

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 graminoids

```
#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(m1_grams, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.t

#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(m2_grams, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.t

#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(m9, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.t
```

```

# 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(m14, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "none")

# 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(m5, terms = c("SLA_s[SLA_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "none")

#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))

#levels(GramDat$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)")

#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$SLA_s, trait = "scaled(Specific Leaf Area) (g/cm2)"))
#levels(RugDat_G$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)")

#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 'trait' into factor

#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 Graminoid 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)")),
theme_classic()+
theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fill = "white",
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 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(m3, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "xy")

#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(m4, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "xy")

#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(m11, terms = c("RDMC_s[RDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "xy")

#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(m16, terms = c("RDiam_s[RDiam_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "xy")

#for SLA
SLA_vals <- seq(min(CO_point_SLA$SLA_s, na.rm = TRUE), max(CO_point_SLA$SLA_s, na.rm = TRUE), length.out = 100)
SLA_F_dat <- ggpredict(m6, terms = c("SLA_s[SLA_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = "xy")

#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$RDiam_s, trait = "scaled(Average Root Diameter) (mm)",
RugDat_F <- rbind(RugDat_F, data.frame(rug = CO_point_all$SLA_s, trait = "scaled(Specific Leaf Area) (g/m^2)",

#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)",
  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 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 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") +
  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)")),
  theme_classic()+
  theme(legend.position = "bottom", legend.title = element_blank(), legend.background = element_rect(fill = "white", stroke = "black", size = 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 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 = 10)
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 = 10)
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)
)

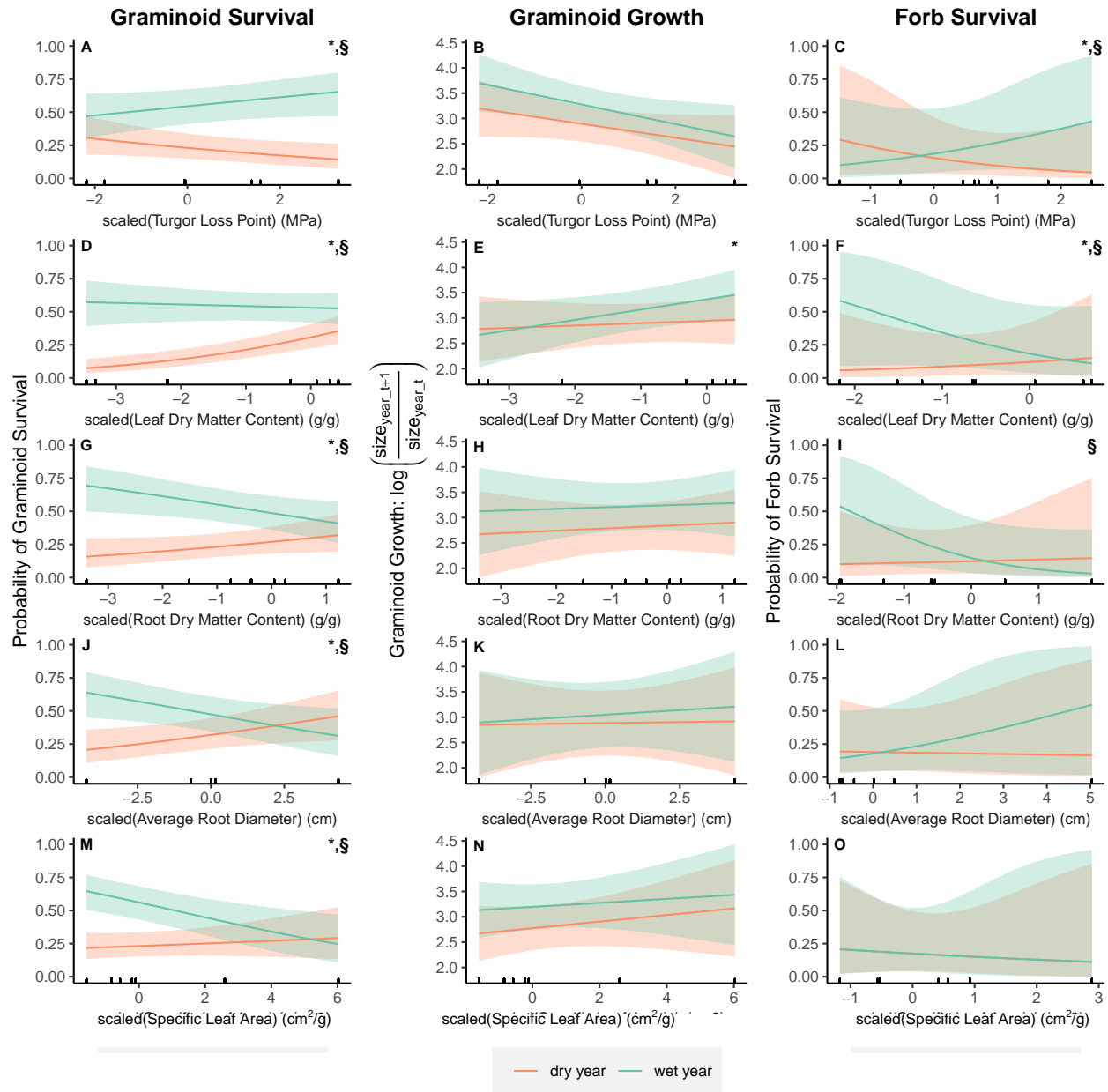
#make a multipanel figure
GrowthExtraFig <- ggplot(data = GrowthDat) +
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, Growth, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat) +
  labs(title = "Graminoid Growth") +
  xlab(NULL) +
  ylab(expression("Graminoid Growth: log" ~ bgroup("(", frac(size[year_t+1], size[year_t]), ")")))) +
  scale_color_manual(labels = c("dry year", "wet year"), values = c("#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", stroke = "black", size = 1))

```

Combine into one figure

```
mainObs <- cowplot::plot_grid( gramSurvFigure, GrowthExtraFig, forbSurvFigure, ncol = 3, align = "h", as
cowplot::ggdraw() +
cowplot::draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white"))) ,hjust = 0, vjust =
cowplot::draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white"))) ,hjust = 0, vjust =
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/CrossSiteClimateCom
#
#
# #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 + area_s + neighbors_10_s + as.factor(near

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

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

AreaEffectSurv <- ggplot() +
  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", "grey60", "grey60", "grey60", "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

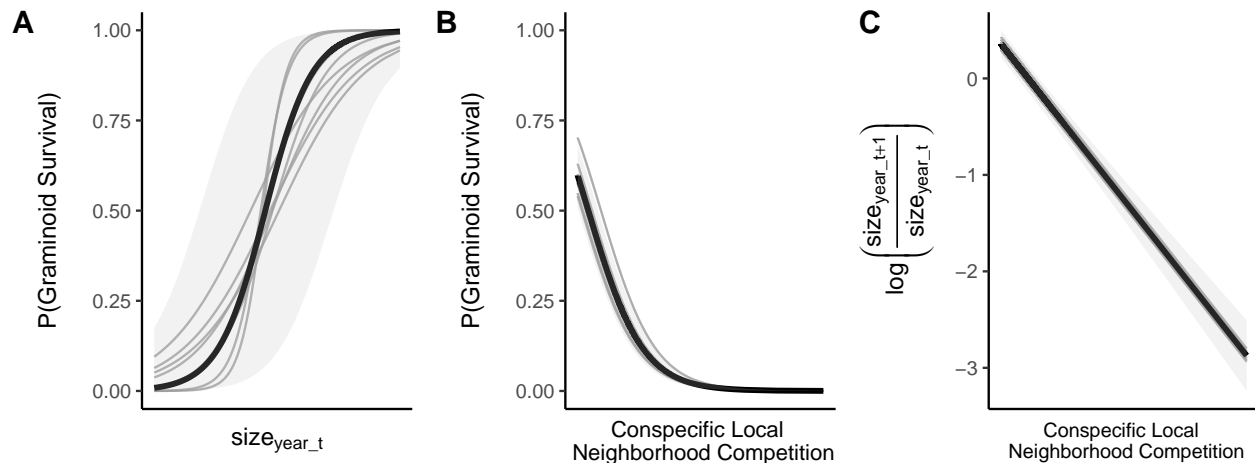
```

sppNeighPreds_s <- ggpredict(m2_fac, terms = c("neighbors_10_s[all]", "species"), type = "random")
sppNeighPreds_s <- data.frame("x" = sppNeighPreds_s$x, "preds" = sppNeighPreds_s$predicted, "spp" = sppNe

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

NeighEffectSurv <- ggplot() +
  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

```

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(m10, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.trans = 0.5)
```

```
#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.trans = 0.5)
```

```
#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)"

#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 Graminoid 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(~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", size = 1))
  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(m12, terms = c("RTD_s[RTD_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.transform = "none")

#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(m15, terms = c("SRL_s[SRL_vals]", "SPEI_s[spei_vals]"), type = "fixed", back.transform = "none")

#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$x, ForbSurv = RTD_F_dat$ForbSurv)

ForbDat <- rbind(ForbDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_F_dat$x, ForbSurv = SRL_F_dat$ForbSurv))

#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 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(fill = "white", stroke = "black", stroke.width = 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)", "scaled(Specific Root Length) (m/g)"), x = RTD_grow_dat$x, Growth = RTD_grow_dat$ForbSurv)
GrowthDat <- rbind(GrowthDat, data.frame(trait = c("scaled(Specific Root Length) (m/g)"), x = SRL_grow_dat$x, Growth = SRL_grow_dat$ForbSurv))

#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(1.2, 1.2)
)

#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("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(fill = "white", stroke = "black", stroke.width = 1))

```

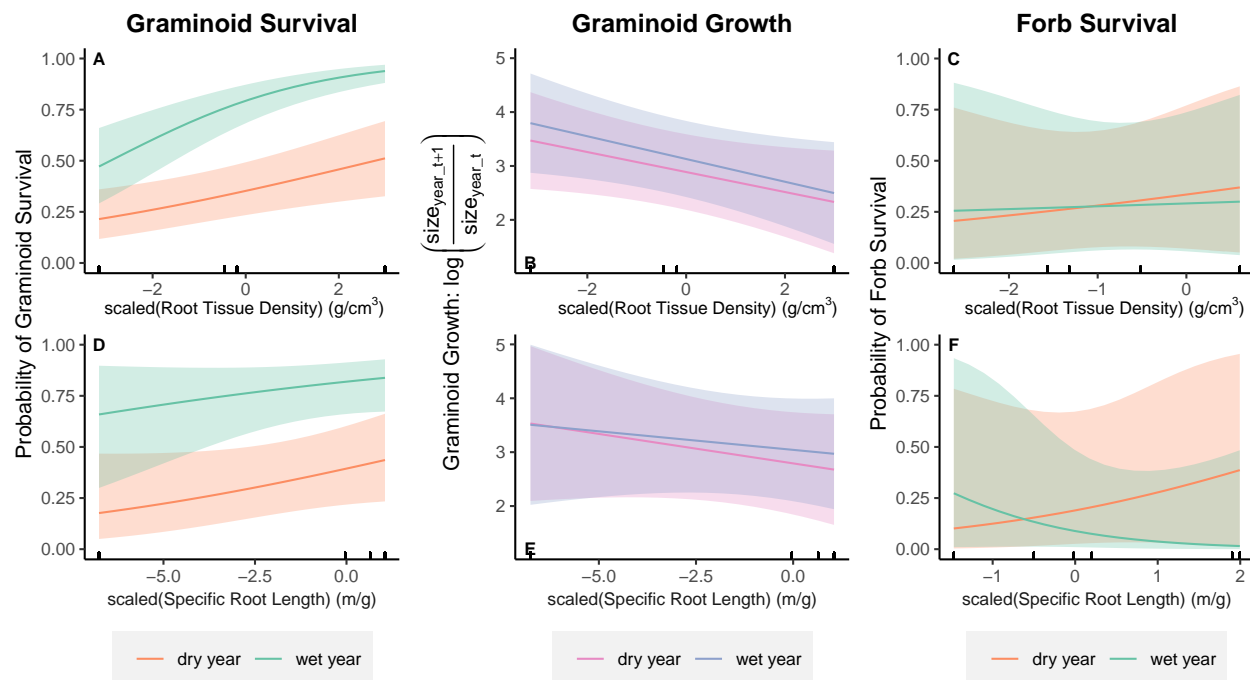
Combine into one figure

```

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 = .1,
  draw_grob(grid::rectGrob(gp = grid::gpar(fill = "white", col = "white"))) ,hjust = 0, vjust = 0, x = .2)

mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Root Tissue Density) (g/c"*m^3*")"),x = .55, y = 1.2))
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Root Tissue Density) (g/c"*m^3*")"),x = .19, y = 1.2))
mainObs <- ggdraw(add_sub(mainObs, label = bquote("scaled(Root Tissue Density) (g/c"*m^3*")"),x = .873, y = 1.2))
mainObs

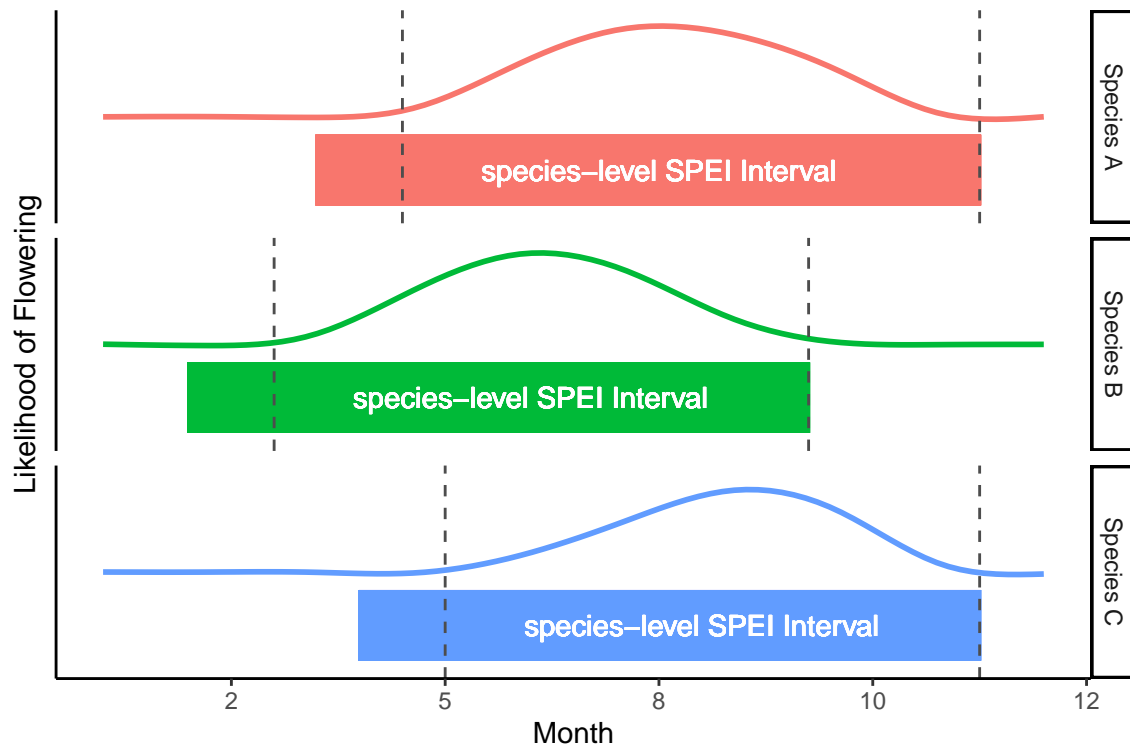
```



make a plot of SPEI intervals

```
#make a fake dataset
phenDat <- data.frame(species = "Species A", month = c(1:12), flowering = c(0,0,0,0,.2,.6,.9,.9,.7,.3,0
phenDat <- rbind(phenDat, data.frame(species = "Species B", month = c(1:12), flowering = c(0,0,0,.3,.7,
phenDat <- rbind(phenDat, data.frame(species = "Species C", month = c(1:12), flowering = c(0,0,0,0,0,.2

ggplot( data = phenDat) +
  geom_smooth(aes(y = flowering, x = month, col = species), method = 'gam', se = FALSE) +
  geom_rect(aes(xmin = xmin,xmax = xmax, ymin = ymin, ymax = ymax, col = species, fill = species)) +
  geom_vline(aes(xintercept = xInt), lty = 2, col = "grey30") +
  geom_vline(aes(xintercept = xInt2), lty = 2, col = "grey30") +
  geom_text(aes(label = "species-level SPEI Interval", x = (xInt+3), y = -.55), colour =
    "white") +
  facet_grid(species~.) +
  ylim(c(-1,1)) +
  xlim(c(1,12)) +
  xlab("Month") +
  ylab("Likelihood of Flowering") +
  scale_color_discrete(guide = FALSE) +
  scale_fill_discrete(guide = FALSE) +
  scale_x_continuous(labels = scales::number_format(accuracy = 1)) +
  theme_classic() +
  theme(axis.ticks.y = element_blank(),
        axis.text.y = element_blank())
```



Figures for comparing unique to uniform SPEI (TLP and LDMC only)

```
#model objects (unique SPEI): m1_grams, m2_grams, mGrow_TLP, mGrow_LDMC
#model objects (uniform SPEI): m1_SPEI, m2_SPEI, mGrowTLP_SPEI, mGrowLDMC_SPEI

## Make figure of unique SPEI of TLP and LDMC survival
#get 2.5 and 97.5 percentiles of the distribution
meanSPEI<- mean(CO_poly_TLP$SPEI_s)
sdSPEI <- sd(CO_poly_TLP$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
TLP_vals <- seq(min(CO_poly_TLP$TLP_s, na.rm = TRUE), max(CO_poly_TLP$TLP_s, na.rm = TRUE), length.out = 100)
TLP_surv_dat <- ggpredict(m1_grams, terms = c("TLP_s[TLP_vals]", "SPEI_s[spei_vals]"), type = "fixed", lty = 1)

#for LDMC
LDMC_vals <- seq(min(CO_poly_LDMC$LDMC_s, na.rm = TRUE), max(CO_poly_LDMC$LDMC_s, na.rm = TRUE), length.out = 100)
LDMC_surv_dat <- ggpredict(m2_grams, terms = c("LDMC_s[LDMC_vals]", "SPEI_s[spei_vals]"), type = "fixed", lty = 1)

#make a data.frame to contain all of the values for each trait
UniqueSurvDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_surv_dat$x, Surv = TLP_surv_dat$Surv)

UniqueSurvDat <- rbind(UniqueSurvDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_surv_dat$x, Surv = LDMC_surv_dat$Surv))

#make data for rug plot
RugDat_surv <- data.frame(rug = CO_poly_TLP$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")
```



```

RugDat_surv <- rbind(RugDat_surv, data.frame(rug = CO_poly_LDMC$LDMC_s, trait = "scaled(Leaf Dry Matter

#make a multipanel figure that shows only the graminoid survival probs for 3 traits
UniqueSPEI_Surv <- ggplot(data = UniqueSurvDat) +
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, y = Surv, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat_surv) +
  labs(title = "Unique SPEI 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")) +
  #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=

## Make figure of unique SPEI of TLP and LDMC growth
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
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
LDMC_vals <- seq(min(CO_poly_LDMC$LDMC_s, na.rm = TRUE), max(CO_poly_LDMC$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",

#make a data.frame to contain all of the values for each trait
UniqueGrowDat <- data.frame(trait = c("scaled(Turgor Loss Point) (MPa)"), x = TLP_grow_dat$x, grow = TLP_grow_dat$y)

UniqueGrowDat <- rbind(UniqueGrowDat, data.frame(trait = c("scaled(Leaf Dry Matter Content) (g/g)"), x = LDMC_grow_dat$x, grow = LDMC_grow_dat$y)

#make data for rug plot
RugDat_grow <- data.frame(rug = CO_grow_TLP$TLP_s, trait = "scaled(Turgor Loss Point) (MPa)")
RugDat_grow <- rbind(RugDat_grow, data.frame(rug = CO_poly_LDMC$LDMC_s, trait = "scaled(Leaf Dry Matter Content) (g/g)")

#make a multipanel figure that shows only the graminoid survival probs for 3 traits
UniqueSPEI_Grow <- ggplot(data = UniqueGrowDat) +
  geom_ribbon(aes(x = x, ymin = CI_low, ymax = CI_high, fill = SPEI), alpha = 0.3) +
  geom_line(aes(x=x, y = grow, col = SPEI)) +
  geom_rug(aes(x = rug), data = RugDat_grow) +
  labs(title = "Unique SPEI Graminoid Growth") +
  xlab(NULL) +
  ylab(expression("Graminoid Growth: log" ~ bgroup("(",frac(size[year_t+1],size[year_t]),")"))) +
  #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

```