

Growth Model Exploration

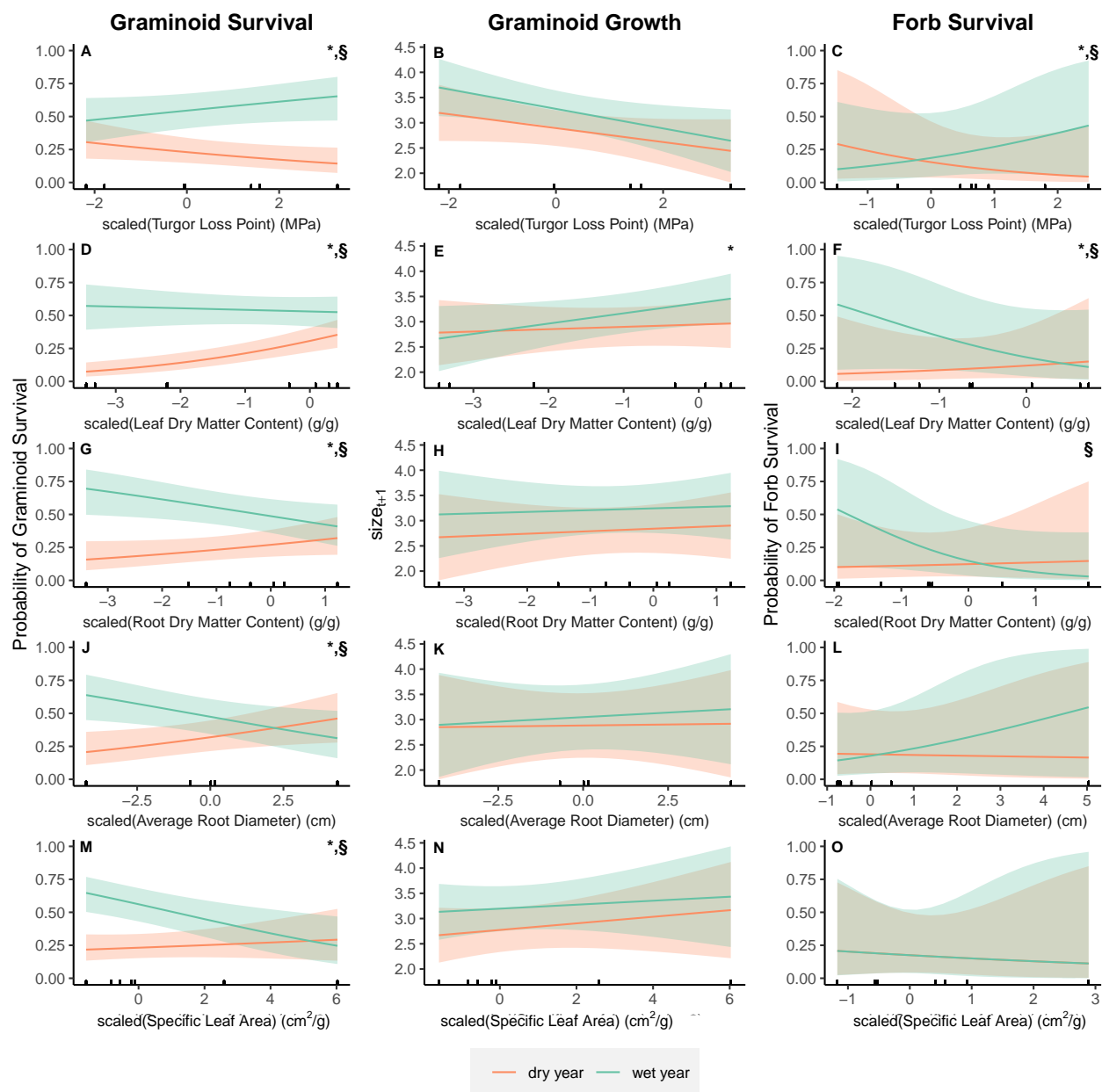
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3/10/2021

Growth Models using size_{t+1} as the response variable

The following growth models use size_{t+1} as the response variable, with both a random slope and a fixed effect of size_t . The figure below shows the updated growth model results for five traits. There is a significant interaction (albeit weak) between SPEI and LDMC for models of growth, but no other significant interactions. Including traits in all growth models actually decreases the AIC of the model in comparison to models without trait data.

Here is a figure showing survival and growth model results for both forbs and graminoids



Here is the model output for these new growth models:

```
##
## =====
##                               Dependent variable:
##                               -----
##                               log(size t+1)
##                               TLP      LDMC      SLA      RDMC      RTD      SRL      RDiam
## area_s      0.51***  0.51***  0.51***  0.51***  0.56***  0.56***  0.49***
##
## neighbors_10_s  -0.12*** -0.12*** -0.12*** -0.12*** -0.13*** -0.13*** -0.13***
```

```
##
## SPEI_s          0.11***  0.12***  0.12***  0.12***  0.07    0.07*   0.05
##
## nearEdge_t      -0.003   -0.003   -0.005   -0.005   -0.03   -0.03   -0.02
##
## Constant        1.34***  1.40***  1.25***  1.30***  1.07***  0.97**  1.30***
##
## Trait           -0.16*    0.12     0.05     0.04    -0.20**  -0.09   -0.02
##
## Trait:SPEI       -0.02    0.05**   -0.01    -0.004   -0.01    0.01    0.01
##
## Marg./Cond. R2   0.23/0.38 0.23/0.39 0.20/0.40 0.20/0.41 0.24/0.49 0.19/0.53 0.17/0.49
## Delta AIC        -10.32   -5.79   -13.17   -12.79    -9.48   -12.19   -13.17
## Observations      9,497    9,497    9,497    9,497    8,802    8,802    9,018
## Akaike Inf. Crit. 30,593.67 30,589.14 30,596.52 30,596.14 28,432.57 28,435.29 29,111.93
## =====
## Note:                                     *p<0.1; **p<0.05; ***p<0.01
```

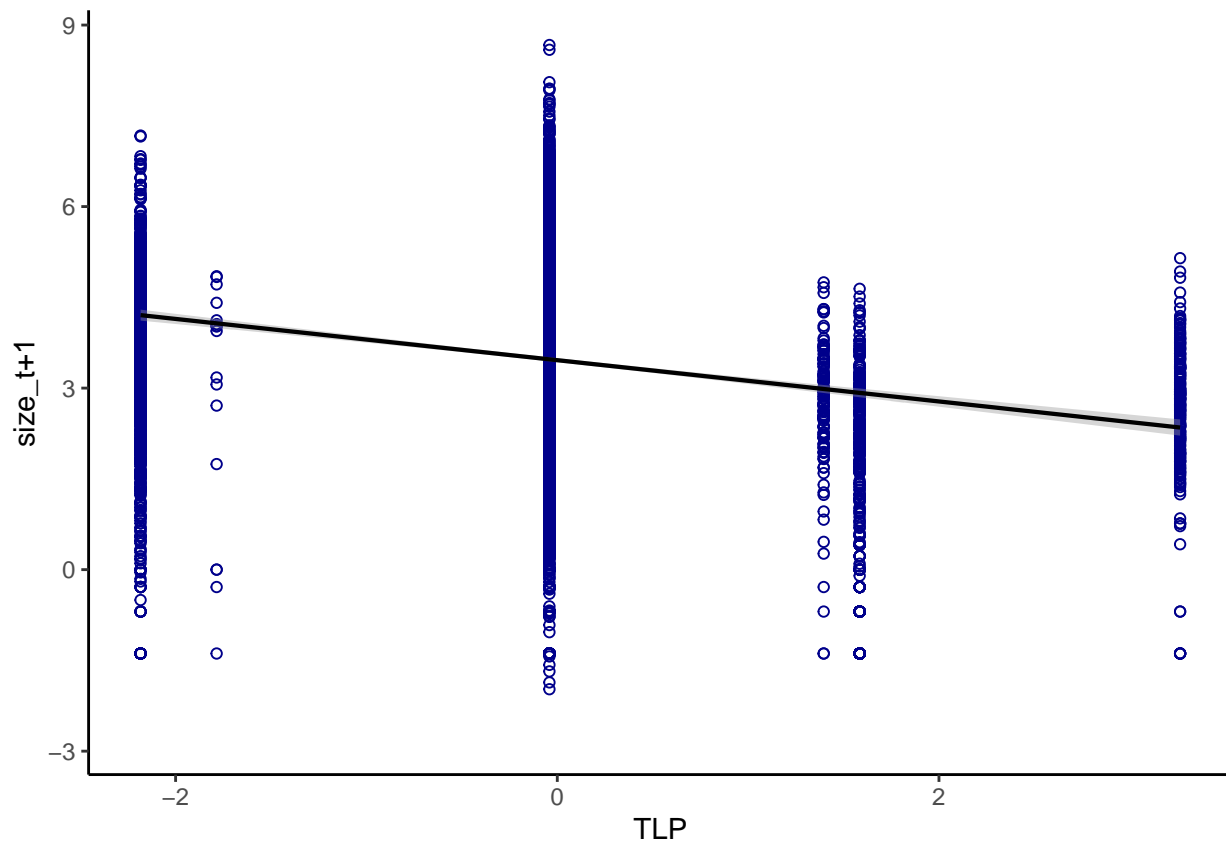
However there is a problem with this modeling approach that I'm not sure how to solve.

If we look at the relationship between trait values and size, we see a negative relationship between TLP and size_{t+1}, such that larger plants tend to have a more negative TLP. So this could get in the way of identifying the interactive effect of SPEI and trait on size in year_{t+1}.

```
#fit a model
modSizeTLP <- lm(CO_grams$area_tplus1_s ~ CO_grams$TLP_s + CO_grams$area_s)

ggplot(data = CO_grams) +
  geom_point(aes(x = TLP_s, y = area_tplus1_s), colour = "darkblue", pch = 1) +
  xlab("TLP") +
  ylab("size_t+1") +
  geom_smooth(aes(x = TLP_s, y = area_tplus1_s), method = "lm", col = "black", lwd = .75) +
  theme_classic()

## `geom_smooth()` using formula 'y ~ x'
## Warning: Removed 22128 rows containing non-finite values (stat_smooth).
## Warning: Removed 22128 rows containing missing values (geom_point).
```



```
summary(modSizeTLP)
```

```
##
## Call:
## lm(formula = CO_grams$area_tplus1_s ~ CO_grams$TLP_s + CO_grams$area_s)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.3515 -0.5166  0.1723  0.7299  4.8210
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.822562   0.032483  25.323 < 2e-16 ***
## CO_grams$TLP_s -0.064800   0.015149  -4.278 1.91e-05 ***
## CO_grams$area_s  0.747473   0.008447  88.487 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.254 on 9494 degrees of freedom
## (22128 observations deleted due to missingness)
## Multiple R-squared:  0.4682, Adjusted R-squared:  0.4681
## F-statistic: 4179 on 2 and 9494 DF, p-value: < 2.2e-16
```

This is problematic. One way we could potentially get around this is to scale size uniquely for each species.

```

# scale size_t and size_tplus1 for each species
spp <- unique(CO_poly_growth$species)

#make an empty column for size in year t and year t+1 scaled per spp
CO_poly_growth$area_t_scaleSpp <- NA
CO_poly_growth$area_tplus1_scaleSpp <- NA

for(i in 1:length(spp)) {
  #unscaled size in year t: CO_poly_growth$area_t
  #scale size in year t for each species
  CO_poly_growth[CO_poly_growth$species==spp[i], "area_t_scaleSpp"] <-
  scale(log(CO_poly_growth[CO_poly_growth$species==spp[i], "area_t"]), center = TRUE)
  #unscaled size in year t+1: CO_poly_growth$area_tplus1
  CO_poly_growth[CO_poly_growth$species==spp[i], "area_tplus1_scaleSpp"] <-
  scale(log(CO_poly_growth[CO_poly_growth$species==spp[i], "area_tplus1"]), center = TRUE)
}

## Then, scale the size variables again all together to make them normally distributed
CO_poly_growth$area_t_scaleSpp <- scale(CO_poly_growth$area_t_scaleSpp, center = TRUE)
CO_poly_growth$area_tplus1_scaleSpp <- scale(CO_poly_growth$area_tplus1_scaleSpp, center = TRUE)

```

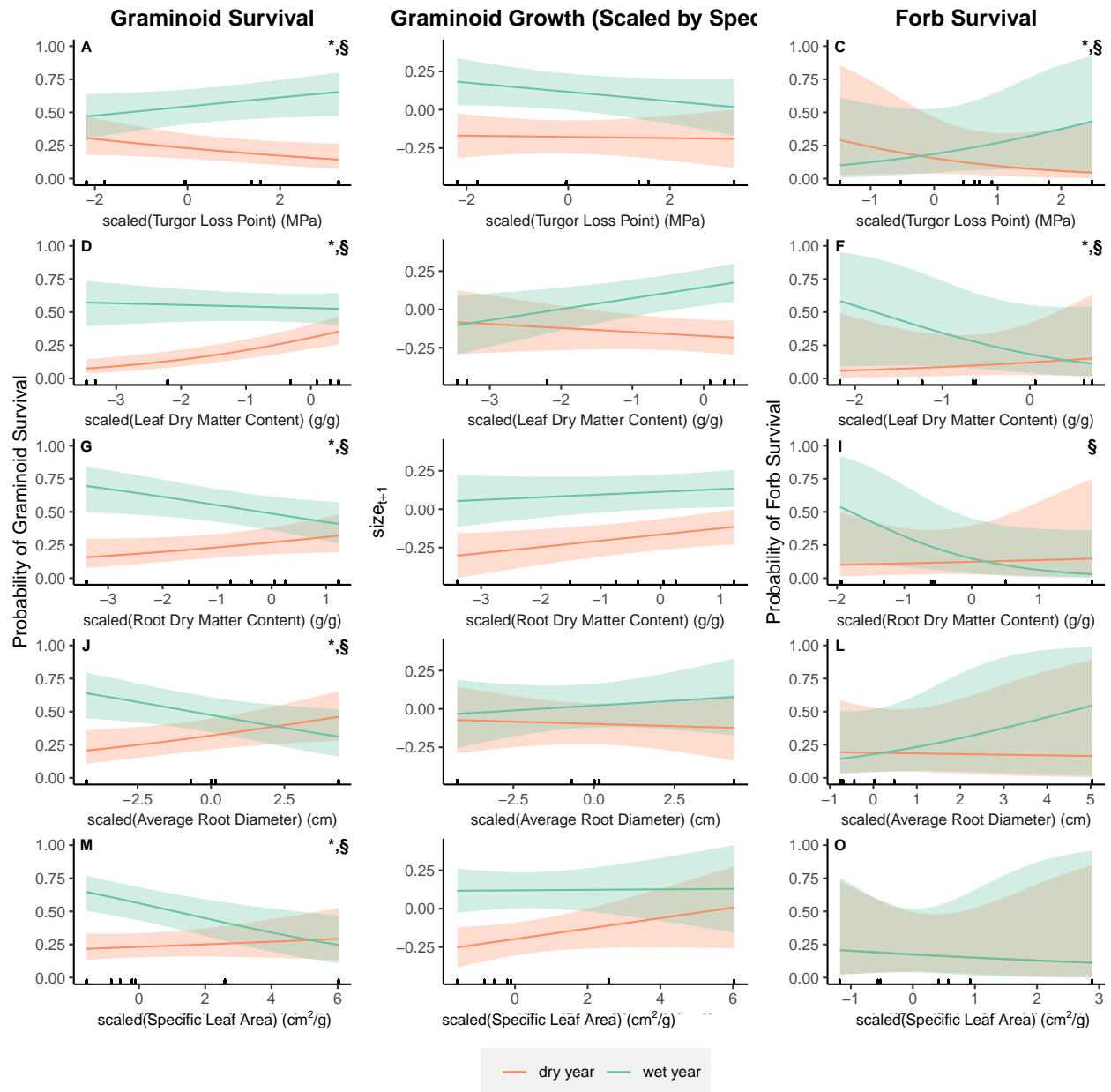
Now, redo the growth models using this new scaled size variable

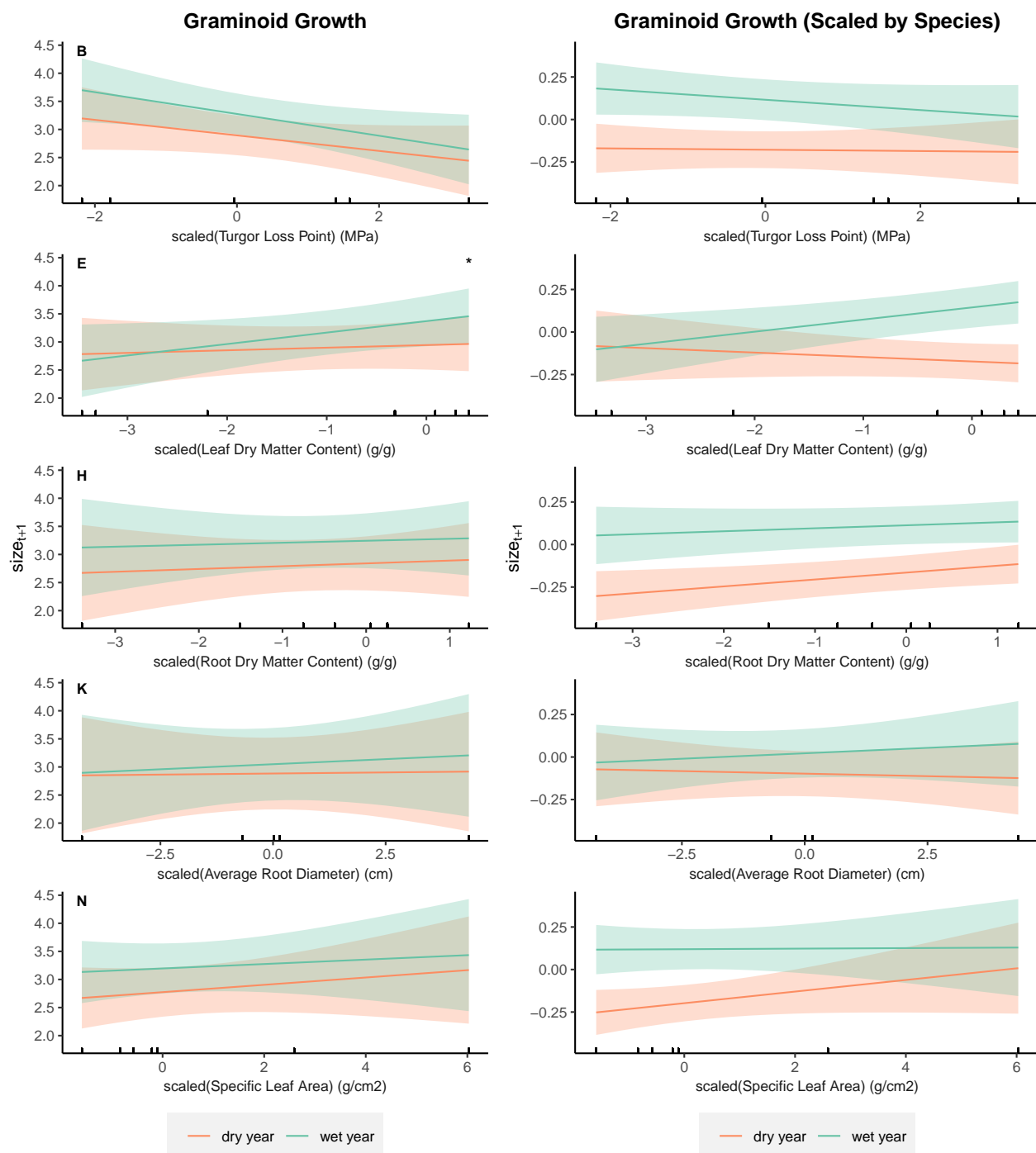
```

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

```

Here are figures showing the model results





Here are the model coefficients and summary statistics

```
##
## =====
##                                     Dependent variable:
## -----
##                                     log(size t+1)
##                                     TLP      LDMC      SLA      RDMC      RTD      SRL      RDiam
## area_t_scaleSpp  0.49***  0.49***  0.49***  0.49***  0.51***  0.51***  0.45***
##
```

```
## neighbors_10_s      -0.07***    -0.07***    -0.08***    -0.08***    -0.08***    -0.08***    -0.08***
##
## SPEI_s              0.09***     0.09***     0.09***     0.08***     0.05*      0.05**      0.03
##
## nearEdge_t          0.003       0.003       0.003       0.003       -0.02      -0.02       -0.01
##
## Constant            0.01        0.02        -0.003      0.01        0.03       -0.001      0.02
##
## Trait               -0.015      0.016       0.020       0.031***    -0.030**   -0.019      0.002
##
## Trait:SPEI          -0.008      0.028**     -0.009      -0.007      -0.008     0.006       0.005
##
## Marg./Cond. R2      0.236/0.310 0.236/0.305 0.232/0.303 0.254 / NA 0.268 / NA 0.246 / 0.334 0.197 / 0.1
## Delta AIC           -16.53     -10.15     -15.67     -13.57     -12.54     -16.70     -17.93
## Observations        9,497      9,497      9,497      9,497      8,802      8,802      9,018
## Akaike Inf. Crit.   21,766.05  21,759.67  21,765.19  21,763.09  19,888.76  19,892.92  20,550.0
## =====
## Note:                                                         *p<0.1; **p<0.05; ***p<0.001
```

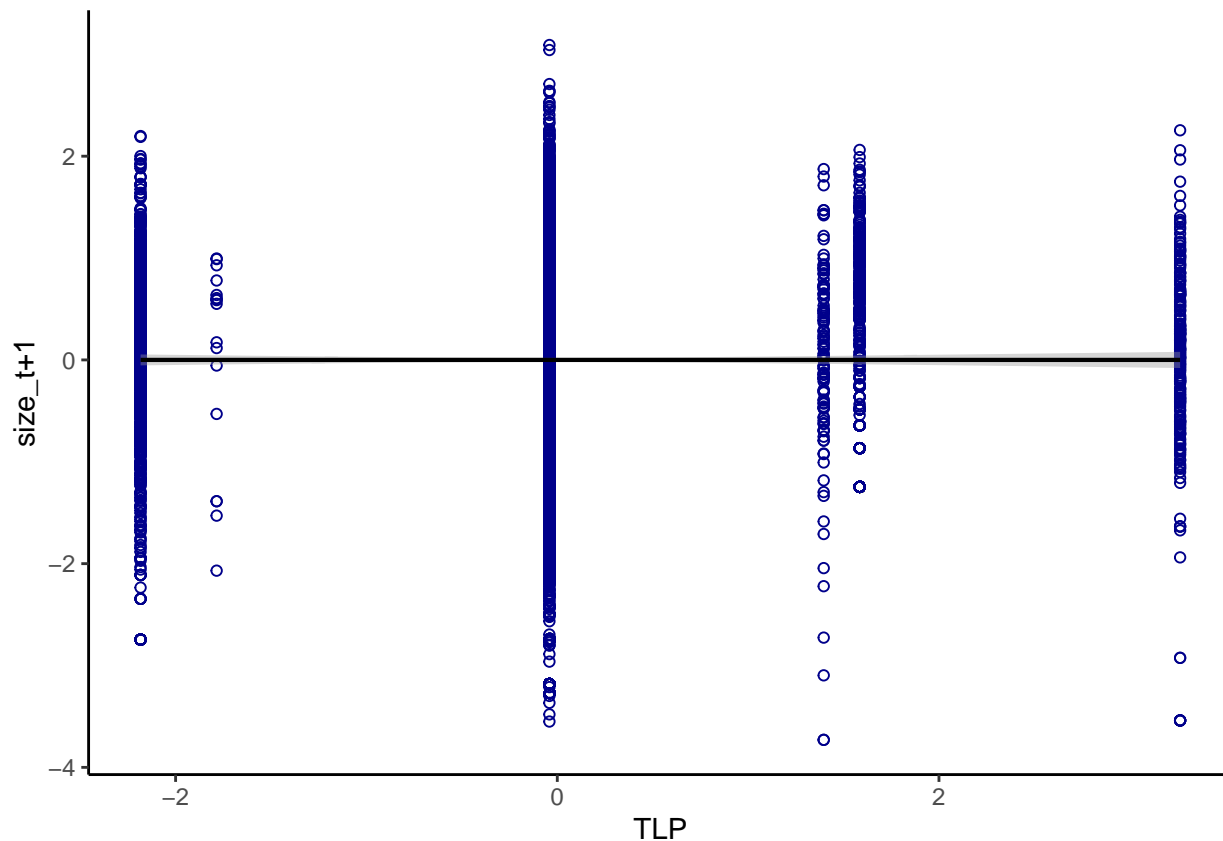
This doesn't seem to do much to make the model fit better... so not too sure how to feel about it except for that it makes more sense theoretically. (note: RDMC and RTD models didn't converge)

Here's a comparison of TLP and size

```
#fit a model
modSizeTLP_spp <- lm(as.numeric(CO_grow_TLP_spp$area_tplus1_scaleSpp) ~
                     as.numeric(CO_grow_TLP_spp$TLP_s) +
                     as.numeric(CO_grow_TLP_spp$area_t_scaleSpp))

ggplot(data = CO_grow_TLP_spp) +
  geom_point(aes(x = TLP_s, y = area_tplus1_scaleSpp), colour = "darkblue", pch = 1) +
  xlab("TLP") +
  ylab("size_t+1") +
  geom_smooth(aes(x = TLP_s, y = area_tplus1_scaleSpp), method = "lm", col = "black", lwd = .75) +
  theme_classic()

## `geom_smooth()` using formula 'y ~ x'
```

```
summary(modSizeTLP_spp)
```

```
##
## Call:
## lm(formula = as.numeric(CO_grow_TLP_spp$area_tplus1_scaleSpp) ~
##     as.numeric(CO_grow_TLP_spp$TLP_s) + as.numeric(CO_grow_TLP_spp$area_t_scaleSpp))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.2521 -0.3205  0.1070  0.4534  2.9686
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept)      1.720e-18  7.993e-03    0.00
## as.numeric(CO_grow_TLP_spp$TLP_s) -1.429e-17  9.200e-03    0.00
## as.numeric(CO_grow_TLP_spp$area_t_scaleSpp) 6.281e-01  7.986e-03  78.66
##              Pr(>|t|)
## (Intercept)              1
## as.numeric(CO_grow_TLP_spp$TLP_s)              1
## as.numeric(CO_grow_TLP_spp$area_t_scaleSpp) <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7782 on 9494 degrees of freedom
## Multiple R-squared:  0.3946, Adjusted R-squared:  0.3944
## F-statistic: 3094 on 2 and 9494 DF, p-value: < 2.2e-16
```

This species-level scaling has dealt with the issue of a significant relationship between TLP and size in t+1,

which seems like a good sign. It would be great to get everyone's opinion on this approach.

Species-level growth models

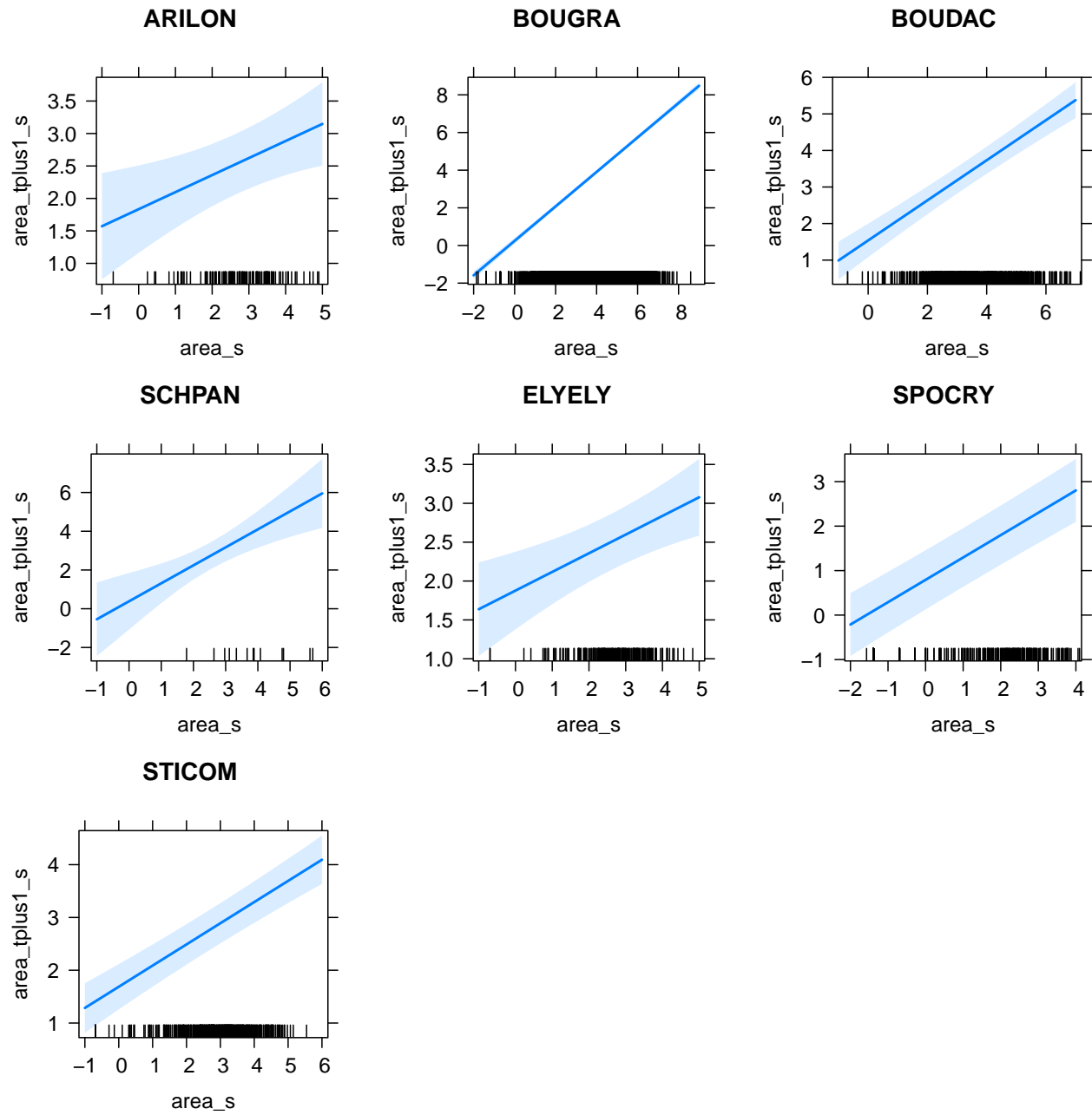
This table shows coefficients and summary statistics of species-level models of plant size in $t+1$ that don't contain trait as a fixed effect or an interaction. These models use the following structure:

```
lme4::lmer(area_tplus1_s ~ area_s + neighbors_10_s + SPEI_s + nearEdge_t + (1|quad) +
  (1|year_t), data = CO_grow_TLP[CO_grow_TLP$species == "Sporobolus cryptandrus",] ,
  control=lmerControl(optimizer="bobyqa"))
```

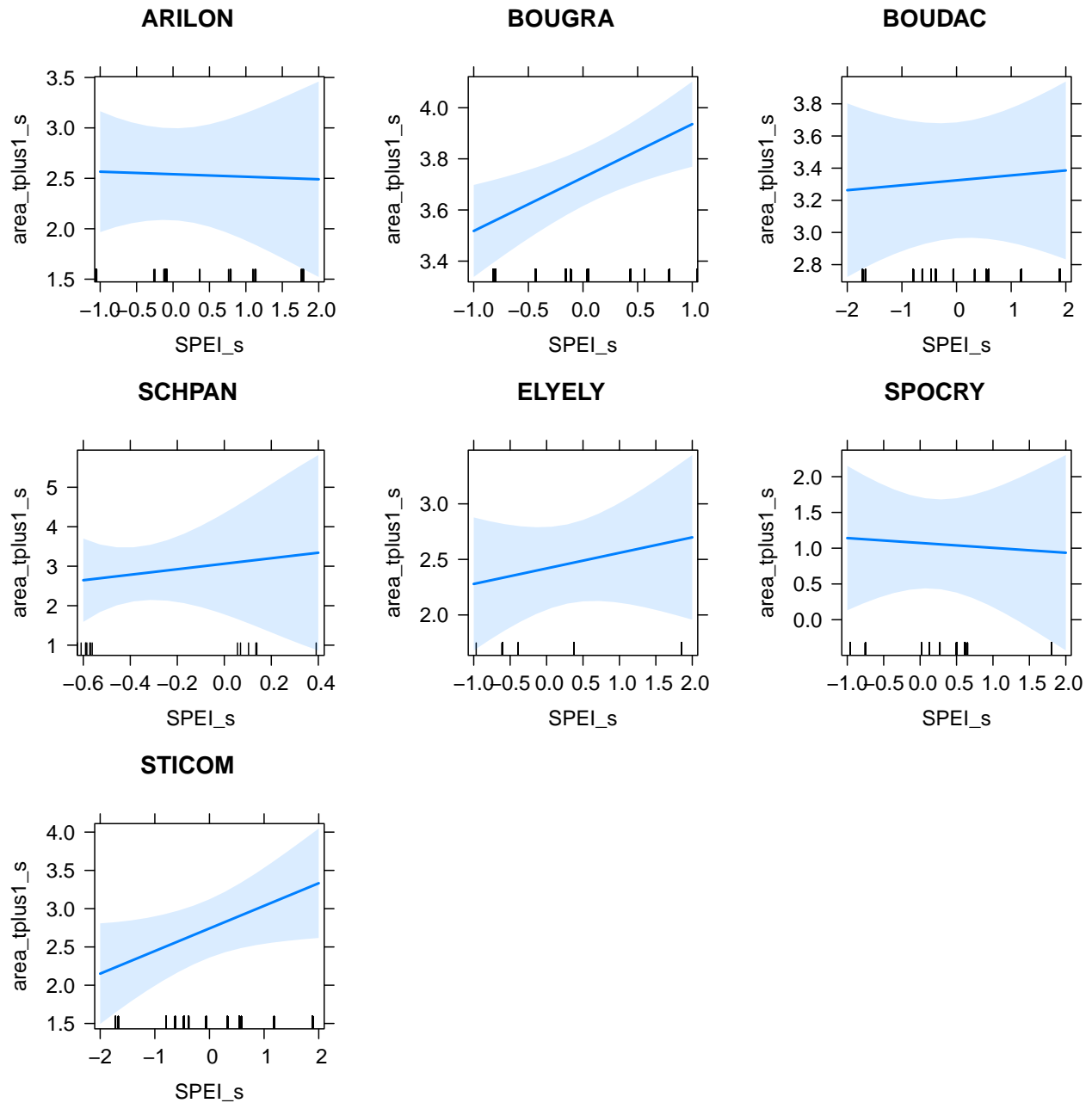
* Important note: the model for *Schedonardus paniculatus* did not converge, likely because there are only 17 observations for that species. * Another Important Note: these models use a response variable of size_t+1 that has been scaled accross the entire dataset, not size_t+1 scaled by species.

```
##
## Species-level models of size(w/out traits)
## =====
##                               Dependent variable:
##                               -----
##                               log(size t+1)
##                               ARILON  BOUDAC  BOUGRA  ELYELY  SCHPAN  SPOCRY  STICOM
## -----
## area_s                0.26***  0.55***  0.92***  0.24***  0.93***  0.50***  0.40***
##                      (0.09)  (0.04)  (0.02)  (0.07)  (0.22)  (0.04)  (0.04)
## neighbors_10_s        -0.10   -0.07   -0.14*** -0.95** -2.72*** -1.99***  0.05
##                      (1.30)  (0.05)  (0.02)  (0.39)  (1.04)  (0.55)  (0.34)
## SPEI_s                -0.03    0.03    0.21***  0.14    0.70   -0.07    0.30**
##                      (0.21)  (0.10)  (0.07)  (0.19)  (1.47)  (0.34)  (0.15)
## nearEdge_t           -0.17   -0.14   -0.04    0.10    0.23    0.08    0.27***
##                      (0.22)  (0.12)  (0.03)  (0.16)  (0.79)  (0.17)  (0.10)
## Constant              1.81*   1.63***  0.36***  1.28*** -0.36   -0.34   1.61***
##                      (0.95)  (0.23)  (0.08)  (0.36)  (0.79)  (0.47)  (0.31)
## -----
## Observations           116      725     7,516     216      17     445     462
## Log Likelihood        -168.72 -1,318.34 -11,739.75 -325.87 -24.09 -815.92 -675.80
## Akaike Inf. Crit.     353.45  2,652.68  23,495.50  667.74  64.18  1,647.84 1,367.60
## Bayesian Inf. Crit.  375.47  2,689.37  23,550.90  694.74  70.85  1,680.63 1,400.68
## =====
## Note:                                     *p<0.1; **p<0.05; ***p<0.01
```

These figures show *the effect of size_t on size_{t+1}* for species-level models



These figures show *the effect of SPEI on size_{t+1}* for species-level models



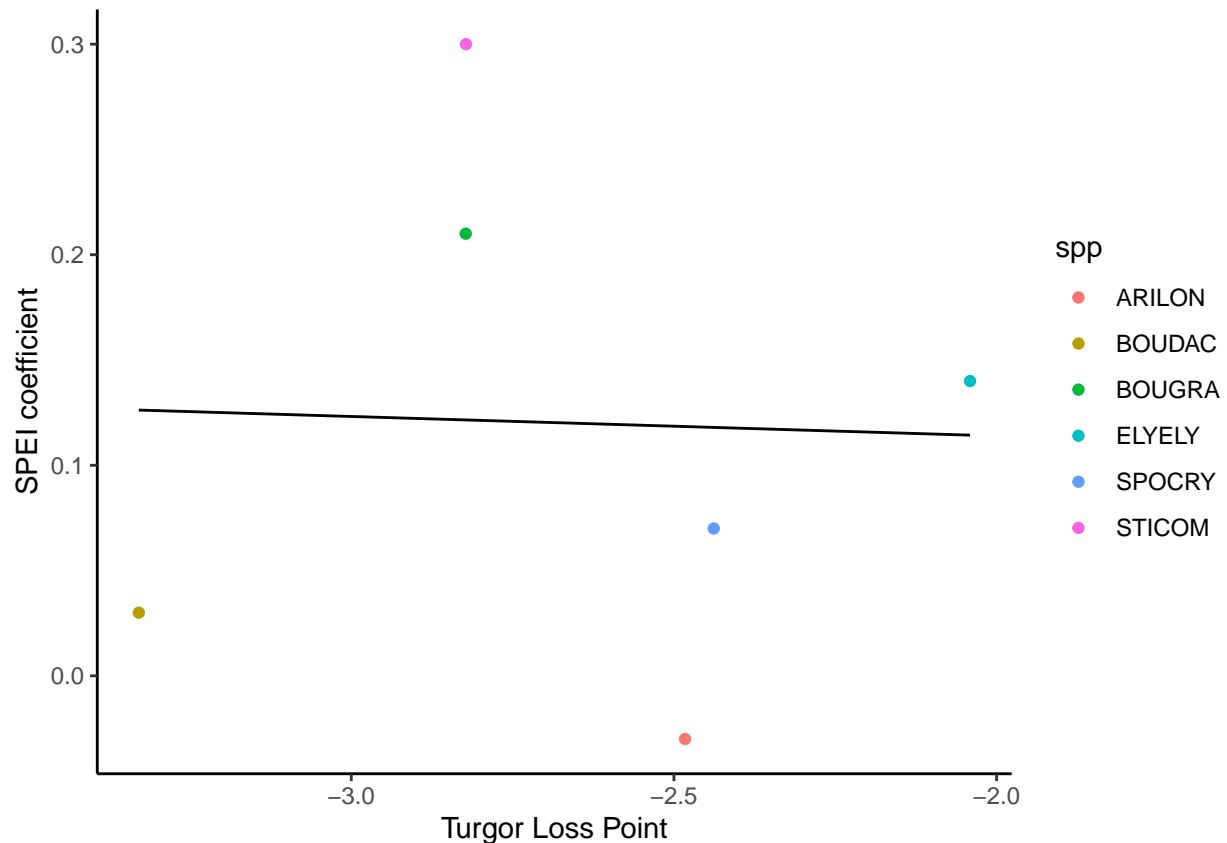
This figure and model compares the effect of SPEI on size in t+1 to TLP value accross species. There is not a significant relationship between SPEI effect and TLP accross the modeled species, which is good sign. There is not a species that responds to SPEI so strongly that it is individually driving the relationship in our cross-species models.

```
#removes SCHPAN results, since the model for that species doesn't converge
sppTest <- data.frame(spp = c("ARILON", "BOUDAC", "BOUGRA", "ELYELY", "SPOCRY", "STICOM"),
  SPEI_coef = c(-0.03, 0.03, 0.21, 0.14, 0.07, 0.30),
  TLP = c(-2.482760, -3.329160, -2.822600, -2.041160, -2.438216, -2.822216))
```

```
modSPEI_TLP <- lm(SPEI_coef ~ TLP , data = sppTest)

ggplot(data = sppTest) +
  geom_point(aes(y = SPEI_coef, x = TLP, col = spp)) +
  xlab("Turgor Loss Point") +
  ylab("SPEI coefficient") +
  geom_smooth(aes(y = SPEI_coef, x = TLP), method = "lm", se = FALSE, col = "black", lwd = .5) +
  theme_classic()
```

```
## `geom_smooth()` using formula 'y ~ x'
```



```
summary(modSPEI_TLP)
```

```
##
## Call:
## lm(formula = SPEI_coef ~ TLP, data = sppTest)
##
## Residuals:
##      1       2       3       4       5       6
## -0.14840 -0.09622  0.08846  0.02568 -0.04799  0.17846
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.09546    0.37190   0.257   0.81
## TLP         -0.00924    0.13845  -0.067   0.95
##
## Residual standard error: 0.1359 on 4 degrees of freedom
```

```
## Multiple R-squared:  0.001112,    Adjusted R-squared:  -0.2486
## F-statistic: 0.004453 on 1 and 4 DF,  p-value: 0.95
```

Now do all this stuff again, but with the species-scaled size values

```
#fit models by species w/ species scaled data

mGrow_ARILON_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE
mGrow_BOUGRA_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE
mGrow_BOUDAC_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE
mGrow_SCHPAN_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE

## boundary (singular) fit: see ?isSingular
#fit is Singular (only 17 data points, so makes sense...)

mGrow_ELYELY_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE
mGrow_SPOCRY_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE
mGrow_STICOM_spp<- lme4::lmer(area_tplus1_scaleSpp ~ area_t_scaleSpp + neighbors_10_s + SPEI_s + nearE

##
## Species-level models of size(w/out traits)
## =====
##                               Dependent variable:
##                               -----
##                               log(size t+1)
##                               ARILON  BOUDAC  BOUGRA  ELYELY  SCHPAN  SPOCRY  STICOM
## -----
## area_t_scaleSpp      0.26***  0.52***  0.73***  0.25***  1.14***  0.52***  0.46***
##                      (0.09)   (0.04)   (0.01)   (0.07)   (0.28)   (0.04)   (0.04)
## neighbors_10_s       -0.09    -0.04   -0.09*** -0.84**  -1.34*** -1.09***  0.04
##                      (1.19)   (0.03)   (0.01)   (0.34)   (0.51)   (0.30)   (0.26)
## SPEI_s               -0.02     0.02    0.13***  0.12     0.34    -0.04    0.23**
##                      (0.19)   (0.06)   (0.04)   (0.17)   (0.72)   (0.19)   (0.11)
## nearEdge_t           -0.15    -0.08   -0.02     0.09     0.11     0.04    0.21***
##                      (0.20)   (0.07)   (0.02)   (0.14)   (0.39)   (0.09)   (0.08)
## Constant             -0.16     0.03    0.10***  -0.64**  -0.37   -0.54**  -0.15
##                      (0.77)   (0.11)   (0.04)   (0.25)   (0.38)   (0.26)   (0.22)
## -----
## Observations          116      725      7,516      216       17      445      462
## Log Likelihood        -158.61 -922.57 -8,194.86 -300.35  -14.65  -551.30  -555.97
## Akaike Inf. Crit.     333.22  1,861.15 16,405.73  616.69   45.30   1,118.61 1,127.93
## Bayesian Inf. Crit.  355.25  1,897.83 16,461.13  643.70   51.97   1,151.39 1,161.02
## =====
## Note:                                     *p<0.1; **p<0.05; ***p<0.01
```

These figures show *the effect of size_t on size_{t+1}* for species-level models w/ species-scaled size

```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
```

```

## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors

## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors

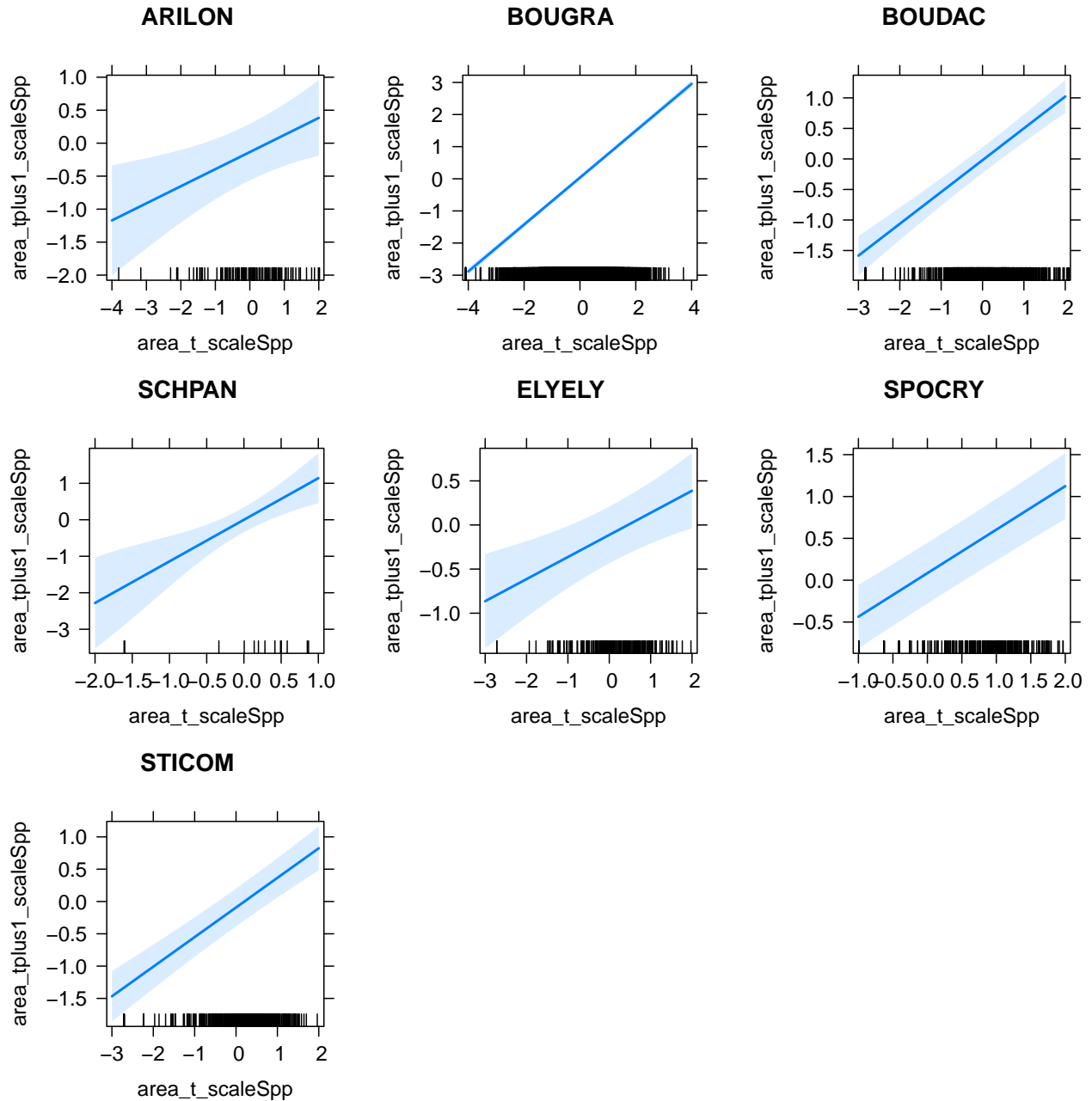
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors

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## were converted to vectors

```



These figures show *the effect of SPEI on size_{t+1}* for species-level models

```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors
```

```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
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## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors
```

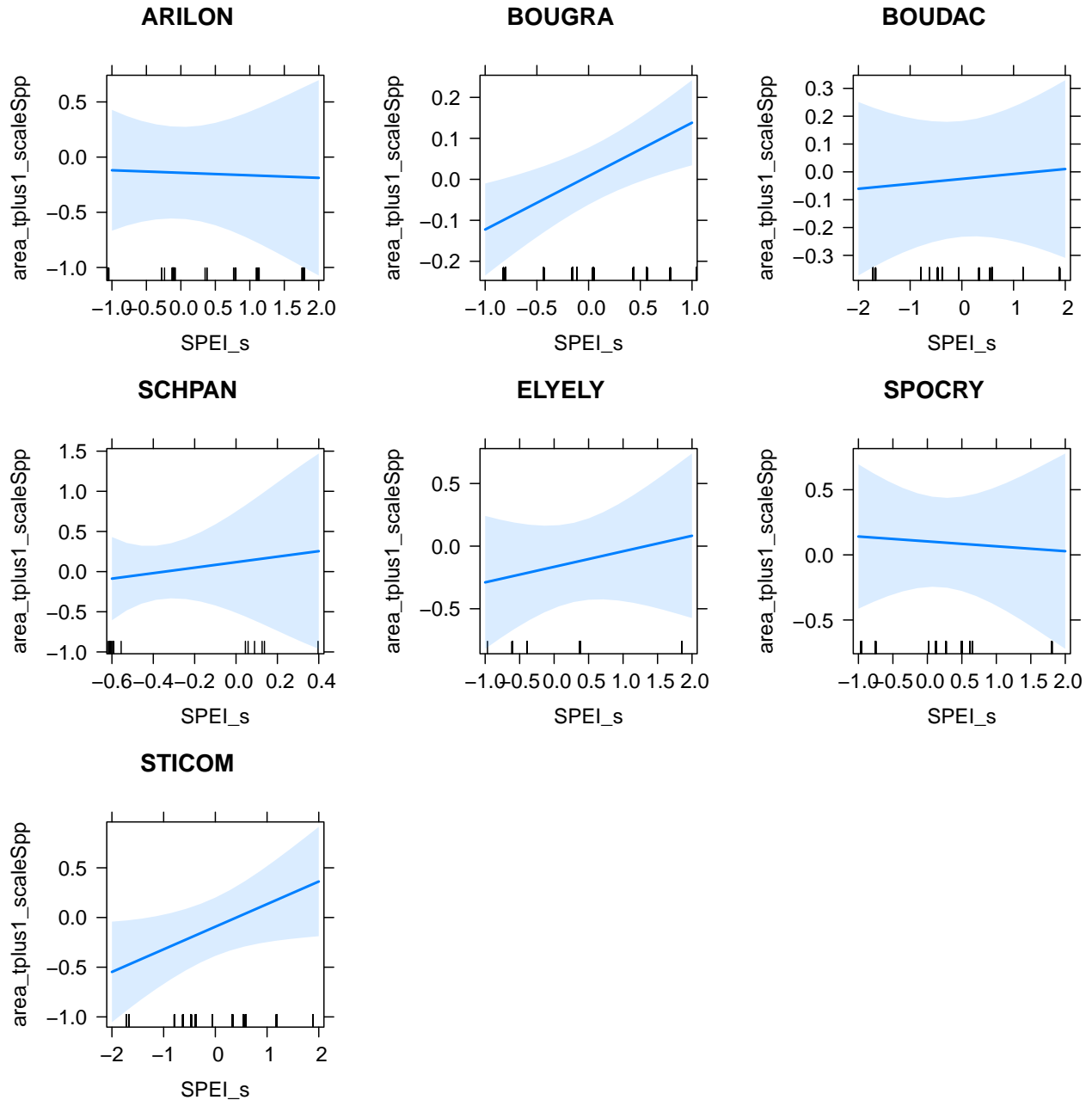


```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors
```

```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors
```

```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors
```

```
## Warning in Analyze.model(focal.predictors, mod, xlevels, default.levels, : the
## predictors area_tplus1_scaleSpp, area_t_scaleSpp are one-column matrices that
## were converted to vectors
```



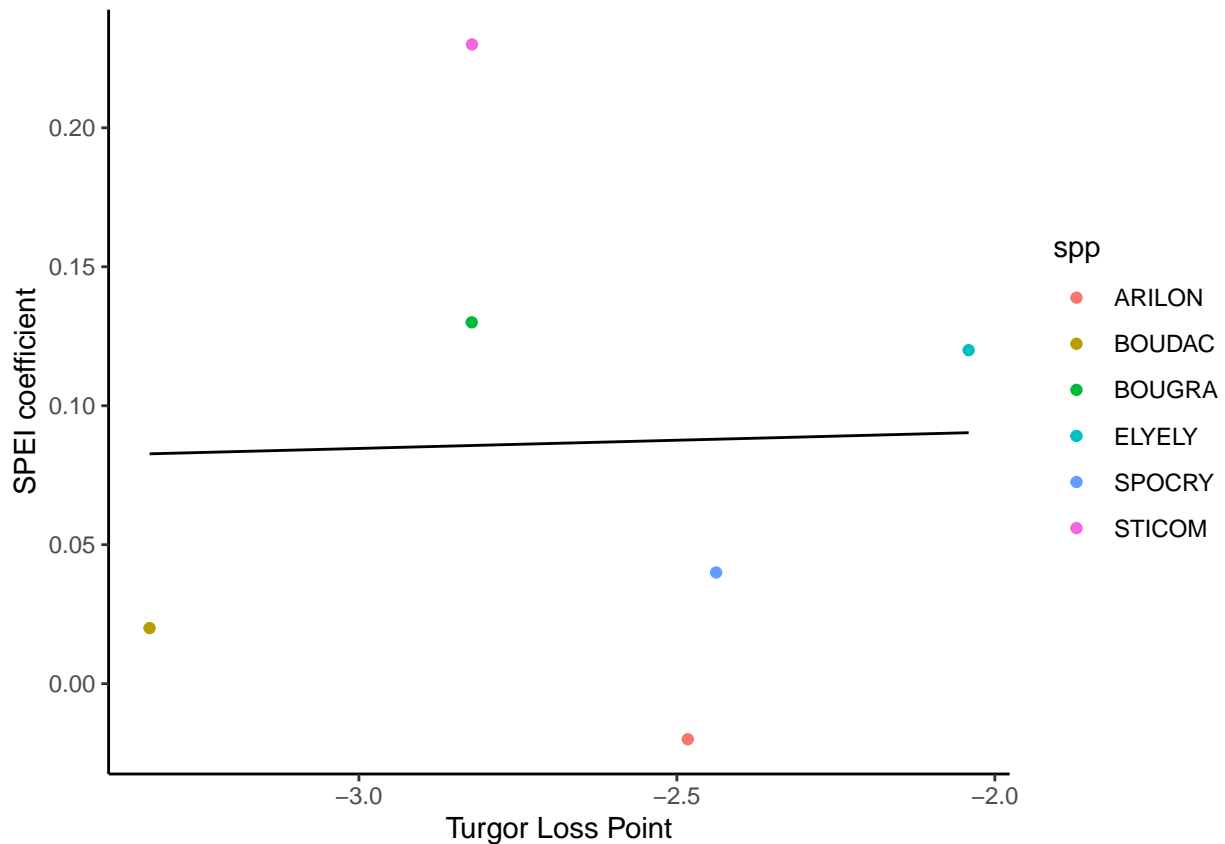
This figure and model compares the effect of SPEI on size in $t+1$ to TLP value accross species. There is not a significant relationship between SPEI effect and TLP accross the modeled species, which is good sign. There is not a species that responds to SPEI so strongly that it is individually driving the relationship in our cross-species models.

```
#removes SCHPAN results, since the model for that species doesn't converge
sppTest <- data.frame(spp = c("ARILON", "BOUDAC", "BOUGRA", "ELYELY", "SPOCRY", "STICOM"),
  SPEI_coef = c(-0.02, 0.02, 0.13, 0.12, 0.04, 0.23),
  TLP = c(-2.482760, -3.329160, -2.822600, -2.041160, -2.438216, -2.822216))

modSPEI_TLP <- lm(SPEI_coef ~ TLP , data = sppTest)
```

```
ggplot(data = sppTest) +
  geom_point(aes(y = SPEI_coef, x = TLP, col = spp)) +
  xlab("Turgor Loss Point") +
  ylab("SPEI coefficient") +
  geom_smooth(aes(y = SPEI_coef, x = TLP), method = "lm", se = FALSE, col = "black", lwd = .5) +
  theme_classic()
```

```
## `geom_smooth()` using formula 'y ~ x'
```



```
summary(modSPEI_TLP)
```

```
##
## Call:
## lm(formula = SPEI_coef ~ TLP, data = sppTest)
##
## Residuals:
##      1       2       3       4       5       6
## -0.10769 -0.06270  0.04432  0.02971 -0.04795  0.14431
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.102333   0.278661   0.367   0.732
## TLP          0.005899   0.103742   0.057   0.957
##
## Residual standard error: 0.1019 on 4 degrees of freedom
## Multiple R-squared:  0.0008075, Adjusted R-squared:  -0.249
## F-statistic: 0.003233 on 1 and 4 DF, p-value: 0.9574
```

There is not a significant relationship between the effect SPEI and TLP for this approach either, which is good.

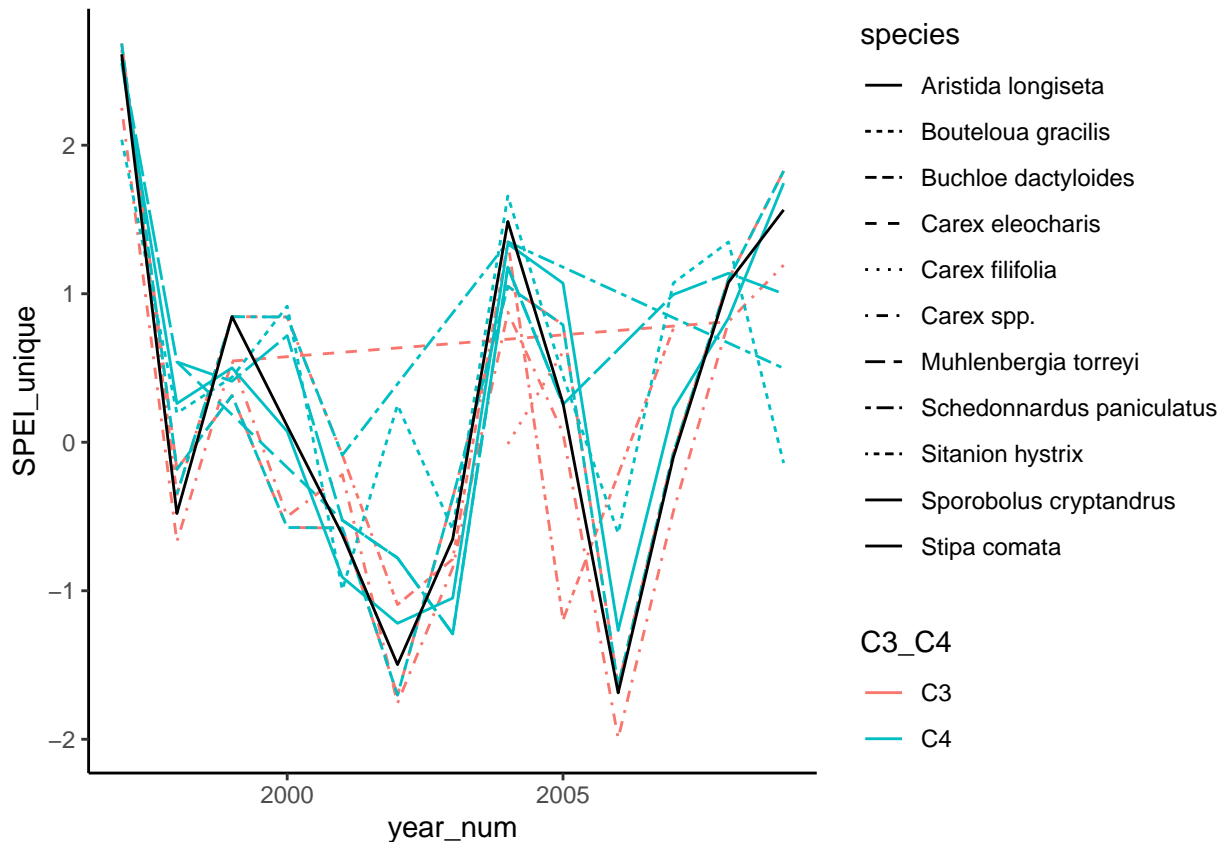
Comparing Unique vs. Uniform SPEI (for graminoids only)s

The following results are for graminoids only

```
## Joining, by = "species"
```

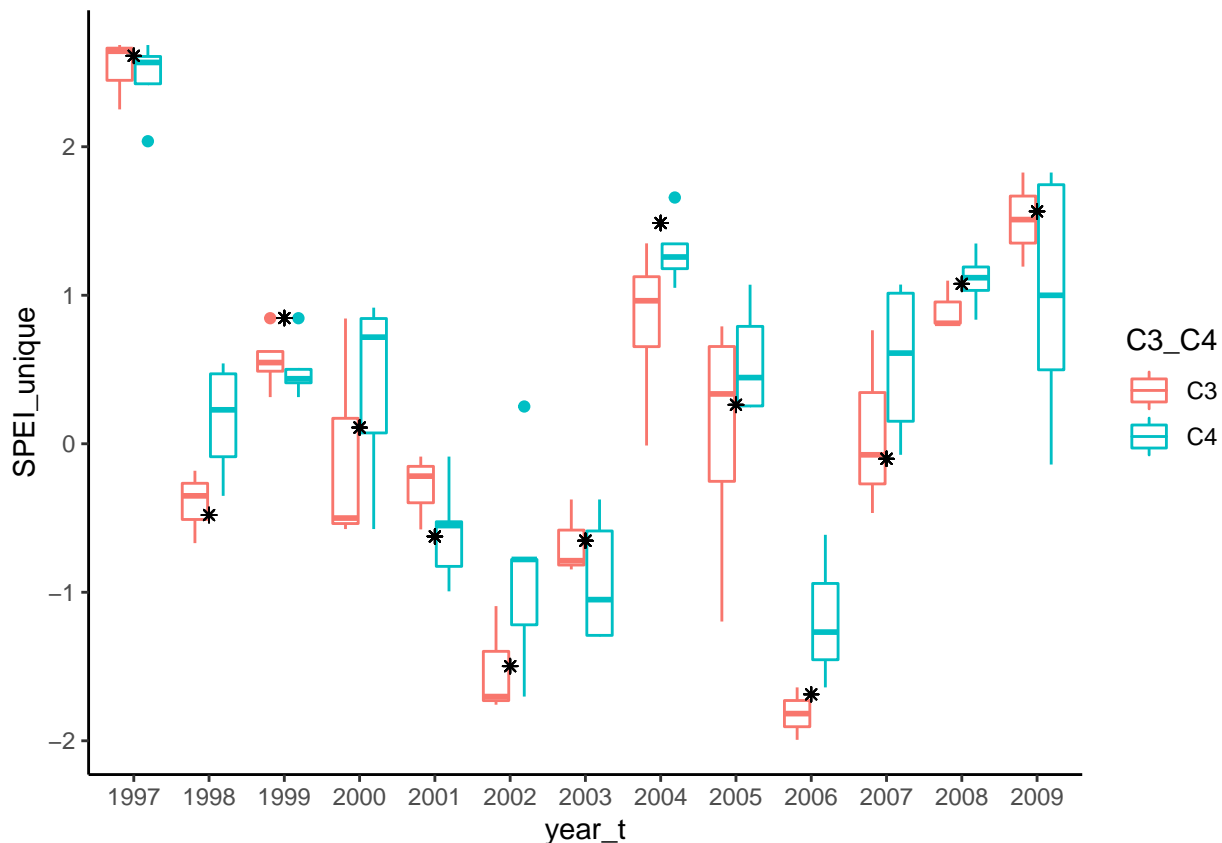
Below are the *unique* SPEI values for each species

The black line shows SPEI when calculated for a uniform interval each year



Below are the *unique* SPEI values for each species, color-coded by photosynthetic pathway (graminoids only)

The black asterisks indicate the value for SPEI when calculated for a uniform interval each year. These patterns are somewhat surprising, since in many years C4 species actually tend to have a more positive SPEI (wetter) than C3 species, which is opposite of what we would expect.



For species-level unique SPEI, year is a significant predictor but species is not.

```
## is the variation between years greater than the variation between species in one year?
testM <- lm(SPEI_unique ~ year_t + species, data = gramsSPEI_unique)
anova(testM)
```

```
## Analysis of Variance Table
##
## Response: SPEI_unique
##           Df Sum Sq Mean Sq F value Pr(>F)
## year_t    12  96.456   8.0380  32.2101 <2e-16 ***
## species    10   2.638   0.2638   1.0572  0.4049
## Residuals  80  19.964   0.2495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#year is a more important predictor than species (is significant, while species isn't)

When photosynthetic pathway is considered as well, year is still the most significant predictor of SPEI. Photosynthetic pathway has a slightly significant effect, while species has no significant effect.

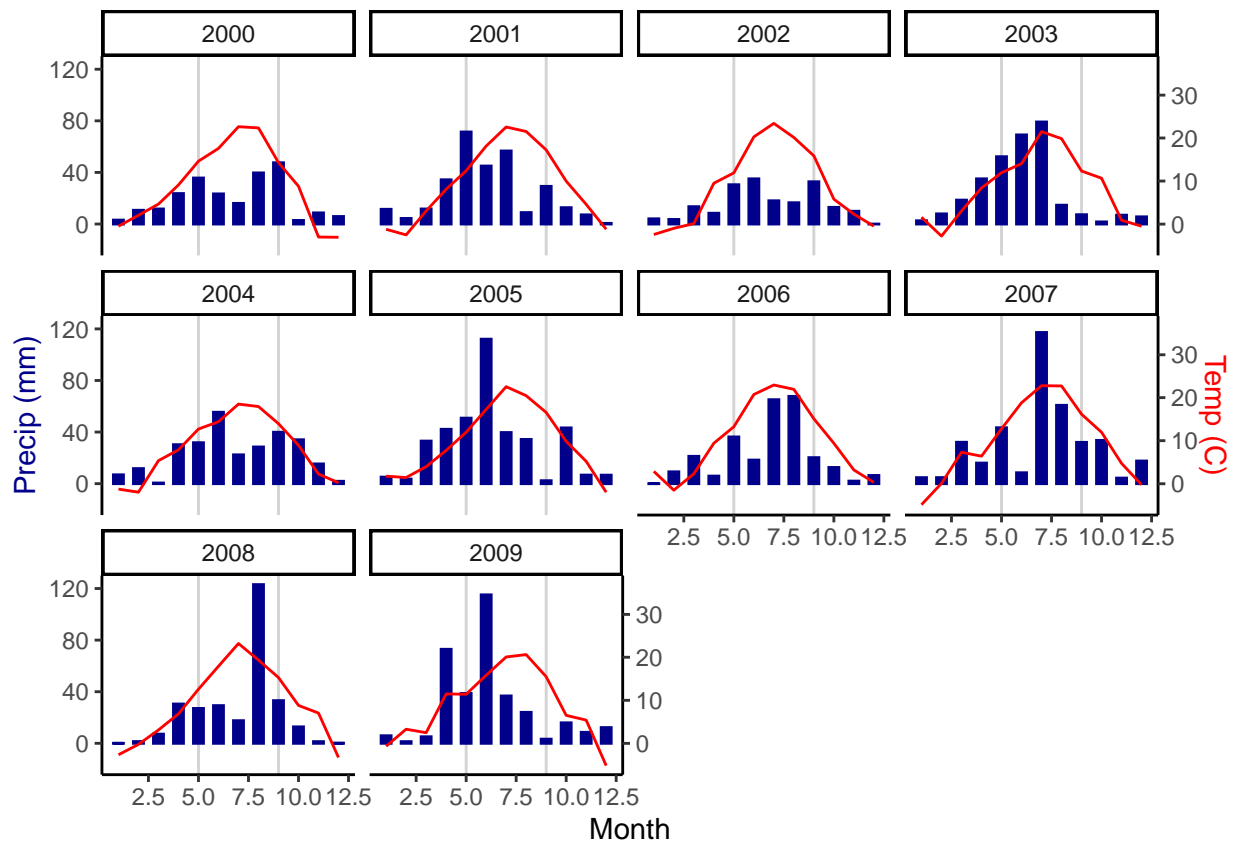
```
testM_photo <- lm(SPEI_unique ~ year_t + C3_C4 + species, data = gramsSPEI_unique)
anova(testM_photo)
```

```
## Analysis of Variance Table
```

```
##
## Response: SPEI_unique
##           Df Sum Sq Mean Sq F value    Pr(>F)
## year_t    12 96.456   8.0380 32.2101 < 2e-16 ***
## C3_C4       1  1.197   1.1972   4.7973 0.03142 *
## species     9  1.441   0.1601   0.6417 0.75820
## Residuals  80 19.964   0.2495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

These results increase my confidence in using species-level SPEI, but I'd like to know what you all think.

These are the yearly precipitation and temperature patterns accross all years included in the demographic dataset



I plotted these patterns to check if it makes sense that sometimes SPEI for C4 species is actually higher (wetter) than for C3 species. It does look like in some years, there is more precip later in the summer. So maybe that pattern of SPEI does make sense.