat$y))

#make data for rug plot
RugDat_F <- data.frame(rug = CO_point_all$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$LDMC_s, trait = "scaled(Leaf Dry Matter Content) (g/g)"))
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$RDMC_s, trait = "scaled(Root Dry Matter Content) (g/g)"))
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$RDiam_s, trait = "scaled(Average Root Diameter) (cm)"))
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$SLA_s, trait = "scaled(Specific Leaf Area) (g/cm2)"))
```

```

#text for labels
dat_text <- data.frame(
  label = c("C", "F", "I", "L", "O"),
  sig = c("","*", "$", "*", "$", "", "*", "$"),
  trait = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dry Matter Content) (g/g)", "scaled(Root Length) (cm)", "scaled(Stem Length) (cm)"),
  x = c(min(TLP_F_dat$x), min(LDMC_F_dat$x), min(RDMC_F_dat$x), min(RDiam_F_dat$x), min(SLA_F_dat$x)),
  y = c(1, 1, 1, 1, 1),
  x1 = c(max(TLP_F_dat$x), max(LDMC_F_dat$x), max(RDMC_F_dat$x), max(RDiam_F_dat$x), max(SLA_F_dat$x)),
  y1 = c(1, 1, 1, 1, 1)
)

#make a multipanel figure that shows only the graminoid survival probs for 5 traits
forbSurvFigure <- ggplot(data = ForbDat) +
  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 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") +
  geom_text(data= dat_text, mapping = aes(x = x1, y = y1, label = sig), size = 3.5, fontface = "bold") +
  scale_fill_manual(values = c("#fc8d62", "#66c2a5"), guide = FALSE) +
  facet_wrap(~factor(trait, levels = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dry Matter Content) (g/g)", "scaled(Root Length) (cm)", "scaled(Stem Length) (cm)")), ncol = 5) +
  theme_classic() +
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fill = "white", stroke = "black", strokeWidth = 1))

```

Make a figure for growth

```

##make figure for graminoid growth models
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI <- mean(CO_grow_TLP$SPEI_s)
sdSPEI <- sd(CO_grow_TLP$SPEI_s)
#get 97.5 quantile of the distribution
SPEI_97_5 <- qnorm(.975, meanSPEI, sdSPEI)
SPEI_2_5 <- qnorm(.025, meanSPEI, sdSPEI)

spei_vals <- c(SPEI_2_5, SPEI_97_5)

#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 = 100)
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.out = 100)
LDMC_grow_dat <- ggpredict(mGrowLDMC, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#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.out = 100)
RDMC_grow_dat <- ggpredict(mGrowRDMC, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#for RDiam_s
RDiam_vals <- seq(min(CO_grow_RDiam$RDiam_s, na.rm = TRUE), max(CO_grow_RDiam$RDiam_s, na.rm = TRUE), length.out = 100)
RDiam_grow_dat <- ggpredict(mGrowRDiam, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed")

```

```

RDiam_grow_dat <- ggpredict(mGrowRDiam, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#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 = 10)
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$x, Growth = TLP_grow_dat$Growth)
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_grow_dat$x, Growth = LDMC_grow_dat$Growth)
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Root Dry Matter Content) (g/g)"), x = RDMC_grow_dat$x, Growth = RDMC_grow_dat$Growth)
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Average Root Diameter) (cm)"), x = RDiam_grow_dat$x, Growth = RDiam_grow_dat$Growth)
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Specific Leaf Area) (g/cm2)"), x = SLA_grow_dat$x, Growth = SLA_grow_dat$Growth)

#make a data.frame with data for the rug plot
RugDat <- data.frame(rug = CO_grow_TLP$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_LDMC$LDMC_s, trait = "scaled(Leaf Dry Matter Content) (g/g)")
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_RDMC$RDMC_s, trait = "scaled(Root Dry Matter Content) (g/g)")
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_RDiam$RDiam_s, trait = "scaled(Average Root Diameter) (cm)")
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(
  label = c("B", "E", "H", "K", "N"),
  sig = c("", "", "", "", "" ),
  trait = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dry Matter Content) (g/g)", "scaled(Average Root Diameter) (cm)", "scaled(Specific Leaf Area) (g/cm2)"),
  x = c(min(TLP_grow_dat$x), min(LDMC_grow_dat$x), min(RDMC_grow_dat$x), min(RDiam_grow_dat$x), min(SLA_grow_dat$x)),
  y = c(4.4, 4.4, 4.4, 4.4, 4.4),
  x1 = c(max(TLP_grow_dat$x), max(LDMC_grow_dat$x), max(RDMC_grow_dat$x), max(RDiam_grow_dat$x), max(SLA_grow_dat$x)),
  y1 = c(4.4, 4.4, 4.4, 4.4, 4.4)
)

#make a multipanel figure
GrowthExtraFig <- ggplot(data = GrowthDat) +
  geom_hline(aes(yintercept = 3.54), col = "darkgrey", lty = 2) + # add an hline to show the average size
  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(ln(size[italic(t+1)]))) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62", "#66c2a5")) +
  scale_fill_manual(values = c("#fc8d62", "#66c2a5"), guide = FALSE) +
  geom_text(data= dat_text, mapping = aes(x = x, y = y, label = label), size = 3, fontface = "bold") +
  geom_text(data = dat_text, mapping = aes(x = x1, y = y1, label = sig), size = 3.5, fontface = "bold") +
  facet_wrap(~factor(trait, levels = c("scaled(Turgor Loss Point) (MPa)", "scaled(Leaf Dry Matter Content) (g/g)", "scaled(Root Dry Matter Content) (g/g)", "scaled(Average Root Diameter) (cm)", "scaled(Specific Leaf Area) (g/cm2)"))) +
  theme_classic() +
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fill = "white", col = "white"))

```

Combine into one figure

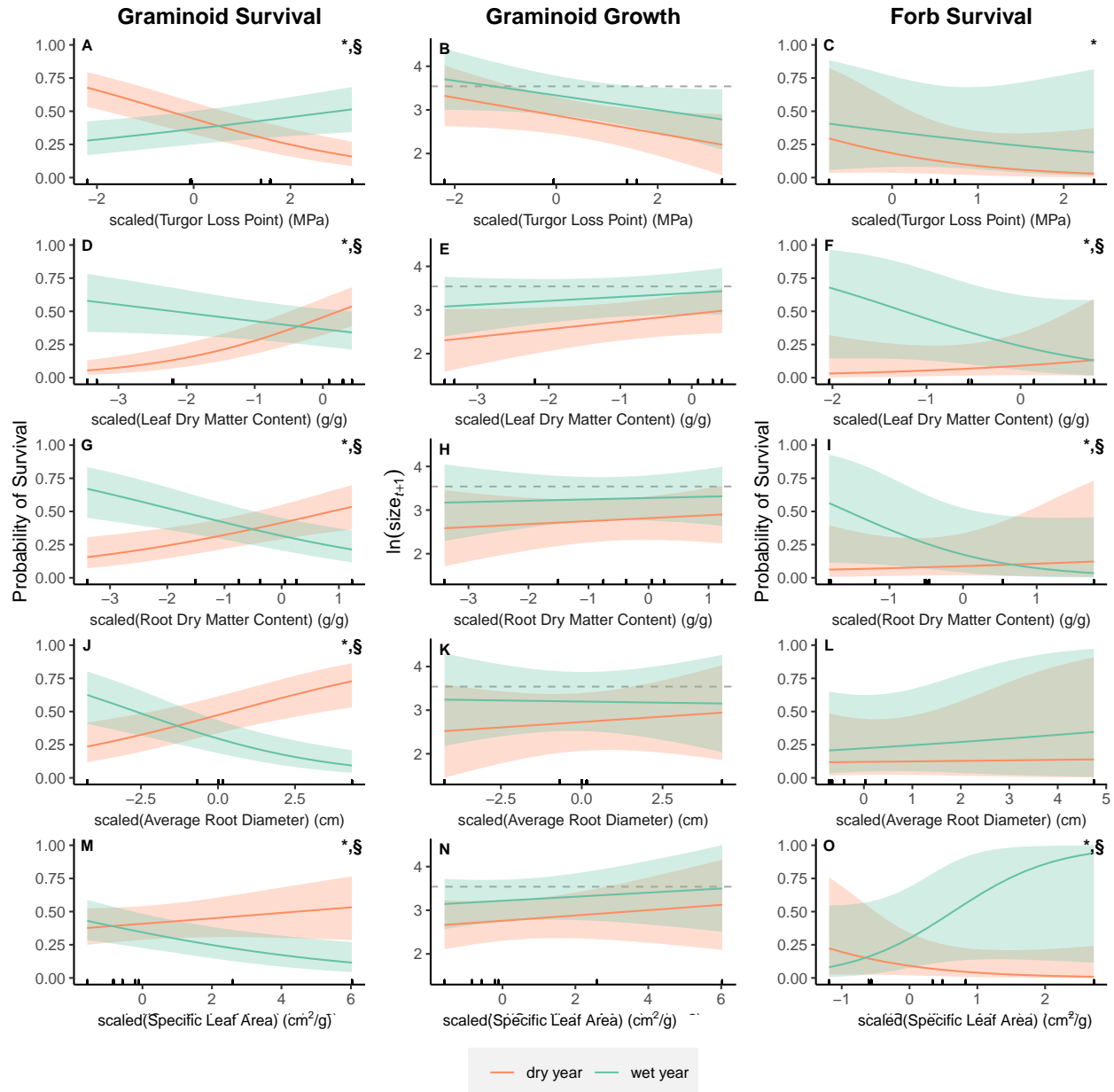
```

mainObs <- cowplot::plot_grid( gramSurvFigure, GrowthExtraFig, forbSurvFigure, ncol = 3, align = "h", as.table = TRUE)
cowplot::ggdraw() +
  cowplot::draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white")), hjust = 0, vjust = 0) +
  cowplot::draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white")), hjust = 0, vjust = 0)

```

```
cowplot::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, y =
mainObs
```



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

```
# source("/Users/Alice/Dropbox/Grad School/Research/Trait Project/Data/Climate Data/CrossSiteClimateComp
#
#
# #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") +
```



```
# 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()
```

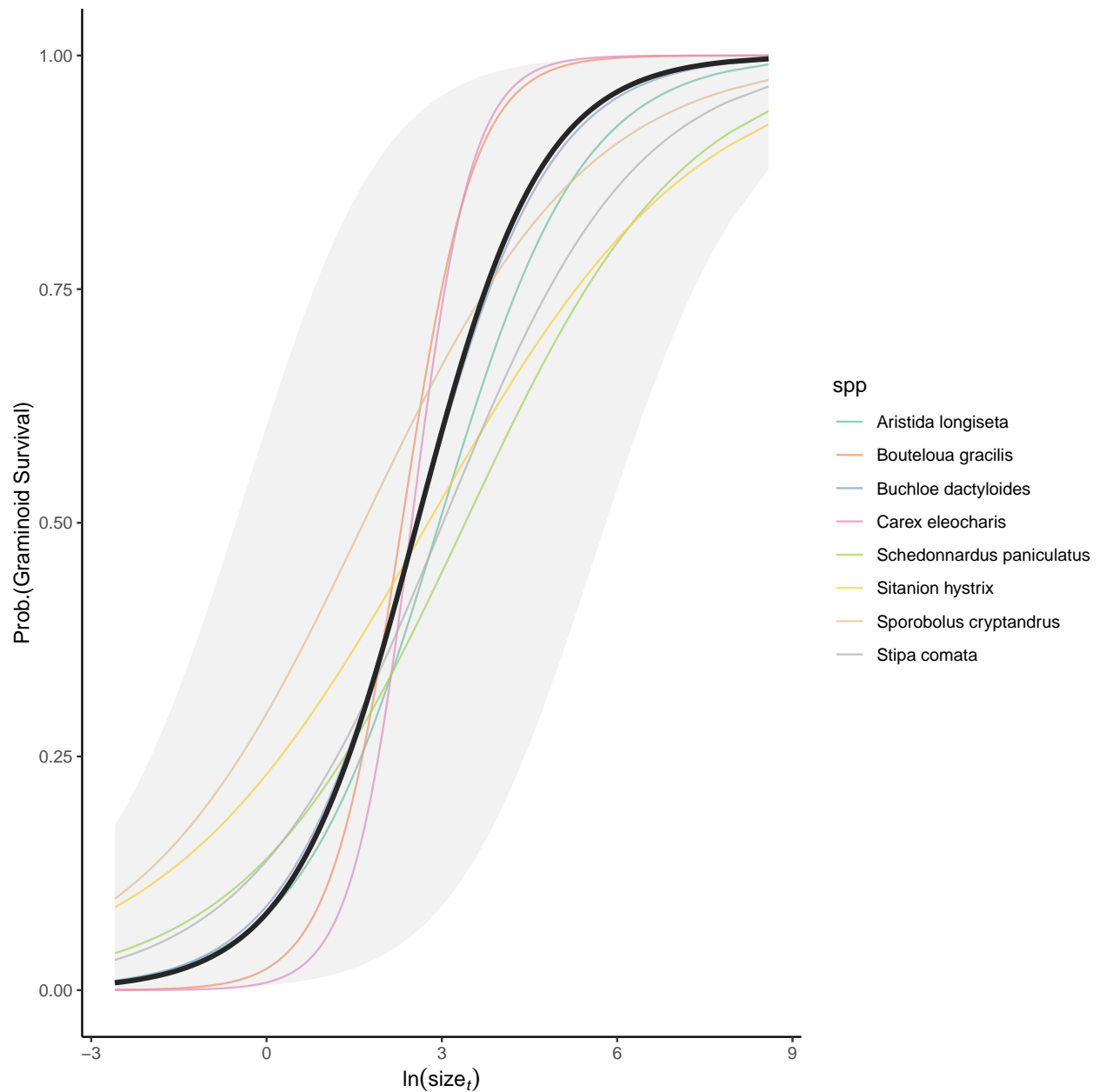
Make a plot of random effects of individual plant size on survival for LDMC model (best model for graminoid survival)

```
#get random effect data
#refit model w/ factors instead of logical values
m2_fac <- glmer(as.factor(survives_tplus1) ~ SPEI_s * LDMC_s + size_t_log + neighbors_10_s + as.factor(spp))

sppAreaPreds_s <- ggpredict(m2_fac, terms = c("size_t_log[all]", "species"), type = "random")
sppAreaPreds_s <- data.frame("x" = sppAreaPreds_s$x, "preds" = sppAreaPreds_s$predicted, "spp" = sppAreaPreds_s$spp)

globPreds_a_s <- ggpredict(m2_fac, terms = c("size_t_log[all]"), type = "random")
globPreds_a_s <- data.frame("x" = globPreds_a_s$x, "preds" = globPreds_a_s$predicted, "spp" = as.factor(sppAreaPreds_s$spp))

(AreaEffectSurv <- ggplot() +
  geom_line(data = sppAreaPreds_s, aes(x = x, y = preds, col = spp), alpha = .75) +
  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$CI_low, rev(globPreds_a_s$CI_high))),
  theme_classic() +
  ylim(c(0,1)) +
  xlab(c(expression(ln(size[italic(t)])))) +
  ylab("Prob.(Graminoid Survival)") +
  scale_color_brewer(palette = "Set2") #+
  #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")
sppNeighPreds_s <- data.frame("x" = sppNeighPreds_s$x, "preds" = sppNeighPreds_s$predicted, "spp" = sppNeighPreds_s$spp)

globPreds_n_s <- ggpredict(m2_fac, terms = c("neighbors_10_s[all]"), type = "fixed")
globPreds_n_s <- data.frame("x" = globPreds_n_s$x, "preds" = globPreds_n_s$predicted, "spp" = as.factor(sppNeighPreds_s$spp))

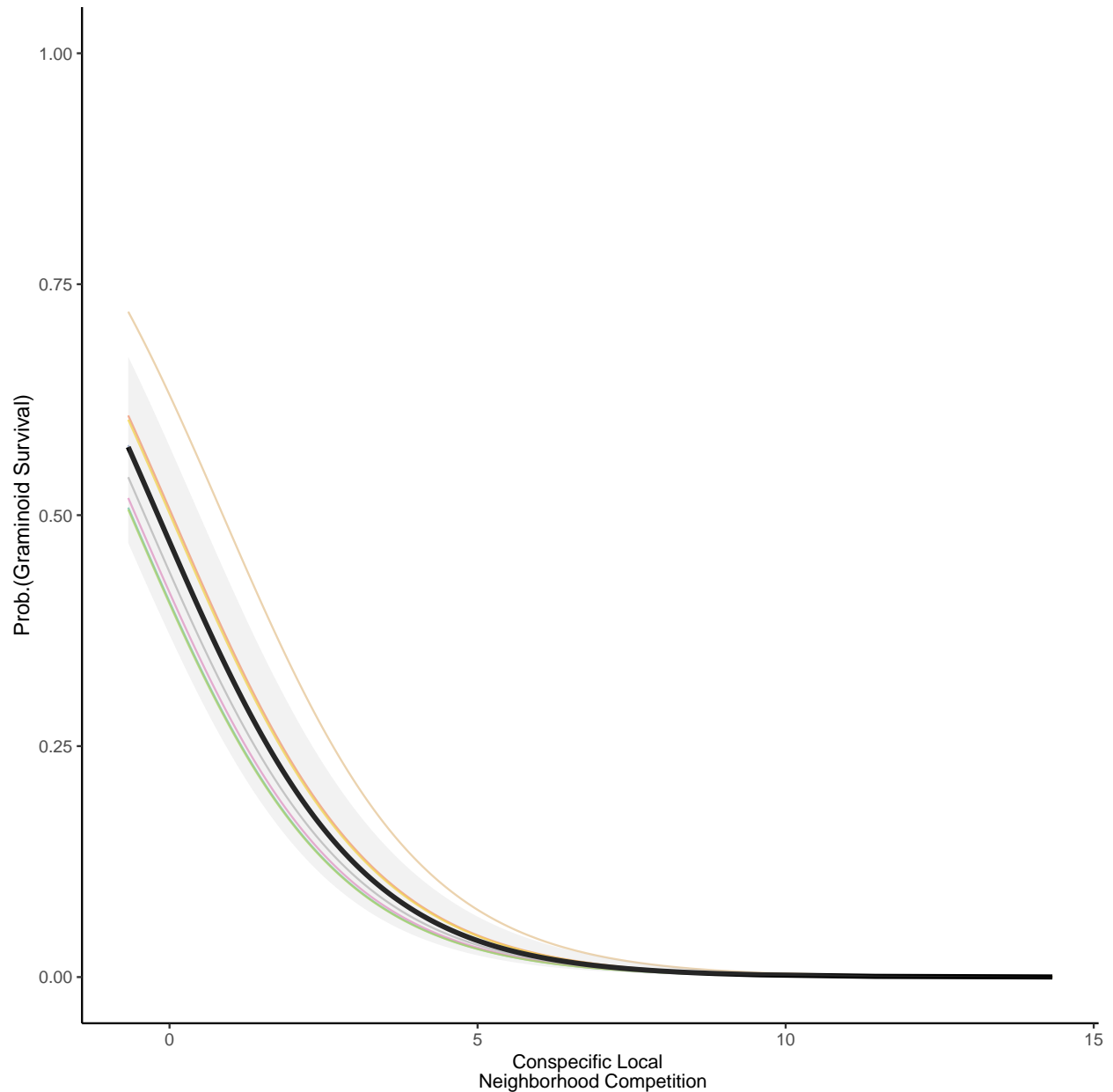
(NeighEffectSurv <- ggplot() +
  geom_line(data = sppNeighPreds_s, aes(x = x, y = preds, col = spp), alpha = .75) +
  geom_line(data = globPreds_n_s, aes(x = x, y = preds), lwd = 1.25) +
  geom_polygon(aes(x = c(globPreds_n_s$x, rev(globPreds_n_s$x)), y = c(globPreds_n_s$CI_low, rev(globPreds_n_s$CI_high))),
  theme_classic() +
  ylim(c(0,1)) +
  xlab("Conspecific Local \n Neighborhood Competition") +
```



```

ylab("Prob.(Graminoid Survival)") +
scale_color_brewer(palette = "Set2") +
theme(#axis.ticks.x.bottom = element_blank(),
      #axis.text.x.bottom = element_blank(),
      axis.title.x.bottom = element_text(size = 9.5),
      legend.position = "none",
      )
)

```



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

```

mGrowTLP_fac<- lme4::lmer(size_tplus1_log ~ size_t_log + neighbors_10_s + TLP_s + SPEI_s * TLP_s + as.f

sppNeighPreds_g <- ggpredict(mGrowTLP_fac, terms = c("neighbors_10_s[all]", "species"), type = "random")
sppNeighPreds_g <- data.frame("x" = sppNeighPreds_g$x, "preds" = sppNeighPreds_g$predicted, "spp" = sppNeighPreds_g$spp)

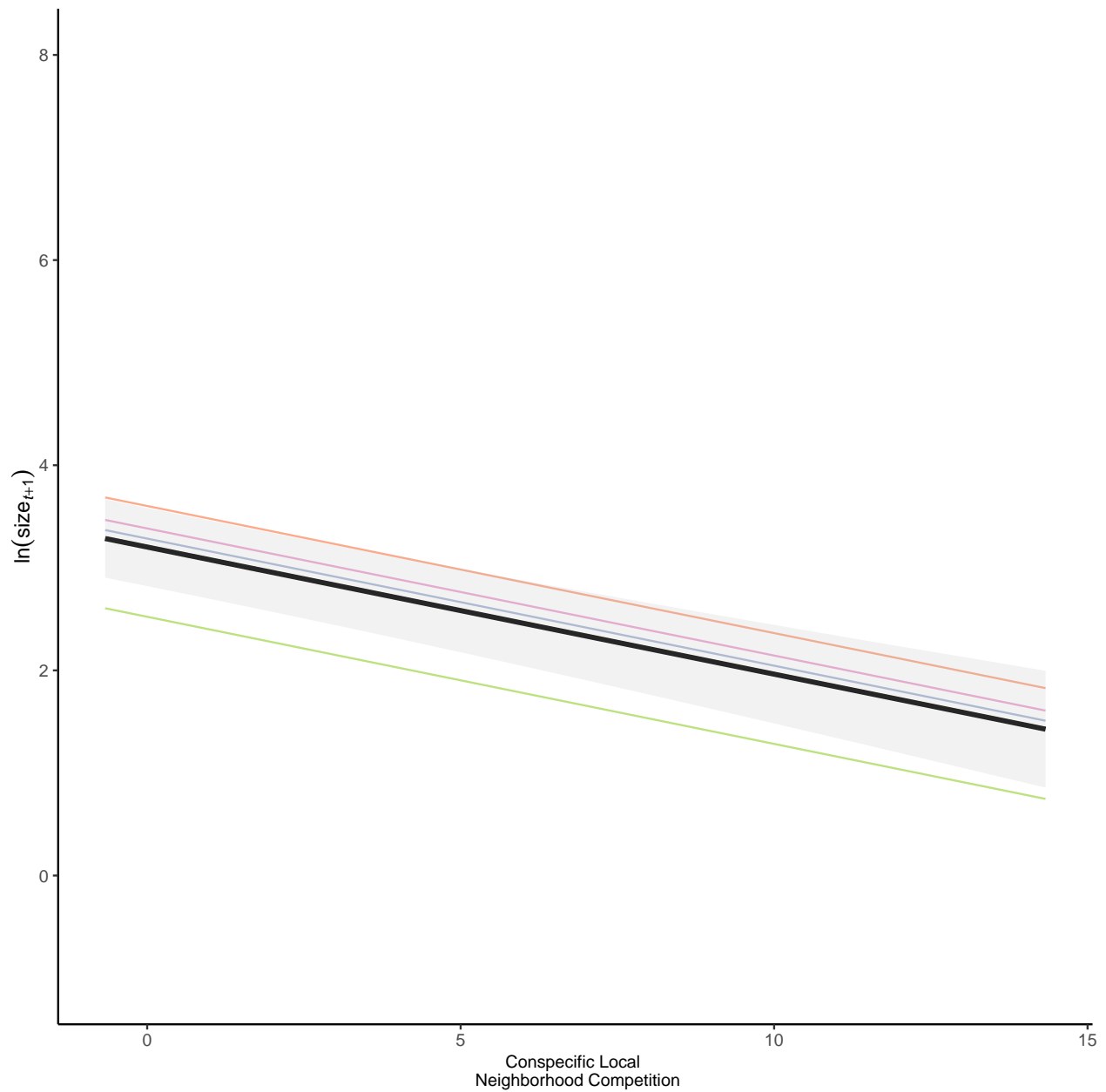
```

```

globPreds_n_g <- ggpredict(mGrowTLP_fac, terms = c("neighbors_10_s[all]"), type = "fixed")
globPreds_n_g <- data.frame("x" = globPreds_n_g$x, "preds" = globPreds_n_g$predicted, "spp" = as.factor

(NeighEffectGrowth <- ggplot() +
  geom_line(data = sppNeighPreds_g, aes(x = x, y = preds, col = spp), alpha = .75)+
  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(ln(size[italic(t+1)]))) +
  ylim(c(-1,8)) +
  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))) +
  scale_color_brewer(palette = "Set2"))

```



Make plot of effect of size_t on size_t+1 using coefficients from TLP model, as well as raw data

#model is mGrowTLP

```
sppSize_Preds_growth <- ggpredict(mGrowTLP_fac, terms = c("size_t_log[all]", "species"), type = "random")
sppSizePreds_growth <- data.frame("x" = sppSize_Preds_growth$x, "preds" = sppSize_Preds_growth$predicted)
```

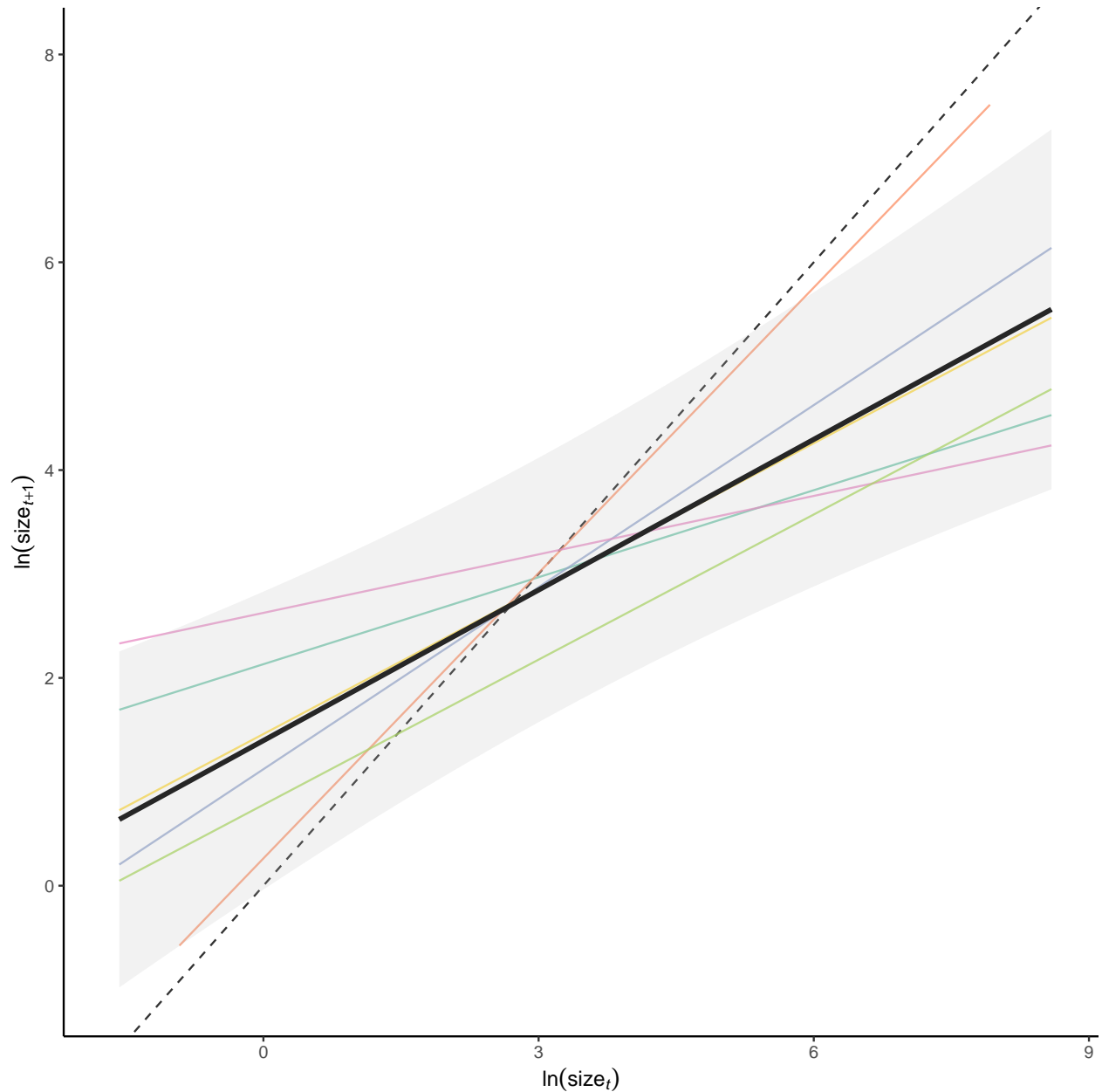
```
globPreds_growth <- ggpredict(mGrowTLP_fac, terms = c("size_t_log[all]"), type = "random")
globPreds_growth <- data.frame("x" = globPreds_growth$x, "preds" = globPreds_growth$predicted, "spp" = spp)
```

```
(AreaEffectGrowth <- ggplot() +
  geom_abline(aes(slope = 1, intercept = 0), lty = 2, alpha = .8) +
  geom_line(data = sppSizePreds_growth, aes(x = x, y = preds, col = spp), alpha = .75) +
  geom_line(data = globPreds_growth, aes(x = x, y = preds), lwd = 1.25) +
  geom_polygon(aes(x = c(globPreds_growth$x, rev(globPreds_growth$x)), y = c(globPreds_growth$CI_low, rev(globPreds_growth$CI_high))), fill = "gray"))
```

```

ylim(c(-1,8)) +
xlim(c(min(CO_grow_TLP$size_t_log)+.2, max(CO_grow_TLP$size_t_log))) +
theme_classic() +
xlab(c(expression(ln(size[italic(t)])))) +
ylab(c(expression(ln(size[italic(t+1)])))) +
theme(legend.position = "none") +
scale_color_brewer(palette = "Set2")

```



Make a figure showing the fitted relationship between size_t and size_{t+1} for each graminoid species

```

## use CO_poly_growth dataset
growTemp <- CO_grow_TLP

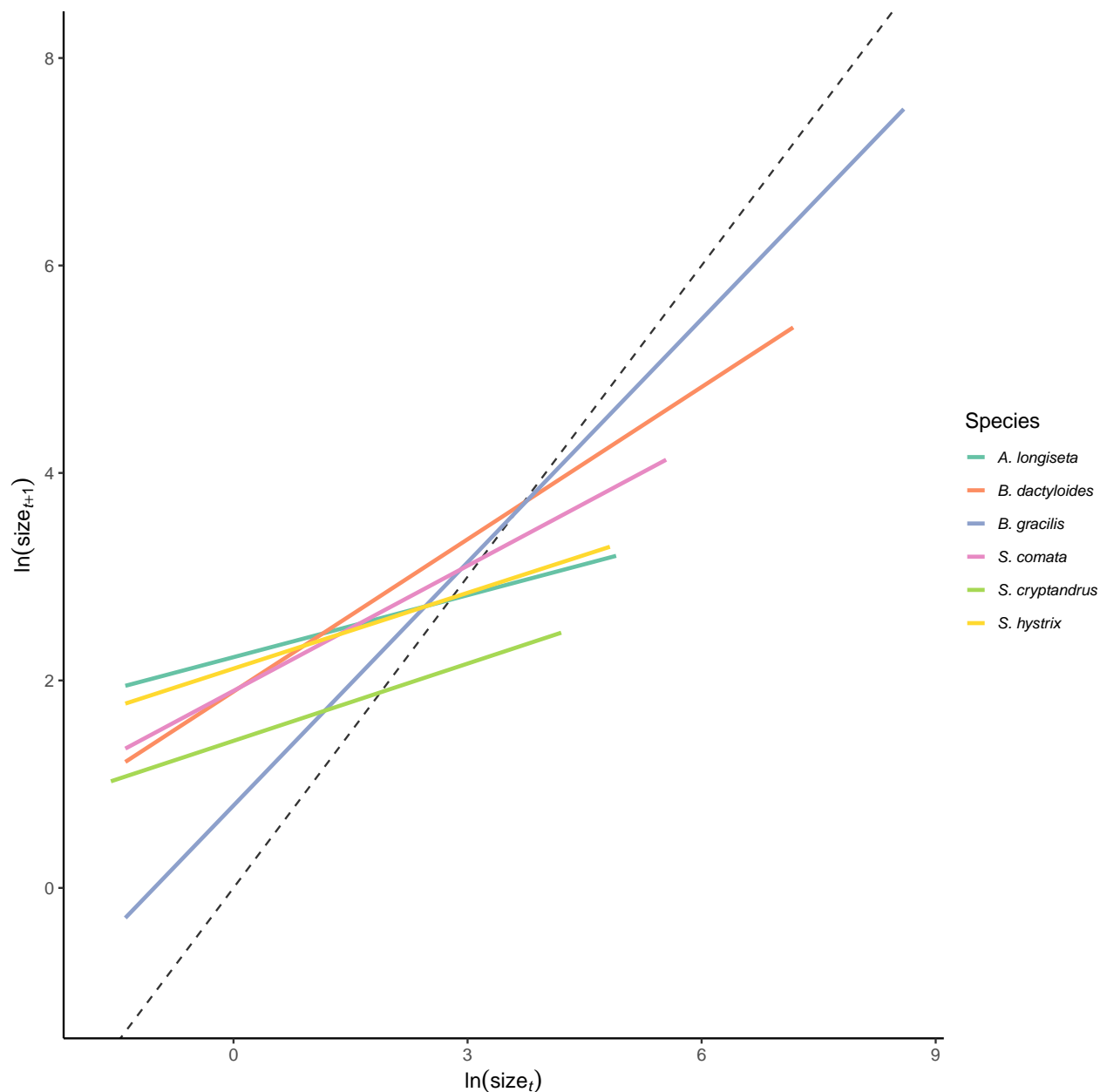
#make abbreviated species names
growTemp$sppName <-

```

```

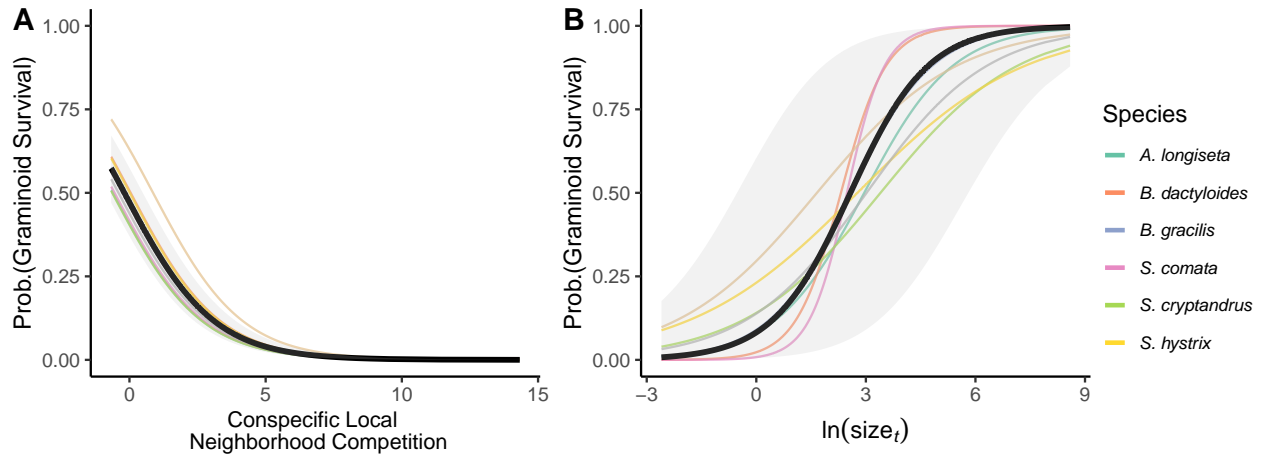
paste0(str_sub(str_split_fixed(CO_grow_TLP$species, " ", n = 2)[,1], start = 1L, end = 1L), ". ", str_sub(
(size_t_size_tplus1 <- ggplot(data = growTemp) +
  geom_abline(aes(slope = 1, intercept = 0), lty = 2, alpha = .8)+
  #geom_point(aes(x = size_t_log, y = size_tplus1_log, col = sppName), alpha = .3) +
  geom_smooth(aes(x = size_t_log, y = size_tplus1_log, col = sppName), method = "lm", se = FALSE) +
  theme_classic() +
  ylim(c(-1,8)) +
  xlim(c(min(CO_grow_TLP$size_t_log)+.2, max(CO_grow_TLP$size_t_log))) +
  xlab(expression(ln(size[italic(t)]))) +
  ylab(expression(ln(size[italic(t+1)]))) +
  theme(legend.text = element_text(face = "italic", size = 8), legend.position = "right", legend.key.wi
  guides(col = guide_legend(title = "Species")) +
  scale_color_brewer(palette = "Set2" ))

```



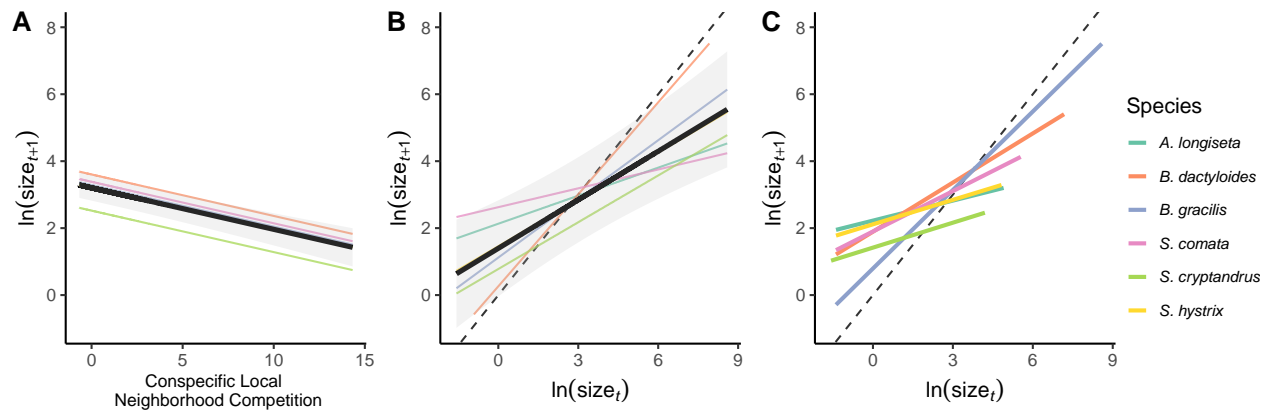
Make figure 3 (combination of figures for effect of size and local neighborhood on LDMC*SPEI effect of graminoid survival)

```
(effectsSurv <- ggarrange(NeighEffectSurv, AreaEffectSurv,
  labels = c("A", "B"),
  ncol = 2, nrow = 1, align = "hv", legend = "right",
  legend.grob = get_legend(sizet_sizetplus1)))
```



Make figure 4 (combination of figures for effect of size and neighbors on LDMC*TLP effect on graminoid growth)

```
(effectsGrowth <- ggarrange(NeighEffectGrowth, AreaEffectGrowth, sizet_sizetplus1,
  labels = c("A", "B", "C"),
  widths = c(1,1,1),
  legend = "right",
  legend.grob = get_legend(sizet_sizetplus1),
  ncol = 3, nrow = 1, align = "hv"))
```



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$SPEI_s, na.rm = TRUE)
sdSPEI_G <- sd(CO_grams$SPEI_s, na.rm = TRUE)
#get 97.5 quantile of the distribution
SPEI_97_5_G <- qnorm(.975, meanSPEI_G, sdSPEI_G)
SPEI_2_5_G <- qnorm(.025, meanSPEI_G, sdSPEI_G)
```

```

spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)

#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(mSurvRTD_grams, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#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(mSurvSRL_grams, 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
GramDat <- data.frame(trait = c("scaled(Root Tissue Density) (g/cm3)"), x = RTD_G_dat$x, GramSurv = RTD_G_dat$y)

GramDat <- rbind(GramDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_G_dat$x, GramSurv = SRL_G_dat$y))

#levels(GramDat$trait) <- c("scaled(Turgor~Loss~Point)~(MPa)", "scaled(Leaf~Dry~Matter~Content)~(g/g)", "scaled(Root~Tissue~Density)~(g/cm3)", "scaled(Specific~Root~Length)~(m/g)")

#make data for rug plot
RugDat_G <- data.frame(rug = CO_grams$RTD_s, trait = "scaled(Root Tissue Density) (g/cm3)")
RugDat_G <- rbind(RugDat_G, data.frame(rug = CO_grams$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)", "scaled(Root~Tissue~Density)~(g/cm3)", "scaled(Specific~Root~Length)~(m/g)")

#text for labels
dat_text <- data.frame(
  label = c("A", "D"),
  trait = c("scaled(Root Tissue Density) (g/cm3)", "scaled(Specific Root Length) (m/g)"),
  x = c(min(RTD_G_dat$x), min(SRL_G_dat$x)),
  y = c(1, 1)
)

#levels(dat_text$trait) <- c("scaled(Turgor~Loss~Point)~(MPa)", "scaled(Leaf~Dry~Matter~Content)~(g/g)", "scaled(Root~Tissue~Density)~(g/cm3)", "scaled(Specific~Root~Length)~(m/g)")

#make a multipanel figure that shows only the graminoid survival probs for 3 traits
gramSurvFigure <- ggplot(data = GramDat) +
  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 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(fill = "white", color = "black"),
        text = element_text(size = 3, fontface = "bold"))
  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$SPEI_s)
sdSPEI_F <- sd(CO_point_all$SPEI_s)
#get 97.5 quantile of the distribution
SPEI_97_5_F <- qnorm(.975, meanSPEI_F, sdSPEI_F)
SPEI_2_5_G <- qnorm(.025, meanSPEI_F, sdSPEI_F)

spei_vals <- c(SPEI_2_5_G, SPEI_97_5_G)

#for RTD
RTD_vals <- seq(min(CO_point_all$RTD_s, na.rm = TRUE), max(CO_point_all$RTD_s, na.rm = TRUE), length.out = 100)
RTD_F_dat <- ggpredict(mSurvRTD_forbs, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed")

#for SRL
SRL_vals <- seq(min(CO_point_all$SRL_s, na.rm = TRUE), max(CO_point_all$SRL_s, na.rm = TRUE), length.out = 100)
SRL_F_dat <- ggpredict(mSurvSRL_forbs, 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
ForbDat <- data.frame(trait = c("scaled(Root Tissue Density) (g/cm3)"), x = RTD_F_dat$x, ForbSurv = RTD_F_dat$y)
ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_F_dat$x, ForbSurv = SRL_F_dat$y))

#make data for rug plot
RugDat_F <- data.frame(rug = CO_point_all$RTD_s, trait = "scaled(Root Tissue Density) (g/cm3)")
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$SRL_s, trait = "scaled(Specific Root Length) (m/g)"))

#text for labels
dat_text <- data.frame(
  label = c("C", "F"),
  trait = c("scaled(Root Tissue Density) (g/cm3)", "scaled(Specific Root Length) (m/g)"),
  x = c(min(RTD_F_dat$x), min(SRL_F_dat$x)),
  y = c(1, 1)
)

#make a multipanel figure that shows only the graminoid survival probs for 3 traits
forbSurvFigure <- ggplot(data = ForbDat) +
  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 Survival") +
  scale_y_continuous(limits = c(0,1)) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62", "#66c2a5"), guide = FALSE) +
  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(fill = "white", stroke = "black", strokewidth = 1))

```

Make figure for graminoid growth models

```

#get 2.5 and 97.5 percentiles of the distribution
meanSPEI <- mean(CO_grow_TLP$SPEI_s)
sdSPEI <- sd(CO_grow_TLP$SPEI_s)
#get 97.5 quantile of the distribution
SPEI_97_5 <- qnorm(.975, meanSPEI, sdSPEI)
SPEI_2_5 <- qnorm(.025, meanSPEI, sdSPEI)

spei_vals <- c(SPEI_2_5, SPEI_97_5)

#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 = 100)
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 = 100)
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$x, Growth = RTD_grow_dat$Growth)
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_grow_dat$x, Growth = SRL_grow_dat$Growth))

#make a data.frame with data for the rug plot
RugDat <- data.frame(rug = CO_grow_RTD$RTD_s, trait = "scaled(Root Tissue Density) (g/cm3)")
RugDat <- rbind(RugDat, data.frame(rug = CO_grow_SRL$SRL_s, trait = "scaled(Specific Root Length) (m/g)"))

#text for labels
dat_text <- data.frame(
  label = c("B", "E"),
  trait = c("scaled(Root Tissue Density) (g/cm3)", "scaled(Specific Root Length) (m/g)"),
  x = c(min(RTD_grow_dat$x), min(SRL_grow_dat$x)),
  y = c(5.3, 5.3)
)

#make a multipanel figure
GrowthExtraFig <- ggplot(data = GrowthDat) +
  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(ln(size[italic(t+1)]))) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#fc8d62", "#66c2a5")) +
  scale_fill_manual(values = c("#fc8d62", "#66c2a5"), 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(fill = "white", col = "white"))

```

Combine into one figure

```

mainObs <- plot_grid( gramSurvFigure, GrowthExtraFig, forbSurvFigure, ncol = 3, align = "h", axis = "tb",
  ggdraw() + draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white"))) ,hjust = 0, vjust = 0,
  draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white"))) ,hjust = 0, vjust = 0, x = .5)

```

```

draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white"))) ,hjust = 0, vjust = 0, x = .
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Root Tissue Density) (g/c*m^3)"),x = .55, y
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Root Tissue Density) (g/c*m^3)"),x = .19, y
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Root Tissue Density) (g/c*m^3)"),x = .873
mainObs

```

