```
### Ecological indices calculated with plant population densities

dens_ind_1720 <- read.csv(here("2-Data/Clean/pldens_indices_1720_clean.csv"))

#convert all id columns to factor
dens_ind_1720 %<>%
  mutate_at(c("Block","Crop_ID", "Year","Corn_weed_management"),
            funs(factor(.)))

dens_ind_1720$Crop_ID <- factor(dens_ind_1720$Crop_ID,
                                levels = c("C2", "S2",
                                           "C3", "S3", "O3",
                                           "C4", "S4", "O4", "A4"))

dens_ind_1720$Crop <- factor(dens_ind_1720$Crop,
                             levels = c("corn", "soybean", "oat", "alfalfa"))
```

```
dens_diversity.lmer1 <- lmer(log(Diversity+1) ~ Block +
                               Crop_ID * Corn_weed_management +
                               (1|Year) +
                               (1|Year:Block) +
                               (1|Year:Crop_ID) +
                               (1|Year:Corn_weed_management) +
                               (1|Year:Crop_ID:Corn_weed_management) +
                               (1|Block:Year:Crop_ID) ,
                   data = dens_ind_1720,
                   control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                     tol = 1e-4)))
summary(dens_diversity.lmer1)$sigma #0.28
```

Seedbank ecological indices

```
## [1] 0.2670657
```

```
min(dens_ind_1720$Evenness[dens_ind_1720$Evenness > 0])
```

```
## [1] 0.01615646
```

```
dens_even.lmer4 <- lmer(log(Evenness+0.016156463) ~  Block +
                          Crop_ID * Corn_weed_management +
                          (1|Year) +
                          (1|Year:Block) +
                          (1|Year:Crop_ID) +
                          (1|Year:Corn_weed_management) +
                          (1|Year:Crop_ID:Corn_weed_management) +
                          (1|Block:Year:Crop_ID) ,
                  data = dens_ind_1720,
                  control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                    tol = 1e-4)))
summary(dens_even.lmer4)$sigma # 0.68 # second best sigma, better than arcsin sqrt transform and more s
```

```
## [1] 0.6831919
```

```
dens_rich.lmer2 <- lmer(log(Richness+1) ~ Block +
                          Crop_ID * Corn_weed_management +
                          (1|Year) +
                          (1|Year:Block) +
                          (1|Year:Crop_ID) +
                          (1|Year:Corn_weed_management) +
                          (1|Year:Crop_ID:Corn_weed_management) +
                          (1|Block:Year:Crop_ID) ,
                  data = dens_ind_1720,
                  control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                    tol = 1e-4)))
summary(dens_rich.lmer2)$sigma  #0.288
```

```
## [1] 0.2881294
```

```
### Ecological indices calculated with plant population biomass densities
biom_ind_1720 <- read_csv("../2-Data/Clean/biom_indices_1720_clean.csv")

#convert all id columns to factor
biom_ind_1720  %<>%  mutate_at(c("Block","Crop_ID", "Year","Corn_weed_management"),funs(factor(.)))

biom_ind_1720$Crop_ID <- factor(biom_ind_1720$Crop_ID,
                                levels = c("C2", "S2",
                                           "C3", "S3", "O3",
                                           "C4", "S4", "O4", "A4"))
```

```
# zero variance: https://rpubs.com/bbolker/6226
# Block is fixed
min(biom_ind_1720$Diversity[biom_ind_1720$Diversity > 0])
```

Biomass ecological indices

```
## [1] 1
```

```
biom_diversity.lmer1 <- lmer(log(Diversity + 1 ) ~  Block +
                               Crop_ID * Corn_weed_management +
                               (1|Year) +
                               (1|Block:Year) +
                               (1|Year:Crop_ID) +
                               (1|Year:Corn_weed_management) +
                               (1|Year:Crop_ID:Corn_weed_management) +
                               (1|Block:Year:Crop_ID)  ,
                  data = biom_ind_1720,
                  control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                    tol = 1e-4)))
summary(biom_diversity.lmer1)$sigma #0.25
```

```
## [1] 0.2571618
```

```r
min(biom_ind_1720$Evenness[biom_ind_1720$Evenness > 0])
```

```
## [1] 0.01510172
```

```r
biom_even.lmer4 <- lmer(log(Evenness + 0.015101721 ) ~ Block +
                          Crop_ID * Corn_weed_management +
                          (1|Year) +
                          (1|Year:Block) +
                          (1|Year:Crop_ID) +
                          (1|Year:Corn_weed_management) +
                          (1|Year:Crop_ID:Corn_weed_management) +
                          (1|Block:Year:Crop_ID) ,
                    data = biom_ind_1720,
                    control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                      tol = 1e-4)))
summary(biom_even.lmer4)$sigma # 0.72 # second best sigma, points more spread-out
```

```
## [1] 0.7268537
```

```r
# Always log-transform positive data: https://statmodeling.stat.columbia.edu/2019/08/21/you-should-usua

min( biom_ind_1720$Richness[ biom_ind_1720$Richness > 0])
```

```
## [1] 1
```

```r
biom_rich.lmer2 <- lmer(log(Richness + 1) ~  Block +
                          Crop_ID * Corn_weed_management +
                          (1|Year) +
                          (1|Year:Block) +
                          (1|Year:Crop_ID) +
                          (1|Year:Corn_weed_management) +
                          (1|Year:Crop_ID:Corn_weed_management) +
                          (1|Block:Year:Crop_ID) ,
                    data = biom_ind_1720,
                    control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                      tol = 1e-4)))
summary(biom_rich.lmer2)$sigma  #0.2935
```

```
## [1] 0.2935653
```

```r
#reduced model
biom_rich.lmer2_r <- lmer(log(Richness + 1) ~  Block +
                            Crop_ID +
                            Corn_weed_management +
                            (1|Year) +
                            (1|Year:Block) +
                            (1|Year:Crop_ID) +
                            (1|Year:Corn_weed_management) +
                            (1|Block:Year:Crop_ID) ,
                    data = biom_ind_1720,
```

Table 1: ANOVAs of crop identity, corn weed management, and their interactive effects on weed community ecological indices

			Stand density		Aboveground mass	
Source of variation	df1	df2	F	p	F	p
(A) - Community diversity						
Crop ID	8	24	1.25	0.3116	5.22	0.0007
Corn weed management	1	3	0.21	0.6804	0.47	0.5439
Crop ID x Corn weed management	8	24	0.54	0.8182	1.35	0.2659
(B) - Community evenness						
Crop ID	8	24	3.66	0.0064	5.87	0.0003
Corn weed management	1	3	0.24	0.6589	0.01	0.9414
Crop ID x Corn weed management	8	24	0.74	0.6547	0.47	0.8632
(C) - Community richness						
Crop ID	8	24	3.23	0.0123	3.19	0.0130
Corn weed management	1	3	1.32	0.3330	1.59	0.2959
Crop ID x Corn weed management	8	24	0.71	0.6803	0.86	0.5635

Note: Corn weed management: low herbicide or conventional. Crop ID: crop species and the cropping system in which it occurred: C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in the 4-year rotation, S2 - soybean in the 2-year rotation, S3 - soybean in the 3-year rotation, S4 - soybean in the 4-year rotation, O3 - oat in the 3-year rotation, and O4 - oat in the 4-year rotation, and A4 - alfalfa in the 4-year rotation.

```
                  control=lmerControl(check.conv.singular = .makeCC(action = "ignore",
                                                                    tol = 1e-4)))
summary(biom_rich.lmer2_r)$sigma  #0.3143426
```

```
## [1] 0.3143426
```

ANOVAs of ecological indices

How did rotation system, crop species, and corn weed management affect community ecological indices? Crop identity (i.e., rotation system x crop phase combination) affected weed community stand density evenness (p = 0.0064) and richness (p = 0.0123, Table 1C) and aboveground mass diversity (p = 0.0007, Table 1A), evenness (p = 0.0003, Table 1B), and richness (p =0.013). For all the differences in ecological indices, crop types were more influential than rotations, with larger differences found between crop types than between rotations (Figure 1, Tables **??** and 3. .

Arrow plots for ecological indices *In general, the hypothesis that "weed communities in the more diverse cropping systems are more diverse" was supported.*

Averaged over crop phases within each rotation system (Table **??**A), the weed community stand diversity index for the 3-year and 4-year rotation systems was comparable with that in the 2-year rotation (p = 0.0535 and p = 0.1575, respectively). For the individual crops (Table **??**B), the weed stand density diversity index was comparable among rotations (p > 0.05). For different crop types (Table **??**C), the weed community stand density diversity index in the average for the cool-season crops (O3, O4, and A4) was 1.2-fold greater than that in the average for the warm-season crops (C2, S2, C3, S3, C4, and S4) (p = 0.0145), but similar between

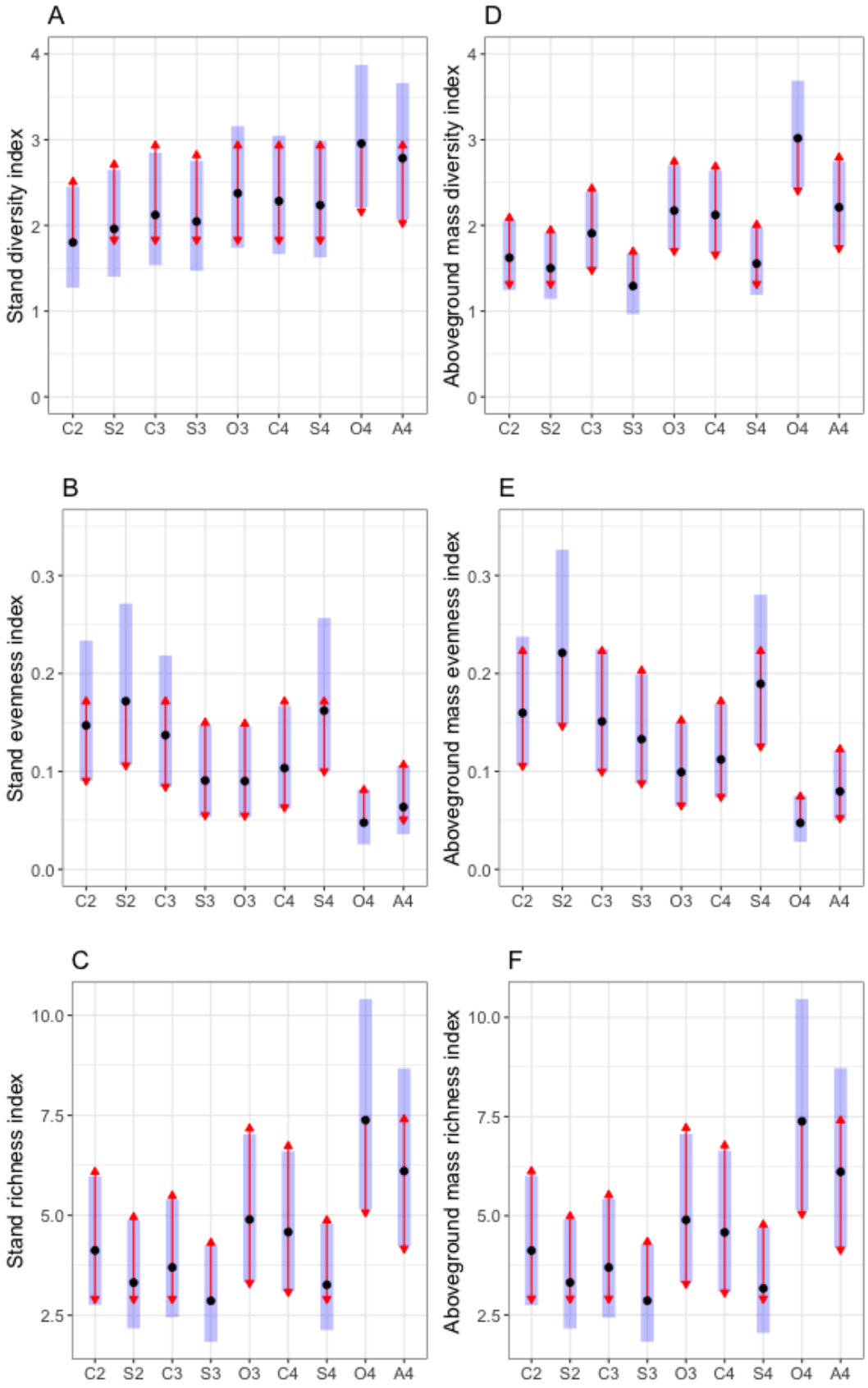

Figure 1: Weed community stand diversity (A), evenness (B), and richness (C) and community aboveground diversity (D), evenness (E), and richness (F). The abbreviations on the x-axis are crop identities, which are the combinations of the first letter in crop species names and the rotation in which it occurred (C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in the 4-year rotation, S2 - soybean in the 2-year rotation, S3 - soybean in the 3-year rotation, S4 - soybean in the 4-year rotation, O3 - oat in the

the warm-season and cool-season crops in the same rotations (p = 0.4666 and p = 0.0987, respectively). The weed stand density diversity index was similar between oat and alfalfa (p = 0.7762).

Averaged over crop phases within the same rotation (Table 3A), the weed community aboveground mass diversity index was different between the 2-year rotation and the average of the 3-year and 4-year rotations (p = 0.0148), and between the 3-year and 4-year rotations (p = 0.0209). Averaged over the corn and soybean phases within the same rotation (Table 3A), the weed community aboveground mass diversity index was similar between rotations (p = 0.4217 and p = 0.2426, respectively). For the individual crops (Table **??**B), the weed community aboveground mass diversity index was comparable between rotations, except for oat (p = 0.0351). For different crop types (Table **??**C), the weed community aboveground mass diversity index in the cool-season crops average was 1.3-fold greater than that in the warm-season crops averages, overall (p < 0.0001), and was 1.23-fold and 1.27-fold greater in the cool-season than that in the warm-season crops in the 3-year (p = 0.034) and 4-year rotation (p = 0.0037), respectively. The weed community aboveground mass diversity index was comparable between oat and alfalfa (p = 0.2583).

The hypothesis that "weed communities in the more diverse cropping systems are more even" was partially supported (Figure 1B and E). However, a lower community evenness index can occur because the presence of rarer species decreases the overall evenness index [@stirlingEmpiricalRelationshipsSpecies2001]. More details to support this concept are presented later (Figure 2C and D).

Averaged over crop phases within the same rotation (Table **??**A), the weed community stand density evenness index in the 2-year rotation was 1.6-fold greater than that in the average of the 3-year and 4-year rotations (p = 0.006), but comparable between the 3-year and 4-year rotations (p = 0.2802). Averaged over the corn and soybean phases within the same rotation (Table **??**A), the weed community stand density evenness index was comparable between rotations (p = 0.1539 and p = 0.5031, respectively). For the individual crops (Table **??**B), the weed community stand density evenness index was comparable between rotations (p > 0.05). For different crop types (Table **??**C), the weed community stand density evenness index in the cool-season crops average was half of that in the warm-season crops average (p = 0.0002) and half of that in the cool-season and warm-season crop in the 4-year rotation (p = 0.0012), but similar between the warm-season and cool-season crops in the 3-year rotation (p = 0.4418). The weed community stand density evenness index was comparable between oat and alfalfa (p = 0.8986).

Averaged over crop phases within the same rotation (Table 3A), the weed community aboveground mass evenness index in the 2-year rotation was 1.65-fold greater than that in the average of 3-year and 4-year rotations (p = 0.0012), but similar between the 3-year and 4-year rotations (p = 0.0802). Averaged over the corn and soybean phases within the same rotation (Table 3A), weed community aboveground mass evenness index was comparable between rotations (p = 0.1081 and p = 0.8682, respectively). For the individual crops (Table **??**B), the weed community aboveground mass evenness index was comparable between rotations (p > 0.05), except for oat (p = 0.0189). The weed community aboveground mass evenness index in the warm-season crops average was twice that of the cool-season crops average (p < 0.0001). The weed community aboveground mass evenness index in the warm-season crops was twice that of the cool-season crops in the 4-year rotation (p = 0.0002), but comparable between between the warm-season and cool-season crops in the 3-year rotation (p = 0.141), and between oat and alfalfa (p = 0.5911).

The hypothesis that "the weed communities in the more diverse cropping systems are more species-rich" was supported.

Averaged over crop phases within the same rotation (Table **??**A), the weed community stand density richness index was comparable in the 2-year rotation and in the average of the 3-year and 4-year rotations (p = 0.1819), but the stand density richness index in the 3-year was 0.77 that of the 4-year rotation (p = 0.0257). Averaged over the corn and soybean phases within the same rotation (Table **??**A), weed community aboveground mass richness index was comparable between the 2-year rotation and the 3-year and 4-year rotations average (p = 0.7996) and between the 3-year and 4-year rotations (p = 0.3469). For individual crops (Table **??**B), the weed community stand density richness index was comparable between rotations (p > 0.05). For different crop types (Table **??**C), the weed stand density richness index in the cool-season crops average was 1.33-fold greater that of the warm-season crops average (p = 0.0003). Within the 4-year rotation, the weed stand density richness index in the cool-season was 1.58-fold greater than that in the warm-season crops (p =

0.0034). The weed stand density richness was comparable between the warm-season and cool-season crops in the 3-year rotation (p = 0.0725) and between oat and alfalfa (p = 0.9499).

The same patterns of difference and similarity of weed community richness index calculated with aboveground mass was observed (Table 3).

```
## Coefficients for customized contrasts
C2 <- c(1,rep(0,8)); C3 <- c(0,0,1,rep(0,6)); C4 <- c(rep(0,5),1,rep(0,3))
S2 <- c(0, 1,rep(0,7)); S3 <- c(rep(0,3), 1,rep(0,5)); S4 <- c(rep(0,6),1,rep(0,2))
O3 <- c(rep(0,4), 1, rep(0,4)); O4 <- c(rep(0,7),1,0)
A4 <- c(rep(0,8), 1)


##### Did rotation affect density diversity, average over all crop phases within the same rotation?
## 2-year vs (3-year + 4-year)/2
dens_diversity_2yrvs34yr <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]" =
                                                           ((C2+S2)/2) - ((C3+S3+O3+C4+S4+O4+A4)/7))),
                                  export = TRUE)

## 3-year vs 4-year
dens_diversity_3yrvs4yr = print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                         method = list("[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]" =
                                                         ((C3+S3+O3)/3) - ((C4+S4+O4+A4)/4) )),
                                export = TRUE)
## 2-year vs 3-year
dens_diversity_2yrvs3yr <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                  infer = c(FALSE,TRUE),
                                                  type = "response"),
                                          method = list("[(C2+S2)/2] vs [(C3+S3+O3)/3]" =
                                                          ((C2+S2)/2) - ((C3+S3+O3)/3) )),
                                 export = TRUE)

## 2-year vs 4-year
dens_diversity_2yrvs4yr = print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                         method = list("[(C2+S2)/2] vs [(C4+S4+O4+A4)/4]" =
                                                         ((C2+S2)/2) - ((C4+S4+O4+A4)/4) )),
                                export = TRUE)


## Corn and soybean average: (C2+S2)/2 vs. (C3+S3+C4+S4)/4
dens_diversity_CS2yr_vs_CS34yr <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                         infer = c(FALSE,TRUE),
                                                         type = "response"),
                                                 method = list("[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]" =
                                                                 ((C2+S2)/2) - ((C3+S3+C4+S4)/4) )),
```

```
                                        export = TRUE)

## Corn and soybean average: (C3+S3)/2 vs. C4+S4)/2
dens_diversity_CS3yr_vs_CS4yr <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                        infer = c(FALSE,TRUE),
                                                        type = "response"),
                                                method = list("[(C3+S3)/2] vs [(C4+S4)/2]" =
                                                                ((C3+S3)/2) - ((C4+S4)/2) )),
                                       export = TRUE)


##### Did crop species affect density diversity, across rotations?

#### 3yr: summer vs. cool-season crops: (C3+S3)/2 vs. O3
dens_diversity_CS3_vs_O3 <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("O3 vs [(C3+S3)/2]" = O3 - (C3+S3)/2)),
                                  export = TRUE)

#### 4yr: summer vs. cool-season crops: (C4+S4)/2 vs. (O4+A4)/2
dens_diversity_CS4_vs_OA4 <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                    infer = c(FALSE,TRUE),
                                                    type = "response"),
                                            method = list("[(O4+A4)/2] vs [(C4+S4)/2]" =
                                                            ((A4+O4)/2) - ((C4+S4)/2))),
                                   export = TRUE)

#### all summer vs. all cool-season crops:
dens_diversity_summer_vs_cool <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                        infer = c(FALSE,TRUE),
                                                        type = "response"),
                                                method = list("[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6
                                                                ((O3+A4+O4)/3) - ((C2+S2+C3+S3+C4+S4)/
                                       export = TRUE)

#### Did rotation affect diversity in density composition for the communities grew in the same crop spe
# Corn: C2 vs (C3+C4)/2
dens_diversity_C2vs3_4 <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                         method = list("C2 vs [(C3+C4)/2]" = C2 - ((C3+C4)/2) )),
                                export = TRUE)
# Corn: C3 vs C4
dens_diversity_C3vs4 <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response",
                                               at = list(Crop_ID = c( "C3", "C4"))), "pairwise"),
                              export = TRUE) #not included in the final table


# Soybean: S2 vs (S3+S4)/2
dens_diversity_S2vs3_4 <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
```

```
                                                infer = c(FALSE,TRUE),
                                                type = "response"),
                                          method = list("S2 vs [(S3+S4)/2]" = S2 - ((S3+S4)/2) )),
                                export = TRUE)

# Soybean: S3 vs S4
dens_diversity_S3vs4 <-print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response",
                                              at = list(Crop_ID = c( "S3", "S4"))), "pairwise"),
                             export = TRUE) #not included in the final table


# Oat: O3 vs O4
dens_diversity_oat <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                             infer = c(FALSE,TRUE),
                                             type = "response",
                                             at = list(Crop_ID = c("O3", "O4"))), "pairwise"),
                            export = TRUE)

# oat vs alfalfa
dens_diversity_OA <- print(contrast(emmeans(dens_diversity.lmer1, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(O3+O4)/2] vs A4" = ( ((O3+O4)/2)) - A4)),
                           export = TRUE)


###### Biomass #######
##### Did rotation affect density diversity, average over all crop phases within the same rotation?

#2-year vs (3-year + 4-year)/2
biom_diversity_2yrvs34yr <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]" =
                                                           (C2+S2)/2 - (C3+S3+O3+C4+S4+O4+A4)/7 )),
                                  export = TRUE)

#3-year vs 4-year average
biom_diversity_3yrvs4yr = print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                         method = list("[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]" =
                                                         ((C3+S3+O3)/3) - ((C4+S4+O4+A4)/4) )),
                                export = TRUE)

#2-year vs 3-year average
biom_diversity_2yrvs3yr <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                  infer = c(FALSE,TRUE),
                                                  type = "response"),
                                          method = list("[(C2+S2)/2] vs [(C3+S3+O3)/3]" =
                                                          ((C2+S2)/2) - ((C3+S3+O3)/3) )),
```

```
                                    export = TRUE)

#2-year vs 4-year average
biom_diversity_2yrvs4yr = print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                          method = list("[(C2+S2)/2] vs [(C4+S4+O4+A4)/4]" =
                                                          ((C2+S2)/2) - ((C4+S4+O4+A4)/4) )),
                                  export = TRUE)

#Corn and soybean average: (C2+S2)/2 vs. (C3+S3+C4+S4)/4
biom_diversity_CS2yr_vs_CS34yr <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                         infer = c(FALSE,TRUE),
                                                         type = "response"),
                                                 method = list("[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]" =
                                                                 ((C2+S2)/2) - ((C3+S3+C4+S4))/4)),
                                          export = TRUE)

## Corn and soybean average: (C3+S3)/2 vs. C4+S4)/2
biom_diversity_CS3yr_vs_CS4yr <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                        infer = c(FALSE,TRUE),
                                                        type = "response"),
                                                method = list("[(C3+S3)/2] vs [(C4+S4)/2]" =
                                                                ((C3+S3)/2) - ((C4+S4)/2))),
                                        export = TRUE)


####### Does crop species affect biomass diversity, different crops, averaged across rotations
biom_diversity_CS3_vs_O3 <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("O3 vs [(C3+S3)/2]" = O3 - (C3+S3)/2)),
                                  export = TRUE)

#### 4yr: summer vs. cool-season crops
## (C4+S4)/2 vs. (O4+A4)/2
biom_diversity_CS4_vs_OA4 <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                    infer = c(FALSE,TRUE),
                                                    type = "response"),
                                            method = list("[(O4+A4)/2] vs [(C4+S4)/2]" =
                                                            ((A4+O4)/2) - ((C4+S4)/2))),
                                   export = TRUE)

#### all summer vs. all cool-season crops
biom_diversity_summer_vs_cool <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                        infer = c(FALSE,TRUE),
                                                        type = "response"),
                                                method = list("[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6
                                                                ((O3+A4+O4)/3) - ((C2+S2+C3+S3+C4+S4)/
                                        export = TRUE)


# Corn: C2 vs (C3+C4)/2
```

```
biom_diversity_C2vs3_4 <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                          method = list("C2 vs [(C3+C4)/2]" = C2 - ((C3+C4)/2) )),
                                export = TRUE)
# Corn: C3 vs C4
biom_diversity_C3vs4 <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response",
                                               at = list(Crop_ID = c( "C3", "C4"))), "pairwise"),
                              export = TRUE) #not included in the final table

# S2 vs (S3+S4)/2 and S3 vs S4
biom_diversity_S2vs3_4 <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                                 infer = c(FALSE,TRUE),
                                                 type = "response"),
                                          method = list("S2 vs [(S3+S4)/2]" = S2 - ((S3+S4)/2) )),
                                export = TRUE)

biom_diversity_S3vs4 <-print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response",
                                              at = list(Crop_ID = c( "S3", "S4"))), "pairwise"),
                             export = TRUE) #not included in the final table


# O3 vs O4
biom_diversity_oat <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                             infer = c(FALSE,TRUE),
                                             type = "response",
                                             at = list(Crop_ID = c("O3", "O4"))), "pairwise"),
                            export = TRUE)

# oat vs alfalfa
biom_diversity_OA <- print(contrast(emmeans(biom_diversity.lmer1, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                     method = list("[(O3+O4)/2] vs A4" = ( ((O3+O4)/2)) - A4)),
                           export = TRUE)
```

Contrasts for ecological indices: diversity

```
#### Did rotation affect community stand density evenness?
## Rotation effect, overall:
dens_even_2yrvs34yr <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
                                       method = list("[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]" =
                                                       (C2+S2)/2 - (C3+S3+O3+C4+S4+O4+A4)/7 )),
                             export = TRUE)
```

```
dens_even_3yrvs4yr = print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]" =
                                                    ((C3+S3+O3)/3) - ((C4+S4+O4+A4)/4) )),
                           export = TRUE)


dens_even_2yrvs4yr <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                             infer = c(FALSE,TRUE),
                                             type = "response"),
                                     method = list("[(C2+S2)/2] vs [(C4+S4+O4+A4)/4]" =
                                                     (C2+S2)/2 - (C4+S4+O4+A4)/4 )),
                            export = TRUE)


dens_even_2yrvs3yr = print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C2+S2)/2] vs [(C3+S3+O3)/3]" =
                                                    (C2+S2)/2 - ((C3+S3+O3)/3) )),
                           export = TRUE)

## (C2+S2)/2 vs. (C3+S3+C4+S4)/4
dens_even_CS2yr_vs_CS34yr <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                                    infer = c(FALSE,TRUE),
                                                    type = "response"),
                                            method = list("[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]" =
                                                            ((C2+S2)/2) - ((C3+S3+C4+S4)/4))),
                                   export = TRUE)

## (C3+S3)/2 vs. C4+S4)/2
dens_even_CS3yr_vs_CS4yr <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(C3+S3)/2] vs [(C4+S4)/2]" =
                                                           ((C3+S3)/2) - ((C4+S4)/2))),
                                  export = TRUE)

#### Does crop phenology affect density evenness
dens_evenn_CS3_vs_O3 <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response"),
                                       method = list("O3 vs [(C3+S3)/2]" = O3 - (C3+S3)/2)),
                              export = TRUE)

#### 4yr: summer vs. cool
## (C4+S4)/2 vs. (O4+A4)/2
dens_even_CS4_vs_OA4 <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response"),
                                       method = list("[(O4+A4)/2] vs [(C4+S4)/2]" =
```

```
                                                    ((A4+O4)/2) - ((C4+S4)/2))),
                              export = TRUE)

#### all summer vs. all cool
dens_even_summer_vs_cool <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]" =
                                                         ( ((O3+A4+O4)/3)) - ((C2+S2+C3+S3+C4+S4)/6))),
                                  export = TRUE)

#### Does rotation affect evenness in density composition for the communities grew in the same crop spe
# C2 vs (C3+C4)/2 and C3 vs C4
dens_even_C2vs3_4 <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("C2 vs [(C3+C4)/2]" = C2 - ((C3+C4)/2))),
                           export = TRUE)

dens_even_C3vs4 <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                          infer = c(FALSE,TRUE),
                                          type = "response",
                                          at = list(Crop_ID = c( "C3", "C4"))),"pairwise"),
                         export = TRUE) #not included in the final table

# S2 vs (S3+S4)/2 and S3 vs S4
dens_even_S2vs3_4 <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("S2 vs [(S3+S4)/2]" = S2 - ((S3+S4)/2) )),
                           export = TRUE)

dens_even_S3vs4 <-print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                         infer = c(FALSE,TRUE),
                                         type = "response",
                                         at = list(Crop_ID = c( "S3", "S4"))),"pairwise"),
                        export = TRUE) #not included in the final table

# O3 vs O4
dens_even_oat <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                        infer = c(FALSE,TRUE),
                                        type = "response",
                                        at = list(Crop_ID = c("O3", "O4"))),"pairwise"), export = TRUE)

# oat vs alfalfa
dens_even_OA <- print(contrast(emmeans(dens_even.lmer4, ~ Crop_ID,
                                       infer = c(FALSE,TRUE),
                                       type = "response"),
                               method = list("[(O3+O4)/2] vs A4" = ( ((O3+O4)/2)) - A4)), export = TRUE)

###### Biomass #######
#### Does rotation affect biomass evenness
```

```
biom_even_2yrvs34yr <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
                                      method = list("[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]" =
                                                      (C2+S2)/2 - (C3+S3+O3+C4+S4+O4+A4)/7 )),
                             export = TRUE)


biom_even_3yrvs4yr = print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]" =
                                                    ((C3+S3+O3)/3) - ((C4+S4+O4+A4)/4) )),
                           export = TRUE)


biom_even_2yrvs3yr <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                             infer = c(FALSE,TRUE),
                                             type = "response"),
                                     method = list("[(C2+S2)/2] vs [(C3+S3+O3)/3]" =
                                                     ((C2+S2)/2) - ((C3+S3+O3)/3) )),
                            export = TRUE)


biom_even_2yrvs4yr = print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C2+S2)/2] vs [(C4+S4+O4+A4)/4]" =
                                                    ((C2+S2)/2) - ((C4+S4+O4+A4)/4) )),
                           export = TRUE)


## (C2+S2)/2 vs. (C3+S3+C4+S4)/4
biom_even_CS2yr_vs_CS34yr <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                                    infer = c(FALSE,TRUE),
                                                    type = "response"),
                                            method = list("[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]" =
                                                            ((C2+S2)/2) - ((C3+S3+C4+S4)/4))),
                                   export = TRUE)

## (C3+S3)/2 vs. C4+S4)/2
biom_even_CS3yr_vs_CS4yr <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(C3+S3)/2] vs [(C4+S4)/2]" =
                                                           ((C3+S3)/2) - ((C4+S4)/2))),
                                  export = TRUE)

#### Does crop phenology affect biomass evenness?

biom_even_CS3_vs_O3 <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
```

```
                                        method = list("O3 vs [(C3+S3)/2]" = O3 - ((C3+S3)/2))),
                                export = TRUE)

#### 4yr: summer vs. cool
## (C4+S4)/2 vs. (O4+A4)/2
biom_even_CS4_vs_OA4 <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response"),
                                       method = list("[(O4+A4)/2] vs [(C4+S4)/2]" =
                                                       ((A4+O4)/2) - ((C4+S4)/2))),
                                export = TRUE)

#### all summer vs. all cool
biom_even_summer_vs_cool <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]" =
                                                           ((O3+A4+O4)/3)  - ((C2+S2+C3+S3+C4+S4)/6))),
                                    export = TRUE)

# C2 vs (C3+C4)/2 and C3 vs C4
biom_even_C2vs3_4 <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("C2 vs [(C3+C4)/2]" = C2 - ((C3+C4)/2) )),
                           export = TRUE)

biom_even_C3vs4 <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                          infer = c(FALSE,TRUE),
                                          type = "response",
                                          at = list(Crop_ID = c( "C3", "C4"))), "pairwise"),
                         export = TRUE)

# S2 vs (S3+S4)/2 and S3 vs S4
biom_even_S2vs3_4 <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("S2 vs [(S3+S4)/2]" = S2 - ((S3+S4)/2))),
                           export = TRUE)

biom_even_S3vs4 <-print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                         infer = c(FALSE,TRUE),
                                         type = "response",
                                         at = list(Crop_ID = c( "S3", "S4"))),  "pairwise"),
                        export = TRUE)

# O3 vs O4
biom_even_oat <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                        infer = c(FALSE,TRUE),
                                        type = "response",
                                        at = list(Crop_ID = c("O3", "O4"))),"pairwise"),
                       export = TRUE)
```

```
# oat vs alfalfa
biom_even_OA <- print(contrast(emmeans(biom_even.lmer4, ~ Crop_ID,
                                       infer = c(FALSE,TRUE),
                                       type = "response"),
                               method = list("[(O3+O4)/2] vs A4" = ( ((O3+O4)/2)) - A4)),
                      export = TRUE)
```

Contrasts for ecological indices: evenness

```
#### Did rotation affect density richness?

dens_rich_2yrvs34yr <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
                                      method = list("[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]" =
                                                      ((C2+S2)/2) - ((C3+S3+O3+C4+S4+O4+A4)/7) )),
                             export = TRUE)


dens_rich_3yrvs4yr <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID, infer = c(FALSE,TRUE),
                                             type = "response"),
                                     method = list("[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]" =
                                                     ((C3+S3+O3)/3) - ((C4+S4+O4+A4)/4) )),
                            export = TRUE)

dens_rich_2yrvs3yr <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                             infer = c(FALSE,TRUE),
                                             type = "response"),
                                     method = list("[(C2+S2)/2] vs [(C3+S3+O3)/3]" =
                                                     ((C2+S2)/2) - ((C3+S3+O3)/3) )),
                            export = TRUE)


dens_rich_2yrvs4yr = print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C2+S2)/2] vs [(C4+S4+O4+A4)/4]" =
                                                    ((C2+S2)/2) - ((C4+S4+O4+A4)/4) )),
                           export = TRUE)

## (C2+S2)/2 vs. (C3+S3+C4+S4)/4
dens_rich_CS2yr_vs_CS34yr <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                                    infer = c(FALSE,TRUE),
                                                    type = "response"),
                                            method = list("[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]" =
                                                            ((C2+S2)/2) - ((C3+S3+C4+S4)/4))),
                                   export = TRUE)

## (C3+S3)/2 vs. C4+S4)/2
dens_rich_CS3yr_vs_CS4yr <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
```

```
                                                  infer = c(FALSE,TRUE),
                                                  type = "response"),
                                           method = list("[(C3+S3)/2] vs [(C4+S4)/2]" =
                                                           ((C3+S3)/2) - ((C4+S4)/2))),
                                  export = TRUE)

#### Does crop phenology affect density richness

## (C3+S3)/2 vs. O3
dens_rich_CS3_vs_O3 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
                                       method = list("O3 vs [(C3+S3)/2]" = O3 - (C3+S3)/2)),
                             export = TRUE)

#### 4yr: summer vs. cool
## (C4+S4)/2 vs. (O4+A4)/2
dens_rich_CS4_vs_OA4 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response"),
                                        method = list("[(O4+A4)/2] vs [(C4+S4)/2]" =
                                                        ((A4+O4)/2) - ((C4+S4)/2))),
                              export = TRUE)

#### all summer vs. all cool
dens_rich_summer_vs_cool <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]" =
                                                           ( ((O3+A4+O4)/3)) - ((C2+S2+C3+S3+C4+S4)/6) )
                                  export = TRUE)


#### Does rotation affect richness in density composition for the communities grew in the same crop spe
# C2 vs (C3+C4)/2 and C3 vs C4
dens_rich_C2vs3_4 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("C2 vs [(C3+C4)/2]" = C2 - ((C3+C4)/2))),
                           export = TRUE)


dens_rich_C3vs4 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                          infer = c(FALSE,TRUE),
                                          type = "response",
                                          at = list(Crop_ID = c( "C3", "C4"))),"pairwise"), export = TRU


# S2 vs (S3+S4)/2 and S3 vs S4
dens_rich_S2vs3_4 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("S2 vs [(S3+S4)/2]" = S2 - ((S3+S4)/2) )),
```

```
                            export = TRUE)

dens_rich_S3vs4 <-print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                         infer = c(FALSE,TRUE),
                                         type = "response",
                                         at = list(Crop_ID = c( "S3", "S4"))), "pairwise"),
                        export = TRUE) #not included in the final table

# O3 vs O4
dens_rich_oat <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                        infer = c(FALSE,TRUE),
                                        type = "response",
                                        at = list(Crop_ID = c("O3", "O4"))),"pairwise"), export = TRUE)

#### Does species affect richness in density composition for the communities grew across crop phases?
dens_rich_2y <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                       infer = c(FALSE,TRUE),
                                       type = "response",
                                       at = list(Crop_ID = c("C2", "S2"))),"pairwise"), export = TRUE)

dens_rich_O3vsCS3 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("O3 vs [(C3+S3)/2]" = O3 - ((C3+S3)/2))), export = TRU

dens_rich_C3vsS3 <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID, infer = c(FALSE,TRUE),
                                           type = "response",
                                           at = list(Crop_ID = c("C3", "S3"))), "pairwise"),
                          export = TRUE)

dens_rich_4y <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                       infer = c(FALSE,TRUE),
                                       type = "response",
                                       at = list(Crop_ID = c("C4", "S4", "O4", "A4"))),
                               "pairwise"), export = TRUE)

# oat vs alfalfal
dens_rich_OA <- print(contrast(emmeans(dens_rich.lmer2, ~ Crop_ID,
                                       infer = c(FALSE,TRUE),
                                       type = "response"),
                               method = list("[(O3+O4)/2] vs A4" = ( ((O3+O4)/2)) - A4)),
                      export = TRUE)

###### Biomass #######

#### Does rotation affect biomass diversity
biom_rich_2yrvs34yr <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
                                      method = list("[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]" =
                                                    (C2+S2)/2 - (C3+S3+O3+C4+S4+O4+A4)/7 )),
                             export = TRUE)
```

```
biom_rich_3yrvs4yr = print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]" =
                                                    ((C3+S3+O3)/3) - ((C4+S4+O4+A4)/4) )),
                           export = TRUE)

biom_rich_2yrvs3yr <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                             infer = c(FALSE,TRUE),
                                             type = "response"),
                                     method = list("[(C2+S2)/2] vs [(C3+S3+O3)/3]" =
                                                     (C2+S2)/2 - (C3+S3+O3)/3 )),
                            export = TRUE)


biom_rich_2yrvs4yr = print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("[(C2+S2)/2] vs [(C4+S4+O4+A4)/4]" =
                                                    ((C2+S2)/2) - ((C4+S4+O4+A4)/4) )),
                           export = TRUE)

## (C2+S2)/2 vs. (C3+S3+C4+S4)/4
biom_rich_CS2yr_vs_CS34yr <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                                    infer = c(FALSE,TRUE),
                                                    type = "response"),
                                            method = list("[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]" =
                                                            ((C2+S2)/2) - ((C3+S3+C4+S4)/4))),
                                   export = TRUE)

## (C3+S3)/2 vs. C4+S4)/2
biom_rich_CS3yr_vs_CS4yr <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                           method = list("[(C3+S3)/2] vs [(C4+S4)/2]" =
                                                           ((C3+S3)/2) - ((C4+S4)/2))),
                                  export = TRUE)

##### Does crop phenology affect biomqss richness
## (C3+S3)/2 vs. O3
biom_rich_CS3_vs_O3 <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                              infer = c(FALSE,TRUE),
                                              type = "response"),
                                      method = list("O3 vs [(C3+S3)/2]" = O3 - ((C3+S3)/2))),
                             export = TRUE)

#### 4yr: summer vs. cool
## (C4+S4)/2 vs. (O4+A4)/2
biom_rich_CS4_vs_OA4 <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                               infer = c(FALSE,TRUE),
                                               type = "response"),
                                       method = list("[(O4+A4)/2] vs [(C4+S4)/2]" =
                                                       ((A4+O4)/2) - ((C4+S4)/2))),
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```
                                export = TRUE)

#### all summer vs. all cool
biom_rich_summer_vs_cool <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                                   infer = c(FALSE,TRUE),
                                                   type = "response"),
                                          method = list("[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]" =
                                                          ( ((O3+A4+O4)/3)) - ((C2+S2+C3+S3+C4+S4)/6))),
                                  export = TRUE)

# C2 vs (C3+C4)/2 and C3 vs C4
biom_rich_C2vs3_4 <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("C2 vs [(C3+C4)/2]" = C2 - ((C3+C4)/2) )),
                           export = TRUE)

biom_rich_C3vs4 <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                          infer = c(FALSE,TRUE),
                                          type = "response",
                                          at = list(Crop_ID = c("C3", "C4"))), "pairwise"),
                         export = TRUE) #not included in the final table

# S2 vs (S3+S4)/2 and S3 vs S4
biom_rich_S2vs3_4 <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                            infer = c(FALSE,TRUE),
                                            type = "response"),
                                    method = list("S2 vs [(S3+S4)/2]" = S2 - ((S3+S4)/2))),
                           export = TRUE)

biom_rich_S3vs4 <-print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                         infer = c(FALSE,TRUE),
                                         type = "response",
                                         at = list(Crop_ID = c("S3", "S4"))),  "pairwise"),
                        export = TRUE) #not included in the final table

# O3 vs O4
biom_rich_oat <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                        infer = c(FALSE,TRUE),
                                        type = "response",
                                        at = list(Crop_ID = c("O3", "O4"))), "pairwise"),
                       export = TRUE)

# oat vs alfalfal
biom_rich_OA <- print(contrast(emmeans(biom_rich.lmer2, ~ Crop_ID,
                                       infer = c(FALSE,TRUE),
                                       type = "response"),
                               method = list("[(O3+O4)/2] vs A4" = ( ((O3+O4)/2)) - A4)),
                      export = TRUE)
```

Contrasts for ecological indices: richness

```
##    contrast                                  estimate.x SE.x df.x t.ratio.x
```

```
## 1  [(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]      -0.16 0.08   24     -2.03
## 2        [(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]      -0.11 0.08   24     -1.46
## 3           [(C2+S2)/2] vs [(C3+S3+C4+S4)/4]      -0.10 0.09   24     -1.12
## 4                 [(C3+S3)/2] vs [(C4+S4)/2]      -0.06 0.10   24     -0.56
## 5                           C2 vs [(C3+C4)/2]      -0.13 0.12   24     -1.10
## 6                                    C3 - C4       -0.05 0.14   24     -0.36
## 7                           S2 vs [(S3+S4)/2]      -0.06 0.12   24     -0.48
## 8                                    S3 - S4       -0.06 0.14   24     -0.43
## 9                                    O3 - O4       -0.16 0.14   24     -1.12
## 10 [(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]       0.19 0.07   24      2.63
## 11                          O3 vs [(C3+S3)/2]       0.09 0.12   24      0.74
## 12                [(O4+A4)/2] vs [(C4+S4)/2]       0.17 0.10   24      1.72
## 13                          [(O3+O4)/2] vs A4      -0.04 0.12   24     -0.29
##    p.value.x estimate.y SE.y df.y t.ratio.y p.value.y estimate   SE df t.ratio
## 1       0.05       0.47 0.16   24      3.01      0.01    -0.16 0.11 24   -1.38
## 2       0.16       0.16 0.15   24      1.10      0.28    -0.26 0.11 24   -2.38
## 3       0.27       0.25 0.17   24      1.47      0.15     0.03 0.12 24    0.26
## 4       0.58      -0.13 0.19   24     -0.68      0.50    -0.14 0.14 24   -0.96
## 5       0.28       0.19 0.24   24      0.78      0.44     0.00 0.17 24    0.00
## 6       0.72       0.25 0.28   24      0.90      0.38    -0.17 0.20 24   -0.86
## 7       0.63       0.31 0.24   24      1.30      0.21     0.06 0.17 24    0.36
## 8       0.67      -0.51 0.28   24     -1.86      0.07    -0.10 0.20 24   -0.49
## 9       0.27       0.51 0.28   24      1.86      0.08    -0.35 0.20 24   -1.76
## 10      0.01      -0.60 0.14   24     -4.37      0.00     0.43 0.10 24    4.27
## 11      0.47      -0.19 0.24   24     -0.78      0.44     0.33 0.17 24    1.88
## 12      0.10      -0.72 0.19   24     -3.69      0.00     0.46 0.14 24    3.25
## 13      0.78       0.03 0.24   24      0.13      0.90    -0.01 0.17 24   -0.06
##    p.value
## 1     0.18
## 2     0.03
## 3     0.80
## 4     0.35
## 5     1.00
## 6     0.40
## 7     0.72
## 8     0.63
## 9     0.09
## 10    0.00
## 11    0.07
## 12    0.00
## 13    0.95
```

```
dens_index[,-c(3:5,8:10,12:14)] %>%
  `colnames<-` (c("Contrast", rep(c("ratio", "p"), 3))) %>% #null, SE, df, t.ratio removed
kable(booktabs = TRUE, longtable = FALSE, digits = 2, align = "lrrr",
    caption = "Weed stand density ecological indices contrast significance. The abbreviations on the co
   add_header_above(c(" " = 1, "Diversity index" = 2, "Evenness index" = 2, "Richness index" = 2))  %>%
  pack_rows("(A) - Rotation system effects", 1, 4) %>%
  pack_rows("(B) - Rotation system effects within individual crops", 5, 9) %>%
  pack_rows("(C) - Crop type effects", 10, 13)%>%
  footnote(general = "C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in
```

Table 2: Weed stand density ecological indices contrast significance. The abbreviations on the contrast column are crop identities, which are the combinations of the first letter in crop species names and the rotation in which it occurred.

	Diversity index		Evenness index		Richness index	
Contrast	ratio	p	ratio	p	ratio	p
(A) - Rotation system effects						
[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]	-0.16	0.05	0.47	0.01	-1.38	0.18
[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]	-0.11	0.16	0.16	0.28	-2.38	0.03
[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]	-0.10	0.27	0.25	0.15	0.26	0.80
[(C3+S3)/2] vs [(C4+S4)/2]	-0.06	0.58	-0.13	0.50	-0.96	0.35
(B) - Rotation system effects within individual crops						
C2 vs [(C3+C4)/2]	-0.13	0.28	0.19	0.44	0.00	1.00
C3 - C4	-0.05	0.72	0.25	0.38	-0.86	0.40
S2 vs [(S3+S4)/2]	-0.06	0.63	0.31	0.21	0.36	0.72
S3 - S4	-0.06	0.67	-0.51	0.07	-0.49	0.63
O3 - O4	-0.16	0.27	0.51	0.08	-1.76	0.09
(C) - Crop type effects						
[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]	0.19	0.01	-0.60	0.00	4.27	0.00
O3 vs [(C3+S3)/2]	0.09	0.47	-0.19	0.44	1.88	0.07
[(O4+A4)/2] vs [(C4+S4)/2]	0.17	0.10	-0.72	0.00	3.25	0.00
[(O3+O4)/2] vs A4	-0.04	0.78	0.03	0.90	-0.06	0.95

Note: C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in the 4-year rotation, S2 - soybean in the 2-year rotation, S3 - soybean in the 3-year rotation, S4 - soybean in the 4-year rotation, O3 - oat in the 3-year rotation, O4 - oat in the 4-year rotation, and A4 - alfalfa in the 4-year rotation

Table 3: Weed aboveground mass ecological indices contrast significance. The abbreviations on the contrast column are crop identities, which are the combinations of the first letter in crop species names and the rotation in which it occurred.

	Diversity index		Evenness index		Richness index	
Contrast	ratio	p	ratio	p	ratio	p
(A) - Rotation system effects						
[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]	-0.16	0.01	0.50	0.00	-1.33	0.20
[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]	-0.14	0.02	0.24	0.08	-2.29	0.03
[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]	-0.05	0.42	0.24	0.11	0.30	0.77
[(C3+S3)/2] vs [(C4+S4)/2]	-0.09	0.24	-0.03	0.87	-0.87	0.39
(B) - Rotation system effects within individual crops						
C2 vs [(C3+C4)/2]	-0.14	0.14	0.18	0.38	0.00	1.00
C3 - C4	-0.07	0.51	0.27	0.28	-0.85	0.40
S2 vs [(S3+S4)/2]	0.03	0.72	0.30	0.15	0.42	0.68
S3 - S4	-0.11	0.32	-0.32	0.19	-0.38	0.71
O3 - O4	-0.24	0.04	0.60	0.02	-1.73	0.10
(C) - Crop type effects						
[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]	0.26	NA	-0.68	NA	4.24	0.00
O3 vs [(C3+S3)/2]	0.21	0.03	-0.32	0.14	1.85	0.08
[(O4+A4)/2] vs [(C4+S4)/2]	0.24	0.00	-0.74	0.00	3.27	0.00
[(O3+O4)/2] vs A4	0.11	0.26	-0.11	0.59	-0.06	0.95

Note: C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in the 4-year rotation, S2 - soybean in the 2-year rotation, S3 - soybean in the 3-year rotation, S4 - soybean in the 4-year rotation, O3 - oat in the 3-year rotation, O4 - oat in the 4-year rotation, and A4 - alfalfa in the 4-year rotation

General description of the weed flora Overall, 34 weed species were identified during the four years of data collection (Table 4). Seven weed species, SETFA (*Setaria faberi*), AMATA (*Amaranthus tuberculatus*), CHEAL (*Chenopodium album*), DIGSA (*Digitaria sanguinalis*), ECHCG (*Echinochloa crus-galli*), SETLU (*Setaria glauca*), and TAROF (*Taraxacum officinale*) made up 94.4% of the total weed density and 94.0% of the total weed biomass (Figure 2C and D).

```
## [1] 0.001079214
```

```
## [1] 0.05396072
```

How did rotation, crop species, and corn weed management affect weed community density and growth? Crop identity affected weed community stand density ($p < 0.0001$) and weed community aboveground mass ($p = 0.0057$), but corn weed management and its interaction with crop identity did not affect weed community stand density or biomass (p-values > 0.05) (Tables **??** and 3). Weed community stand density and aboveground mass in each crop identity category, averaged over blocks, years, and corn weed management regimes, are presented in Figure 2A and B. Contributions by the dominant species are presented in Figure 2C and D. Contrasts for the effects of rotation systems, rotation system within individual crops, and crop types on community stand density and aboveground mass are shown in Table 5C.

Weed community density and aboveground mass of the 3-year and 4-year systems averages were comparable to those of the 2-year system ($p = 0.058$ and $p = 0.9451$, respectively; Table 5B1). The weed community density in the 4-year rotation was 2.5-fold greater than that in the 3-year rotation ($p = 0.0368$), but the community aboveground mass was comparable between the 3-year and 4-year rotations.

For the individual crops (Table 5B2), increased rotation diversity tended to decrease weed density and aboveground mass in corn and soybean and increase weed abundance in oat, but these changes were not significant ($p = 0.6354$ and $p = 0.4041$ for corn, $p = 0.1834$ and $p = 0.0739$ for soybean, and $p = 0.3955$ and $p = 0.335$ for oat). The patchiness of weeds, which was reflected in the high standard error values, might have caused the lack of significance for these inconclusive trends.

For different crop types, weed community density and aboveground mass were comparable between the warm-season crops (corn and soybean) and between the cool-season crops (oat and alfalfa) (Table 5B3). Overall, the average weed community density in the cool-season crops was 26-fold greater than that in the warm-season crops ($p < 0.0001$), and the average weed community aboveground mass in cool-season crops was 16-fold greater than that in warm-season crops ($p = 0.0001$). In the 3-year rotation, the weed stand community stand in oat (O3) was 11.5-fold greater than the average in corn and soybean (C3 and S3) ($p = 0.0012$), but the weed community aboveground mass was comparable between O3 and the average of the C3 and S3 phases ($p = 0.1502$). In the 4-year rotation, the weed community stand density in the average of oat and alfalfa (O4 and A4) was 36-fold greater than the average of the corn (C4) and soybean (S4) phases ($p < 0.0001$), and the average weed biomass for the O4 and A4 phases was 29-fold greater than for the C4 and S4 phases ($p < 0.0001$).

```
comm_dens_tab <- emmeans(comm_dens_lmer, ~ Crop_ID | Corn_weed_management,  infer = c(FALSE,TRUE),  type
  broom::tidy() %>%
  select(Crop_ID, Corn_weed_management, response, std.error) %>%
  rename(density = response)
```

```
comm_biom_tab <- emmeans(comm_biom_lmer, ~ Crop_ID | Corn_weed_management,  infer = c(FALSE,TRUE),  type
  broom::tidy()  %>%
  select(Crop_ID, Corn_weed_management, response, std.error) %>%
  rename(biomass = response)
```

Table 4: List of weed species (in alphabetical order) found from 2017 through 2020 field seasons.

Bayer code	Scientific name	Life cycle
(A) - Dicotyledon species		
ABUTH	*Abutilon theophrasti* Medicus	annual
AMARE	*Amaranthus retrofelxus* L.	summer annual
AMATA	*Amaranthus tuberculatus* (Moq.) Sauer var. *rudis*	summer annual
AMBEL	*Ambrosia artemissifolia* L.	erect, branching, summer annual
ARFMI	*Arctium minus* (Hill) Bernh.	biennial
CHEAL	*Chenopodium album* L.	erect summer annual
CIRAR	*Cirsium arvense* (L.) Scop.	rhizomatous perennial
CIRVU	*Cirsium vulgare* (Savi) Tenore	biennial
EPHHT	*Euphorbia humistrata* Engelm. ex Gray	mat-forming summer annual
EPHMA	*Euphorbia maculata* L.	mat-forming summer annual
EUPHY	*Eupatorium hyssopifolium* L.	summer annual
MORAL	*Morus alba* L.	perennial shrub
PHYSU	*Physalis subglabrata* Mackenz. and Bush	rhizomatous perennial
PLAMA	*Plantago major* L.	rosette-forming perennial
POLPE	*Polygonum perfoliatum* L.	spiny summer annual vine
POLPY	*Polygonum pensylvanicum* L.	ascending much-branched summer annual
POROL	*Portulaca oleracea* L.	prostrate mat-forming summer annual
SOLPT	*Solanum ptycanthum* Dun.	erect branching summer annual
SONAR	*Sonchus arvensis* L.	rhizomatous perennial
TAROF	*Taraxacum officinale* Weberin Wiggers	tap-rooted perennial
(B) - Monocotyledon species		
AGRRE	*Elytrigia repens* (L.) Nevski	rhizomatous perennial
BROTE	*Bromus tectorum* L.	summer or winter annual
CCHPA	*Cenchrus longispinus* (Hack.) Fern.	summer annual
CONAR	*Convolvulus arvensis* L.	rhizomatous perennial
CYPES	*Cyperus esculentus* L.	rhizomatous perennial
DACGL	*Dactylis glomerata* L.	clump-forming perennial
DIGSA	*Digitaria sanguinalis* (L.) Scop.	summer annual
ECHCG	*Echinochloa crus − galli* (L.) Beauv.	summer annual
ERBVI	*Eriochloa villosa* (Thunb.) Kunth	erect summer annual
FESSP	*Festuca* spp.	clump-forming perennial
PANCA	*Panicum capillare* L.	summer annual
PANDI	*Panicum dichotomiflorum* Michx.	summer annual
SETFA	*Setaria faberi* Herrm.	clump-forming, erect summer annual
SETLU	*Setaria glauca* (L.) Beauv.	clump-forming, erect summer annual

Table 5: Community density and aboveground mass ANOVA and contrasts. The abbreviations in the contrast column are crop identities, which are the combinations of the first letter in crop species names and the rotation in which it occurred.

			Stand density		Aboveground mass	
Source of variation	df1	df2	F	p	F	p
(A) - ANOVA						
Crop ID	8	24	12.22	<.0001	3.74	0.0057
Corn weed management	1	3	2.13	0.2402	0.02	0.8900
Crop ID x Corn weed management	8	24	1.66	0.1613	0.99	0.4660
Contrasts ratio p ratio p						
(B1) - Rotation system effects						
[(C2+S2)/2] vs [(C3+S3+O3+C4+S4+O4+A4)/7]				-0.87	-0.04	0.64
[(C3+S3+O3)/3] vs [(C4+S4+O4+A4)/4]				-0.92	-0.86	0.61
(B2) - Rotation system effects within individual crops						
C2 vs [(C3+C4)/2]				0.32	0.83	0.98
C3 - C4				-0.53	-0.31	1.13
S2 vs [(S3+S4)/2]				0.91	1.83	0.98
S3 - S4				0.17	0.04	1.13
O3 - O4				-0.67	-1.11	1.13
(B3) - Crop type effects						
[(C2+S2)/2] vs [(C3+S3+C4+S4)/4]				0.62	1.33	0.69
[(C3+S3)/2] vs [(C4+S4)/2]				0.53	1.26	0.80
[(O3+O4+A4)/3] vs [(C2+S2+C3+S3+C4+S4)/6]				3.26	2.77	0.57
O3 vs [(C3+S3)/2]				2.44	1.46	0.98
[(O4+A4)/2] vs [(C4+S4)/2]				3.58	3.36	0.80
[(O3+O4)/2] vs A4				-0.22	0.40	0.98

Note: C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in the 4-year rotation, S2 - soybean in the 2-year rotation, S3 - soybean in the 3-year rotation, S4 - soybean in the 4-year rotation, O3 - oat in the 3-year rotation, O4 - oat in the 4-year rotation, and A4 - alfalfa in the 4-year rotation.

Density and biomass per sq ft

```
left_join(comm_dens_tab, comm_biom_tab, by = c("Crop_ID", "Corn_weed_management")) %>%
  select(Crop_ID, Corn_weed_management,
         density, std.error.x,
         biomass, std.error.y) %>%
  mutate(across(where(is.numeric), ~ as.numeric(sprintf('%.1f', .)))) %>%
  mutate(`density (SE)` = paste0(density, " (", std.error.x, ")") ,
         `biomass (SE)` = paste0(biomass, " (", std.error.y, ")")) %>%
  select(Crop_ID, Corn_weed_management, `density (SE)`,  `biomass (SE)`) #%>%
```

Combined table: metric

```
## # A tibble: 18 x 4
##    Crop_ID Corn_weed_management ‘density (SE)‘ ‘biomass (SE)‘
##    <chr>   <chr>                <chr>          <chr>
##  1 C2      conv                 7.7 (4.4)      4 (3.7)
##  2 S2      conv                 1.3 (0.8)      4.5 (4.1)
##  3 C3      conv                 2.9 (1.7)      1 (0.9)
##  4 S3      conv                 0.7 (0.4)      1.2 (1.1)
##  5 O3      conv                 32 (18)        17 (15.4)
##  6 C4      conv                 8 (4.5)        1.9 (1.8)
##  7 S4      conv                 0.3 (0.2)      0.5 (0.5)
##  8 O4      conv                 64 (36)        52.1 (47.3)
##  9 A4      conv                 69 (38.7)      24.3 (22.1)
## 10 C2      low                  7.6 (4.3)      3.5 (3.2)
## 11 S2      low                  1.4 (0.8)      4.4 (4)
## 12 C3      low                  6.1 (3.4)      1.9 (1.7)
## 13 S3      low                  0.5 (0.3)      0.4 (0.4)
## 14 O3      low                  44.3 (24.9)    18.2 (16.5)
## 15 C4      low                  6.5 (3.7)      1.9 (1.7)
## 16 S4      low                  0.6 (0.4)      0.9 (0.9)
## 17 O4      low                  84 (47.2)      55 (49.9)
## 18 A4      low                  62.2 (35)      17.4 (15.8)
```

```
  # pivot_wider(names_from = Corn_weed_management,
  #             values_from = c(`density (SE)`,  `biomass (SE)` ))
```

```
left_join(comm_dens_tab, comm_biom_tab, by = c("Crop_ID", "Corn_weed_management")) %>%
  mutate(density_sq_yd = density/1.2,
         density_sq_yd_se = std.error.x/1.2,
         biomass_sq_yd = biomass* 0.0353/1.2,
         biomass_sq_yd_se = std.error.y * 0.0353/1.2) %>%
  select(Crop_ID, Corn_weed_management,
         density_sq_yd, density_sq_yd_se,
         biomass_sq_yd, biomass_sq_yd_se) %>%
  mutate(across(where(is.numeric), ~ as.numeric(sprintf('%.1f', .)))) %>%
```

```
  mutate(`density (SE)` = paste0(density_sq_yd, " (", density_sq_yd_se, ")") ,
         `biomass (SE)` = paste0(biomass_sq_yd, " (", biomass_sq_yd_se, ")")) %>%
  select(Crop_ID, Corn_weed_management, `density (SE)`,  `biomass (SE)`)%>%
  pivot_wider(names_from = Corn_weed_management,
              values_from = c(`density (SE)`,  `biomass (SE)` ))
```

Combined table: imperial

```
## # A tibble: 9 x 5
##   Crop_ID `density (SE)_conv` `density (SE)_low` `biomass (SE)_conv`
##   <chr>   <chr>               <chr>              <chr>
## 1 C2      6.4 (3.6)           6.3 (3.6)          0.1 (0.1)
## 2 S2      1.1 (0.6)           1.1 (0.7)          0.1 (0.1)
## 3 C3      2.5 (1.4)           5.1 (2.9)          0 (0)
## 4 S3      0.6 (0.3)           0.4 (0.2)          0 (0)
## 5 O3      26.6 (15)           36.9 (20.8)        0.5 (0.5)
## 6 C4      6.7 (3.8)           5.4 (3.1)          0.1 (0.1)
## 7 S4      0.3 (0.2)           0.5 (0.3)          0 (0)
## 8 O4      53.3 (30)           70 (39.3)          1.5 (1.4)
## 9 A4      57.5 (32.3)         51.8 (29.1)        0.7 (0.6)
## # i 1 more variable: `biomass (SE)_low` <chr>
```

```
# remove rows that sum to zeros https://www.tutorialspoint.com/how-to-remove-rows-that-contains-all-zer
#dens_1720_clean <- dens_1720[rowSums(dens_1720[,13:46])>0,]

dens_1720_clean$Crop <- factor(dens_1720_clean$Crop,
                               levels = c("corn", "soybean", "oat", "alfalfa"))
dens_1720_clean$Crop_ID <- factor(dens_1720_clean$Crop_ID,
                                  levels = c("C2", "S2",
                                             "C3", "S3", "O3",
                                             "C4", "S4", "O4", "A4"))

#biom_1720_clean <- biom_1720[rowSums(biom_1720[,13:46])>0,]
biom_1720_clean$Crop <- factor(biom_1720_clean$Crop,
                               levels = c("corn", "soybean", "oat", "alfalfa"))

biom_1720_clean$Crop_ID <- factor(biom_1720_clean$Crop_ID,
                                  levels = c("C2", "S2",
                                             "C3", "S3", "O3",
                                             "C4", "S4", "O4", "A4"))

dens_1720_clean %<>%
  mutate_at(c("Block","Crop_ID", "Year","Corn_weed_management"),
            funs(factor(.)))

biom_1720_clean %<>%
  mutate_at(c("Block","Crop_ID", "Year","Corn_weed_management"),
            funs(factor(.)))

# Find minimum non-zero in each matrix, or in the Prop column of the long-format dframe

# convert wide to long format
```

```r
dens_1720_long <- dens_1720_clean %>%
  pivot_longer(!c(Crop:Corn_weed_management),
               names_to = "Species",
               values_to =  "Density")

min(dens_1720_long$Density[dens_1720_long$Density>0]) #0.05396072
```

```
## [1] 0.05396072
```

```r
biom_1720_long <- biom_1720_clean %>%
  pivot_longer(!c(Crop:Corn_weed_management),
               names_to = "Species",
               values_to =  "Biomass")

min(biom_1720_long$Biomass[biom_1720_long$Biomass>0]) # 0.0005396072
```

```
## [1] 0.0005396072
```

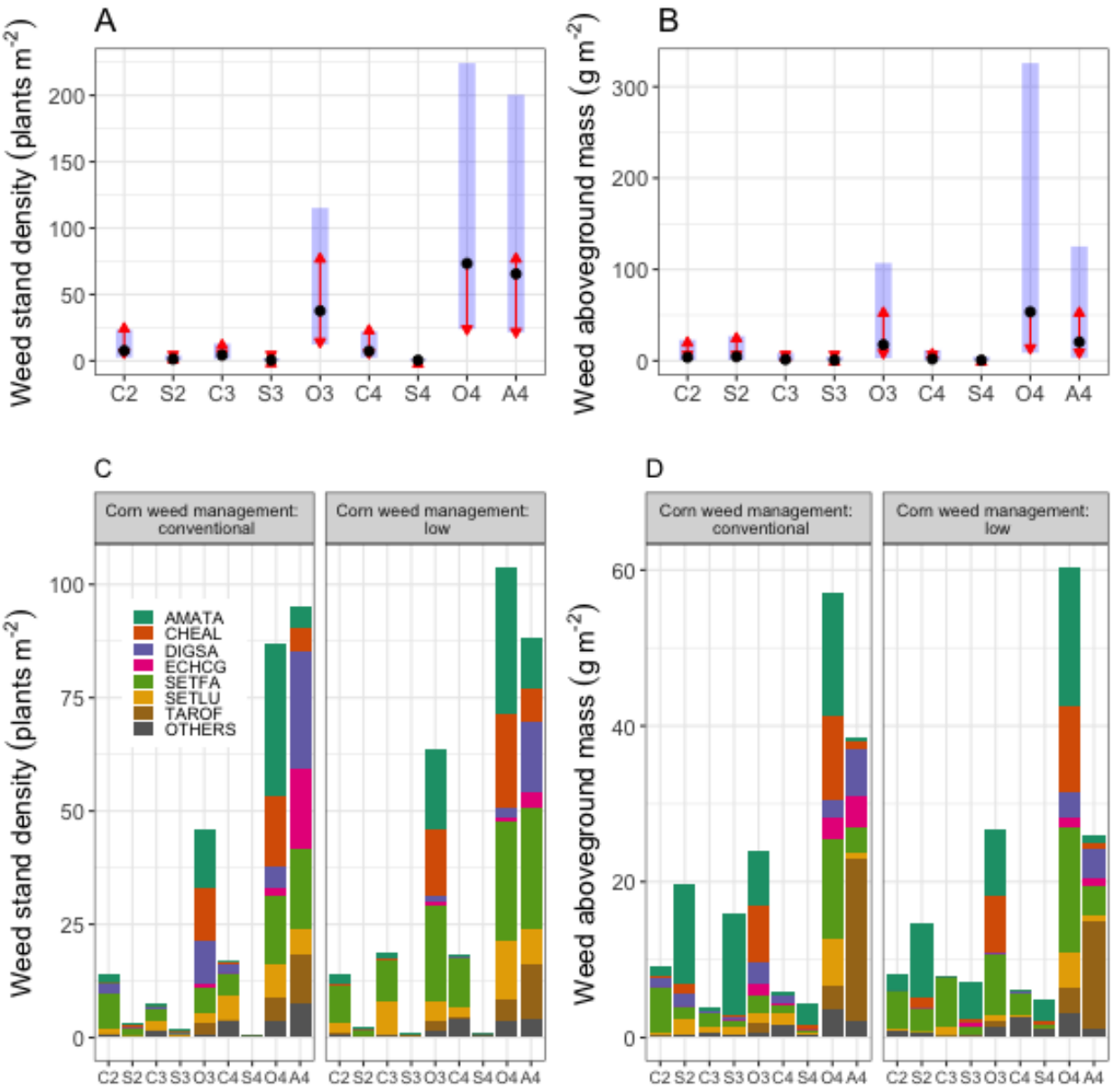

Figure 2: In panels A and B: weed community stand density and aboveground mass were averaged over four blocks, four years, and two corn weed management regimes; the black dots are estimated marginal means; the blue bars are 95% confidence intervals; the red arrows reflect the comparisons among means; overlapping arrows indicate non-significant differences. In panels C and D: the contribution of the seven most abundant weed species and the rarer species (species ordered eighth and above grouped in OTHERS) in each crop identity, averaged over four blocks and four years, are ordered alphabetically. The abbreviations on the x-axis are crop identities, which are the combinations of the first letter in crop species names and the rotation in which it occurred (C2 - corn in the 2-year rotation, C3 - corn in the 3-year rotation, C4 - corn in the 4-year rotation, S2 - soybean in the 2-year rotation, S3 - soybean in the 3-year rotation, S4 - soybean in the 4-year rotation, O3 - oat in the 3-year rotation, O4 - oat in the 4-year rotation, and A4 - alfalfa in the 4-year rotation.) The less abundant weed species which made up 6% of the whole community are grouped in OTHERS. The means displayed on panels A and B were estimated marginal means, calculated based on the analysis model (with `emmip` function) but the means displayed on panels C and D were arithmetic means, calculated from the data so they are slightly different.