Cover

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```
library(lme4)
```

```
## Loading required package: Matrix
```

```
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
##
##     lmer
```

```
## The following object is masked from 'package:stats':
##
##     step
```

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------------------- tidyverse 1.2.1 --
```

```
## v ggplot2 3.2.1     v purrr   0.3.2
## v tibble  2.1.3     v dplyr   0.8.3
## v tidyr   1.0.0     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.4.0
```

```
## -- Conflicts ------------------------------------------------------- tidyverse_conflicts() --
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x tidyr::pack()   masks Matrix::pack()
## x tidyr::unpack() masks Matrix::unpack()
```

```
library(lsmeans)
```

```
## Loading required package: emmeans
```

```
## The 'lsmeans' package is now basically a front end for 'emmeans'.
## Users are encouraged to switch the rest of the way.
## See help('transition') for more information, including how to
## convert old 'lsmeans' objects and scripts to work with 'emmeans'.
```

```
library(car)
```

```
## Loading required package: carData
```

```
## Registered S3 methods overwritten by 'car':
##   method                          from
##   influence.merMod                lme4
##   cooks.distance.influence.merMod lme4
##   dfbeta.influence.merMod         lme4
##   dfbetas.influence.merMod        lme4
```

```
##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some
```

```
library(multcomp)
```

```
## Loading required package: mvtnorm

## Loading required package: survival

## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##     geyser
```

```
library(multcompView)
library(ggplot2)
library(betareg)
library(glmmTMB)
library(effects)
```

```
## lattice theme set by effectsTheme()
## See ?effectsTheme for details.
```

```
library(broom)
```

```
Corn2 <- Data %>%
       filter(crop == "corn")

Corn2$herbicide <- factor(Corn2$herbicide, levels=c("Zemax + Halex GT",   "SureStart", "Stinger",  "Acc
```

Corn

```
Oat <- Corn2 %>%
  filter(species =="oat")

model1 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Oat)
#summary(model1)
```

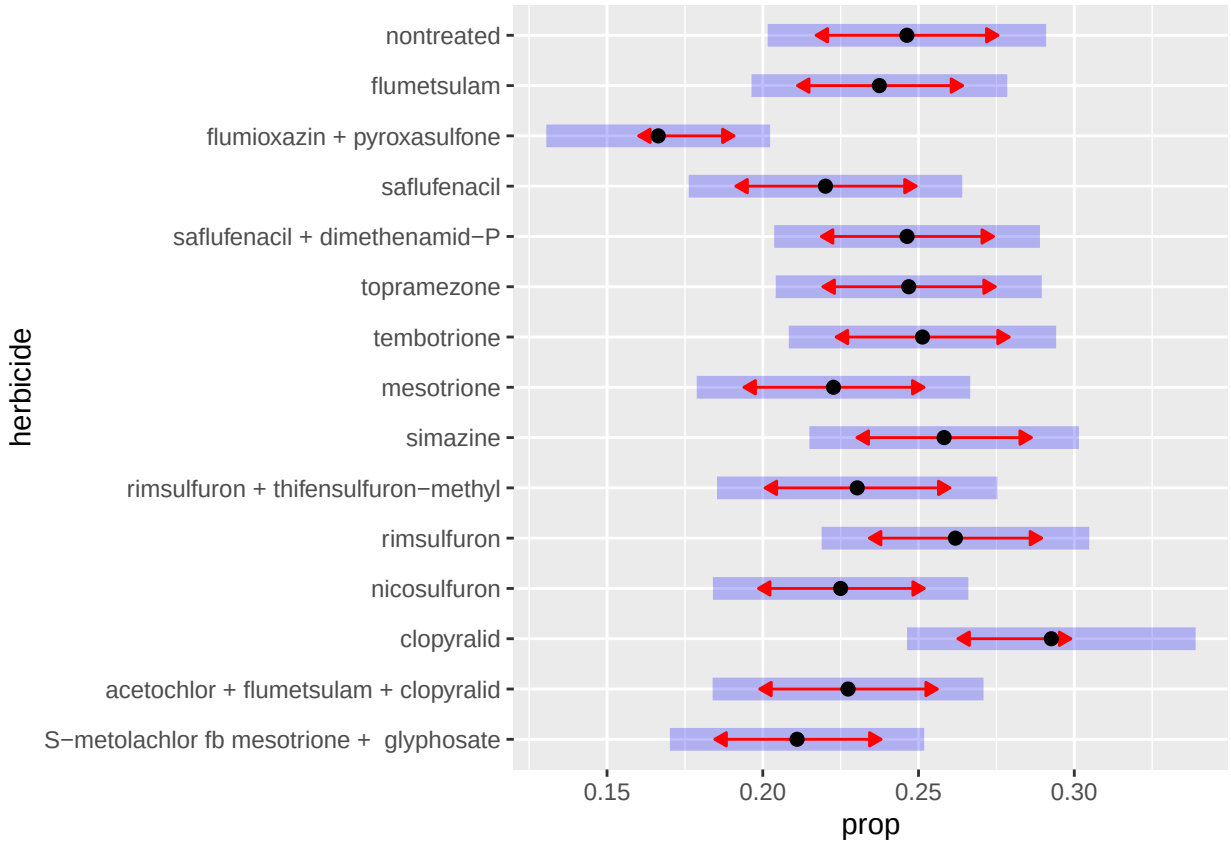
```
Anova(model1, test.statistic = "Chisq", type = "II")
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                    Chisq Df Pr(>Chisq)
## herbicide         54.194 14   1.19e-06 ***
## year            2700.701  1  < 2.2e-16 ***
## herbicide:year    14.691 14     0.3996
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm1=emmeans(model1, ~ herbicide|year, contr="pairwise", adjust="none", type="response")

lsmh=emmeans(model1 , ~ "herbicide", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

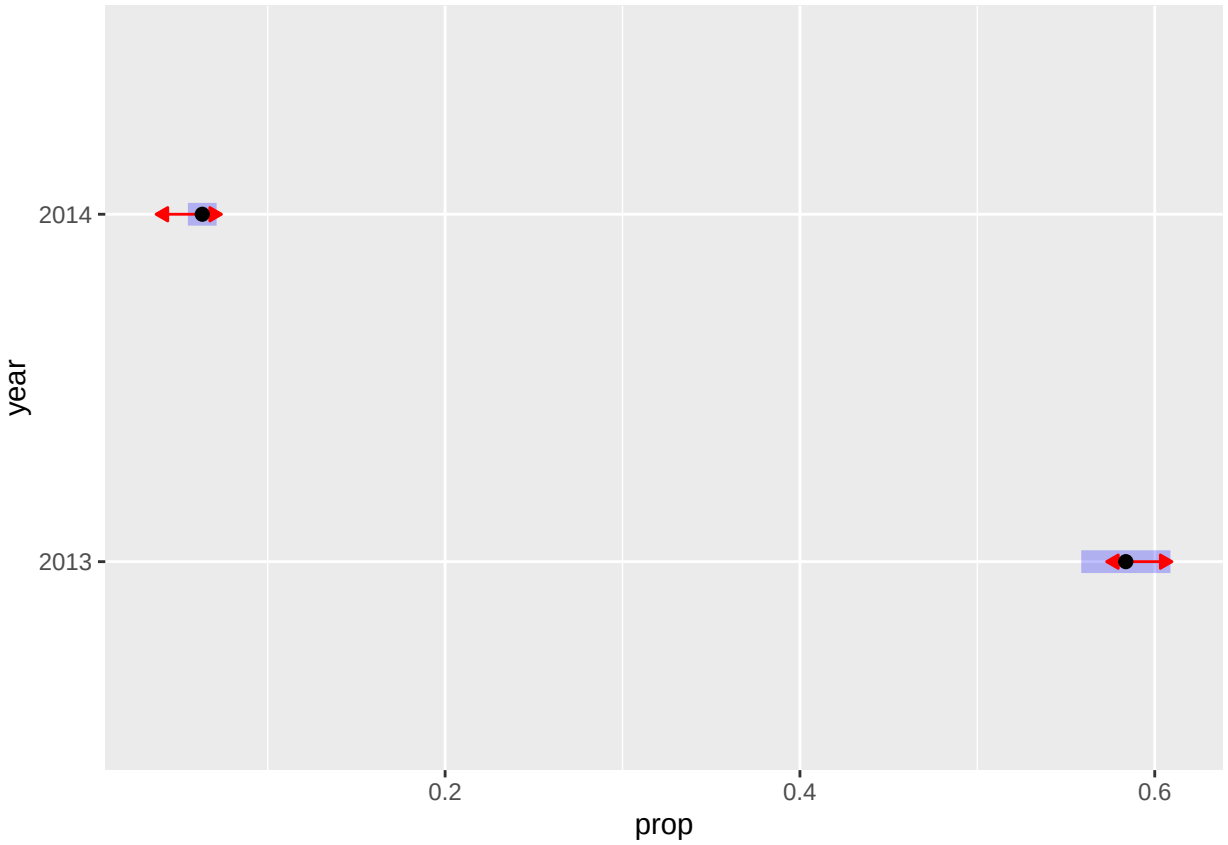
```
plot(lsmh, comparisons =TRUE, adjust="none")
```




```
lsmy=lsmeans(model1 , ~ "year", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
plot(lsmy, comparisons =TRUE, adjust="none")
```




```
CDLh=CLD(lsmh, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmh, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
CDLy=CLD(lsmy, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmy, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oa
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm1 <- as.data.frame(lsm1$emmeans)
```

```r
Ots1 <- data.frame(crop, lsm1)
```

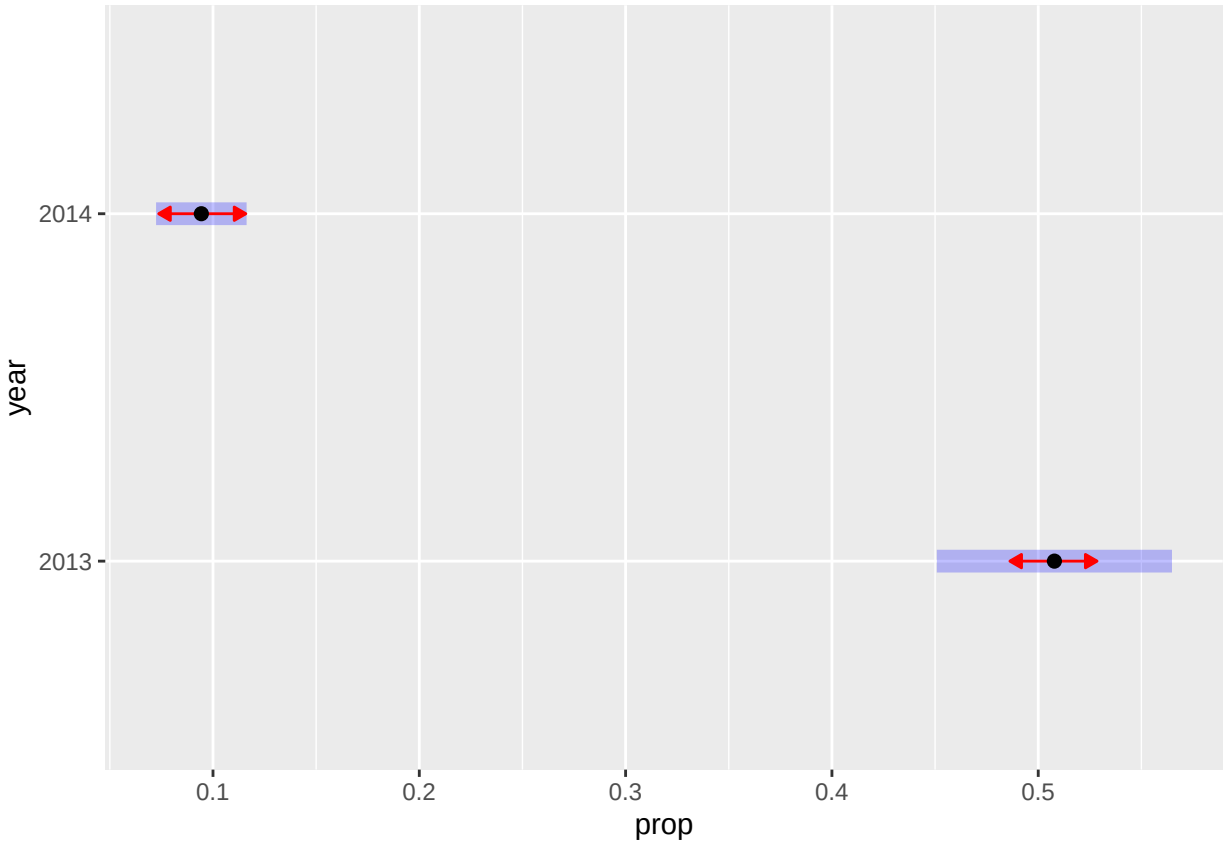
```r
Radish <- Corn2 %>%
  filter(species =="radish")

model2 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Radish)
#summary(model2)

Anova(model2)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                   Chisq Df Pr(>Chisq)
## herbicide       14.841 14     0.3891
## year           668.506  1     <2e-16 ***
## herbicide:year  17.967 14     0.2083
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
lsm2=emmeans(model2, ~ herbicide|year, contr="pairwise", adjust="none", type="response")

lsmy=lsmeans(model2 , ~ "year", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```r
plot(lsmy, comparisons =TRUE, adjust="none")
```



```
CDLy=CLD(lsmy, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmy, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("Radish","Radish","Radish","Radish","Radish","Radish","Radish","Radish","Radish","Radish","Ra
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm2 <- as.data.frame(lsm2$emmeans)
Rad1 <- data.frame(crop, lsm2)
```

```
Winter <- Corn2 %>%
  filter(species =="winter rye")

model3 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Winter)
summary(model3)
```

```
##  Family: beta  ( logit )
## Formula:          cover ~ herbicide * year + (1 | rep)
## Data: Winter
##
##      AIC      BIC   logLik deviance df.resid
##   -233.4   -144.2    148.7   -297.4       88
##
## Random effects:
##
## Conditional model:
##  Groups Name        Variance Std.Dev.
##  rep    (Intercept) 0.01425  0.1194
## Number of obs: 120, groups:  rep, 4
##
## Overdispersion parameter for beta family (): 42.3
##
## Conditional model:
##                                                    Estimate
## (Intercept)                                        -0.11847
## herbicideacetochlor + flumetsulam + clopyralid      0.18954
## herbicideclopyralid                                 0.25841
## herbicidenicosulfuron                              -0.21056
## herbiciderimsulfuron                                0.08894
## herbiciderimsulfuron + thifensulfuron-methyl       -0.01309
## herbicidesimazine                                  -0.09322
## herbicidemesotrione                                -0.09540
## herbicidetembotrione                               -0.23032
## herbicidetopramezone                               -0.03022
## herbicidesaflufenacil + dimethenamid-P              0.19730
## herbicidesaflufenacil                               0.08870
## herbicideflumioxazin + pyroxasulfone               -0.05874
## herbicideflumetsulam                               -0.23962
```

```
## herbicidenontreated                                          -0.08965
## year2014                                                     -1.11579
## herbicideacetochlor + flumetsulam + clopyralid:year2014      -0.53729
## herbicideclopyralid:year2014                                 -0.35727
## herbicidenicosulfuron:year2014                                0.09058
## herbiciderimsulfuron:year2014                                -0.02003
## herbiciderimsulfuron + thifensulfuron-methyl:year2014         0.18171
## herbicidesimazine:year2014                                    0.11919
## herbicidemesotrione:year2014                                 -0.06934
## herbicidetembotrione:year2014                                 0.25699
## herbicidetopramezone:year2014                                 0.07790
## herbicidesaflufenacil + dimethenamid-P:year2014              -0.11269
## herbicidesaflufenacil:year2014                               -0.25689
## herbicideflumioxazin + pyroxasulfone:year2014                -0.16998
## herbicideflumetsulam:year2014                                 0.47201
## herbicidenontreated:year2014                                  0.17378
##                                                           Std. Error z value
## (Intercept)                                                  0.16421  -0.721
## herbicideacetochlor + flumetsulam + clopyralid               0.21538   0.880
## herbicideclopyralid                                          0.21595   1.197
## herbicidenicosulfuron                                        0.21697  -0.970
## herbiciderimsulfuron                                         0.21600   0.412
## herbiciderimsulfuron + thifensulfuron-methyl                 0.21557  -0.061
## herbicidesimazine                                            0.21632  -0.431
## herbicidemesotrione                                          0.21674  -0.440
## herbicidetembotrione                                         0.21772  -1.058
## herbicidetopramezone                                         0.21603  -0.140
## herbicidesaflufenacil + dimethenamid-P                       0.21592   0.914
## herbicidesaflufenacil                                        0.21616   0.410
## herbicideflumioxazin + pyroxasulfone                         0.21630  -0.272
## herbicideflumetsulam                                         0.21775  -1.100
## herbicidenontreated                                          0.21658  -0.414
## year2014                                                     0.23610  -4.726
## herbicideacetochlor + flumetsulam + clopyralid:year2014      0.34358  -1.564
## herbicideclopyralid:year2014                                 0.33643  -1.062
## herbicidenicosulfuron:year2014                               0.33697   0.269
## herbiciderimsulfuron:year2014                                0.33184  -0.060
## herbiciderimsulfuron + thifensulfuron-methyl:year2014        0.32971   0.551
## herbicidesimazine:year2014                                   0.33343   0.357
## herbicidemesotrione:year2014                                 0.33877  -0.205
## herbicidetembotrione:year2014                                0.33406   0.769
## herbicidetopramezone:year2014                                0.33257   0.234
## herbicidesaflufenacil + dimethenamid-P:year2014              0.33115  -0.340
## herbicidesaflufenacil:year2014                               0.33831  -0.759
## herbicideflumioxazin + pyroxasulfone:year2014                0.34087  -0.499
## herbicideflumetsulam:year2014                                0.32983   1.431
## herbicidenontreated:year2014                                 0.33186   0.524
##                                                           Pr(>|z|)
## (Intercept)                                                  0.471
## herbicideacetochlor + flumetsulam + clopyralid               0.379
## herbicideclopyralid                                          0.231
## herbicidenicosulfuron                                        0.332
## herbiciderimsulfuron                                         0.681
## herbiciderimsulfuron + thifensulfuron-methyl                 0.952
```

```
## herbicidesimazine                                              0.667
## herbicidemesotrione                                            0.660
## herbicidetembotrione                                           0.290
## herbicidetopramezone                                           0.889
## herbicidesaflufenacil + dimethenamid-P                         0.361
## herbicidesaflufenacil                                          0.682
## herbicideflumioxazin + pyroxasulfone                           0.786
## herbicideflumetsulam                                           0.271
## herbicidenontreated                                            0.679
## year2014                                                    2.29e-06 ***
## herbicideacetochlor + flumetsulam + clopyralid:year2014        0.118
## herbicideclopyralid:year2014                                   0.288
## herbicidenicosulfuron:year2014                                 0.788
## herbiciderimsulfuron:year2014                                  0.952
## herbiciderimsulfuron + thifensulfuron-methyl:year2014          0.582
## herbicidesimazine:year2014                                     0.721
## herbicidemesotrione:year2014                                   0.838
## herbicidetembotrione:year2014                                  0.442
## herbicidetopramezone:year2014                                  0.815
## herbicidesaflufenacil + dimethenamid-P:year2014                0.734
## herbicidesaflufenacil:year2014                                 0.448
## herbicideflumioxazin + pyroxasulfone:year2014                  0.618
## herbicideflumetsulam:year2014                                  0.152
## herbicidenontreated:year2014                                   0.601
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

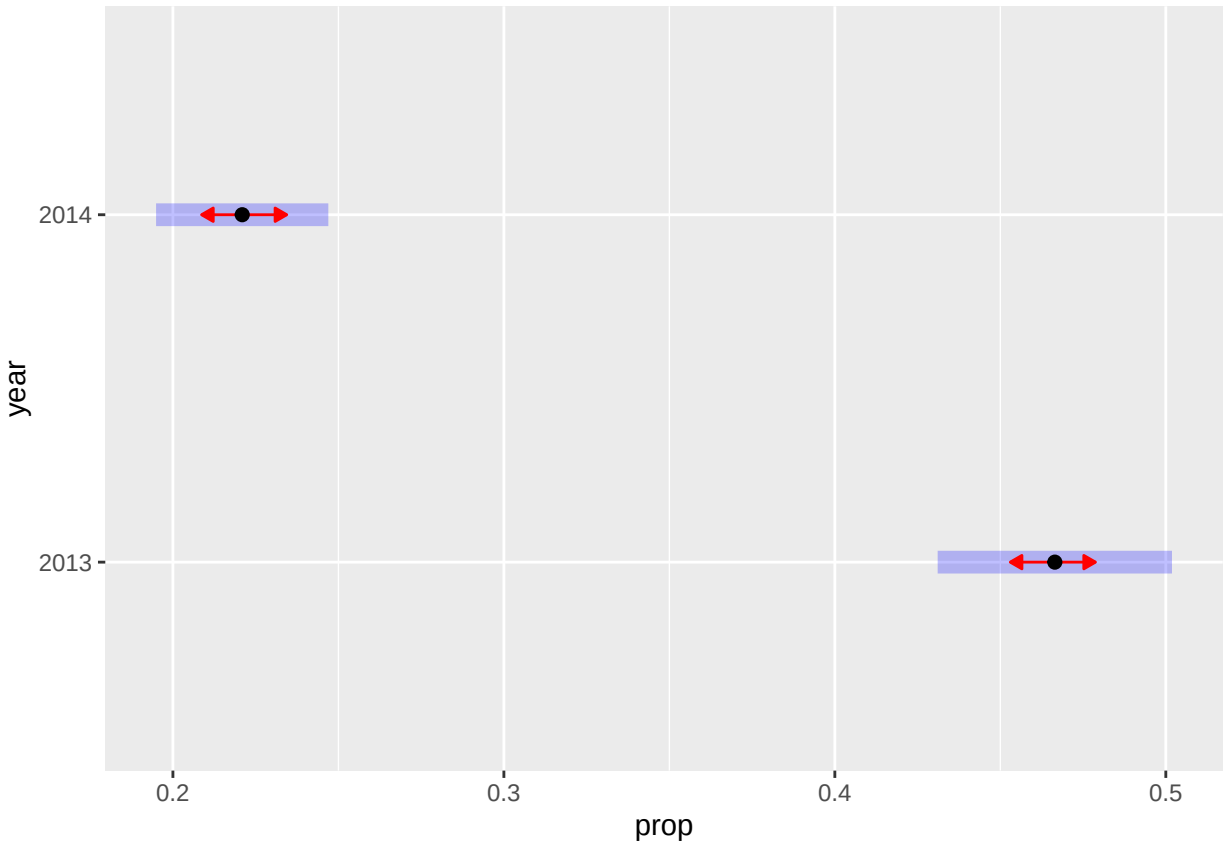
```
Anova(model3)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                   Chisq Df Pr(>Chisq)
## herbicide        8.7872 14     0.8444
## year           330.4926  1     <2e-16 ***
## herbicide:year  15.8232 14     0.3243
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm3=emmeans(model3, ~ herbicide|year, contr="pairwise", adjust="none", type="response")

lsmy=lsmeans(model3, ~ "year", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
plot(lsmy, comparisons =TRUE, adjust="none")
```




```
CDLy=CLD(lsmy, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmy, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("Winter rye","Winter rye","Winter rye","Winter rye","Winter rye","Winter rye","Winter rye","W
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm3 <- as.data.frame(lsm3$emmeans)
Win1 <- data.frame(crop, lsm3)
```

```
Bruiser <- Corn2 %>%
  filter(species =="bruiser annual ryegrass")

model4 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Bruiser)
#summary(model4)

Anova(model4)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
```

```
##                  Chisq Df Pr(>Chisq)
## herbicide       36.925 14  0.0007574 ***
## year           577.080  1  < 2.2e-16 ***
## herbicide:year  17.505 14  0.2302488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm4=emmeans(model4, ~ herbicide|year, contr="pairwise", adjust="none", type="response")

lsmh=lsmeans(model4, ~ "herbicide", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
lsmy=lsmeans(model4, ~ "year", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
CDLh=CLD(lsmh, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmh, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
CDLy=CLD(lsmy, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmy, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("Buiser annual rye","Buiser annual rye","Buiser annual rye","Buiser annual rye","Buiser annual
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm4 <- as.data.frame(lsm4$emmeans)
Bru1 <- data.frame(crop, lsm4)
```

```
King <- Corn2 %>%
  filter(species =="king annual rye")

model5 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=King)
#summary(model5)

Anova(model5)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                  Chisq Df Pr(>Chisq)
## herbicide       70.557 14   1.53e-09 ***
```

```
## year           620.792  1  < 2.2e-16 ***
## herbicide:year  36.496 14  0.0008791 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm5=emmeans(model5, ~ herbicide|year, contr="pairwise", adjust="none", type="response")

lsm=lsmeans(model5, ~ herbicide|year, contr="pairwise", adjust="none", type="response")
CDL=CLD(lsm, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsm, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("King annual rye", "King annual rye","King annual rye","King annual rye","King annual rye","K
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm5 <- as.data.frame(lsm5$emmeans)
Kin1 <- data.frame(crop, lsm5)
```

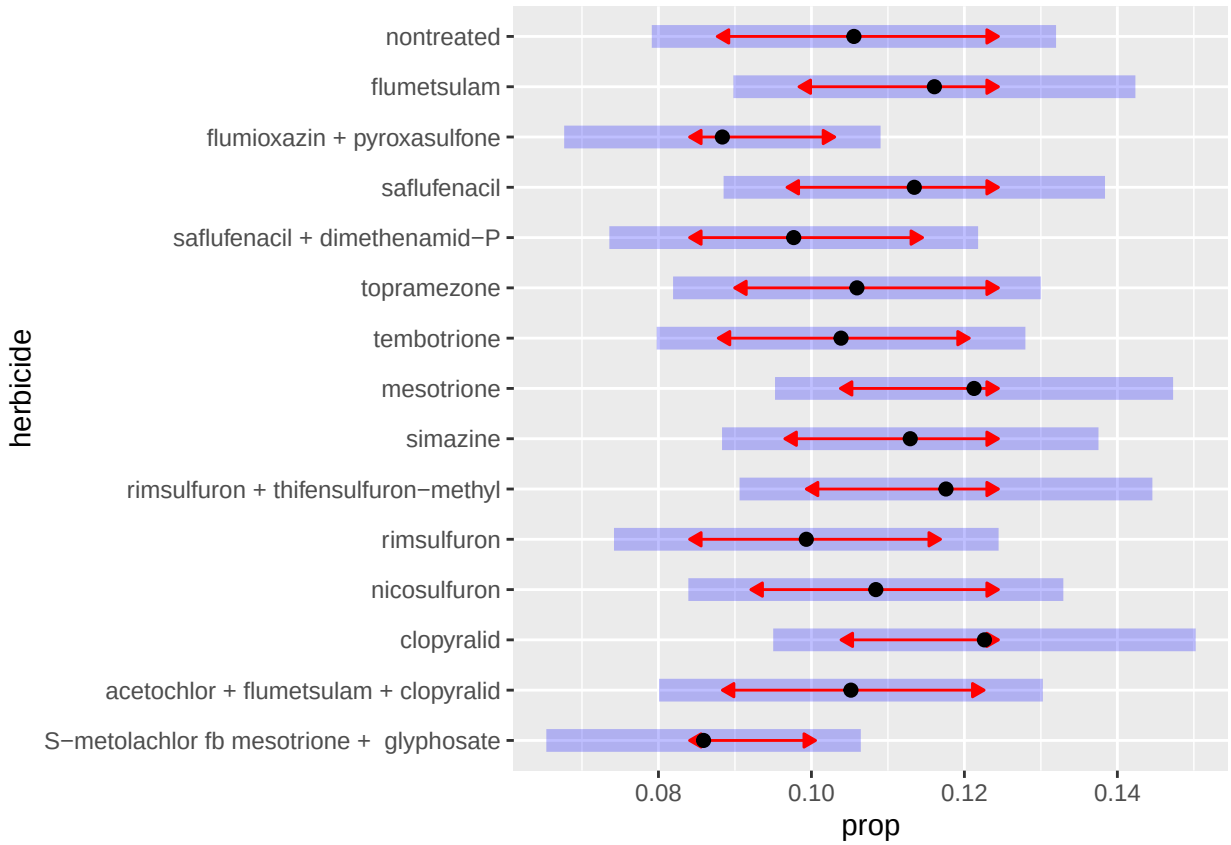
```
Crimson <- Corn2 %>%
  filter(species =="crimson")

model6 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Crimson)
#summary(model6)

Anova(model6)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                   Chisq Df Pr(>Chisq)
## herbicide        73.758 14  3.996e-10 ***
## year           1835.629  1  < 2.2e-16 ***
## herbicide:year   17.113 14     0.2502
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm6=emmeans(model6, ~ herbicide|year, contr="pairwise", adjust="none", type="response")

lsmh=lsmeans(model6, ~ "herbicide", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

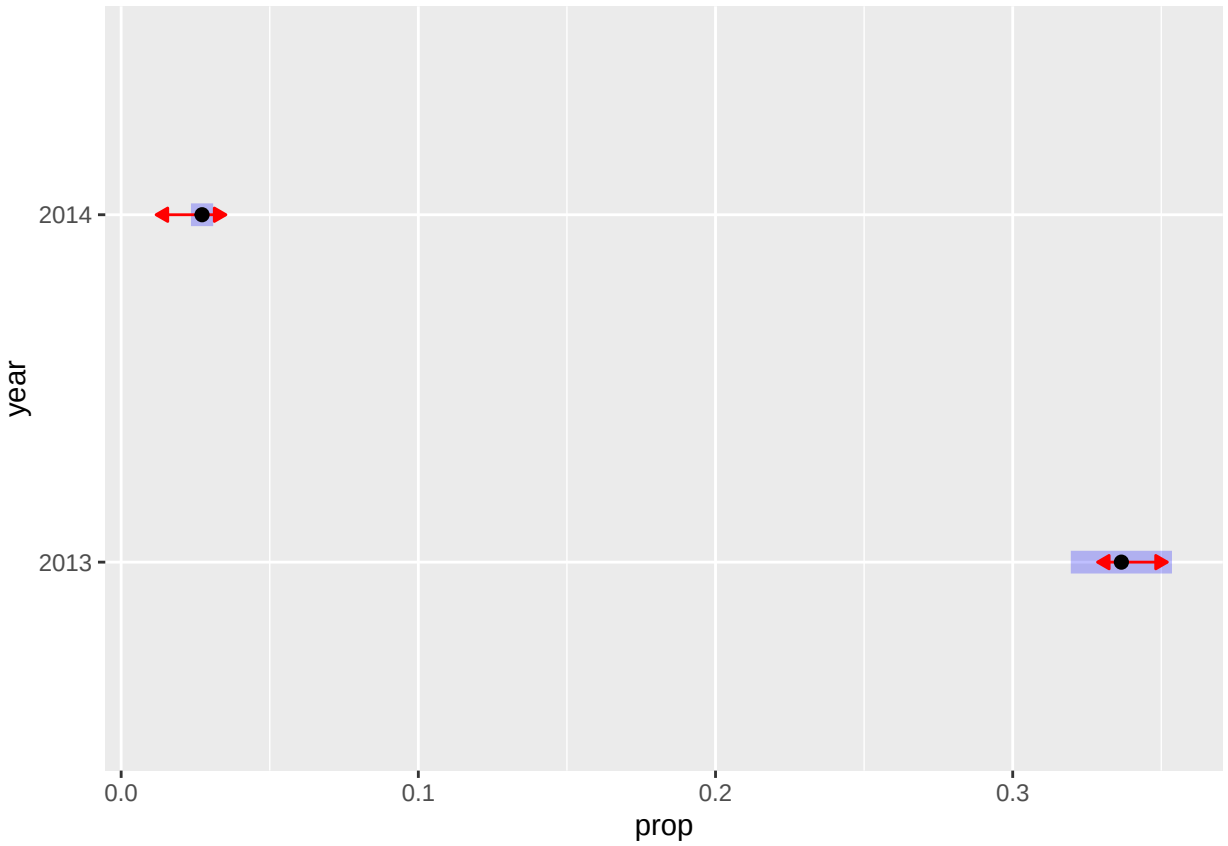
```
plot(lsmh, comparisons =TRUE, adjust="none")
```




```
lsmy=lsmeans(model6, ~ "year", contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
plot(lsmy, comparisons =TRUE, adjust="none")
```




```
CDLh=CLD(lsmh, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmh, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
CDLy=CLD(lsmy, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsmy, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("Crimson clover","Crimson clover","Crimson clover","Crimson clover","Crimson clover","Crimson
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm6 <- as.data.frame(lsm6$emmeans)
Cri1 <- data.frame(crop, lsm6)
```

```
NewC <- bind_rows(Bru1, Cri1, Kin1, Ots1, Rad1, Win1)
```

```
## Warning in bind_rows_(x, .id): Unequal factor levels: coercing to character
```

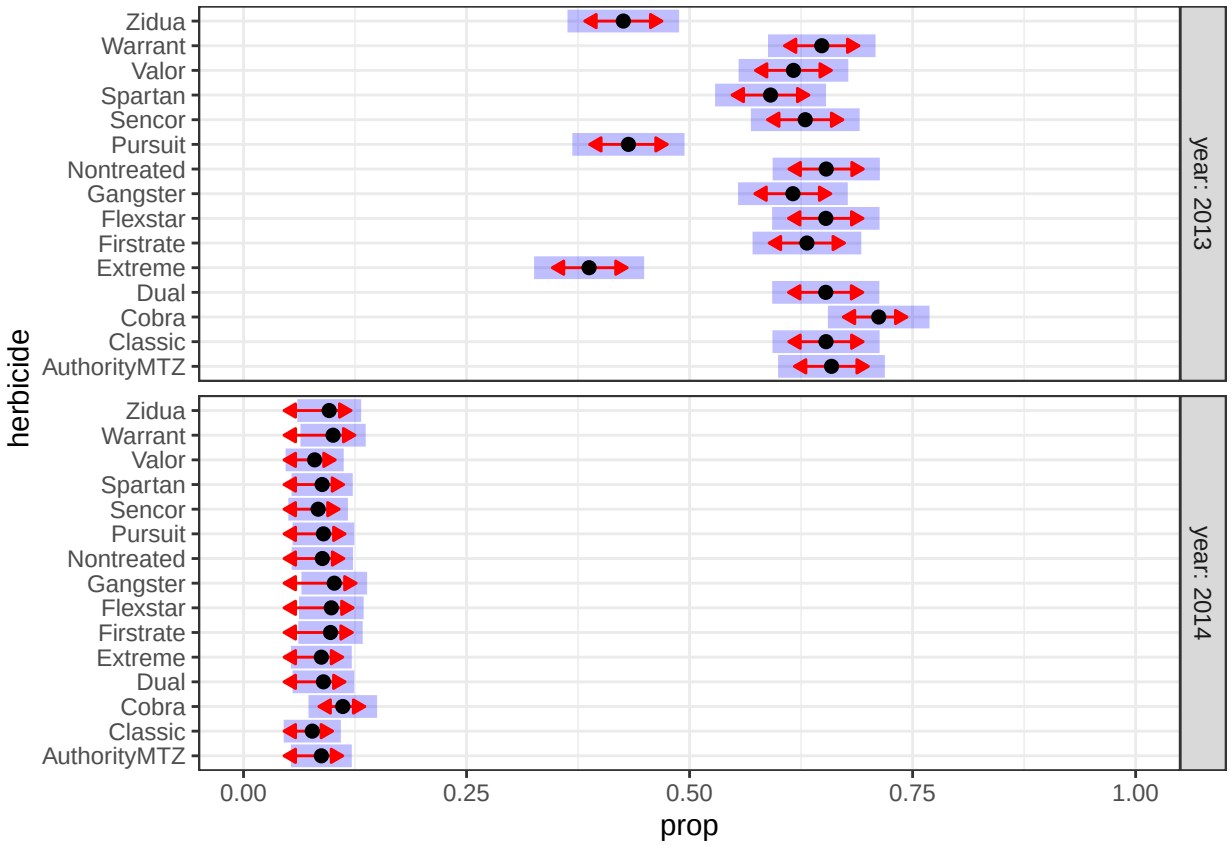
```
## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector
```

Soybean

```
Oat <- Data %>%
  filter(crop == "soybean" & species =="oat")

model7 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Oat)
#summary(model7)

Anova(model7)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                   Chisq Df Pr(>Chisq)
## herbicide       105.115 14  4.927e-16 ***
## year           1727.879  1  < 2.2e-16 ***
## herbicide:year   37.177 14  0.0006935 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm7=emmeans(model7 , ~ herbicide|year, contr="pairwise", adjust="none", type="response")

plot(lsm7, comparisons =TRUE, adjust="none") + xlim(0,1) + theme_bw()
```




```
CDL=CLD(lsm, alpha=0.05, Letters=letters, adjust="none", reversed = TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(lsm, alpha = 0.05, Letters = letters, adjust =
## "none", : `CLD()` called with a list of 2 objects. Only the first one was
## used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
crop <- c("Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oat/Pea","Oa
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm7 <- as.data.frame(lsm7$emmeans)
Ots <- data.frame(crop, lsm7)
```

```
Radish <- Data %>%
  filter(crop == "soybean" & species =="radish")

model8 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Radish)
#summary(model8)

Anova(model8)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
```

```
##                   Chisq Df Pr(>Chisq)
## herbicide      122.363 14  < 2.2e-16 ***
## year           402.120  1  < 2.2e-16 ***
## herbicide:year  85.824 14  2.319e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm8=emmeans(model8 , ~ herbicide|year, contr="pairwise", adjust="none", type="response")
```

```
crop <- c("Radish","Radish","Radish","Radish","Radish","Radish","Radish","Radish","Radish","Radish","Ra
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm8 <- as.data.frame(lsm8$emmeans)
Rad <- data.frame(crop, lsm8)
```

```
Winter <- Data %>%
  filter(crop == "soybean" & species =="winter rye")

model9 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Winter)
#summary(model9)

Anova(model9)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                    Chisq Df Pr(>Chisq)
## herbicide       25.7467 14    0.02787 *
## year           420.2011  1    < 2e-16 ***
## herbicide:year   7.1706 14    0.92793
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm9=emmeans(model9, ~  herbicide|year, contr="pairwise", adjust="none", type="response")
```

```
crop <- c("Winter rye","Winter rye","Winter rye","Winter rye","Winter rye","Winter rye","Winter rye","W
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm9 <- as.data.frame(lsm9$emmeans)
Win <- data.frame(crop, lsm9)
```

```
Bruiser <- Data %>%
  filter(crop == "soybean" & species =="bruiser annual ryegrass")

model10 <- glmmTMB(cover ~ herbicide*year + (1/rep), beta_family(link = "logit"), data=Bruiser)
#summary(model10)

Anova(model10)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                   Chisq Df Pr(>Chisq)
## herbicide       20.869 14     0.1051
## year           311.411  1     <2e-16 ***
## herbicide:year  15.245 14     0.3616
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm10=emmeans(model10 , ~ herbicide|year, contr="pairwise", adjust="none", type="response")
```

```
crop <- c("Buiser annual rye","Buiser annual rye","Buiser annual rye","Buiser annual rye","Buiser annual
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm10 <- as.data.frame(lsm10$emmeans)
Bru <- data.frame(crop, lsm10)
```

```
King <- Data %>%
  filter(crop == "soybean" & species =="king annual rye")

model11 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=King)
#summary(model11)

Anova(model11)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                  Chisq Df Pr(>Chisq)
## herbicide       65.323 14  1.340e-08 ***
## year           691.512  1  < 2.2e-16 ***
## herbicide:year  54.409 14  1.093e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm11=emmeans(model11 , ~ herbicide|year, contr="pairwise", adjust="none", type="response")
```

```
crop <- c("King annual rye", "King annual rye","King annual rye","King annual rye","King annual rye","K
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm11 <- as.data.frame(lsm11$emmeans)
Kin <- data.frame(crop, lsm11)
```

```
Crimson <- Data %>%
  filter(crop == "soybean" & species =="crimson")

model12 <- glmmTMB(cover ~ herbicide*year + (1|rep), beta_family(link = "logit"), data=Crimson)
#summary(model12)

Anova(model12)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cover
##                    Chisq Df Pr(>Chisq)
## herbicide        28.2475 14    0.01319 *
## year           2555.8036  1    < 2e-16 ***
## herbicide:year    8.7819 14    0.84476
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm12=emmeans(model12 , ~ herbicide|year, contr="pairwise", adjust="none", type="response")
```

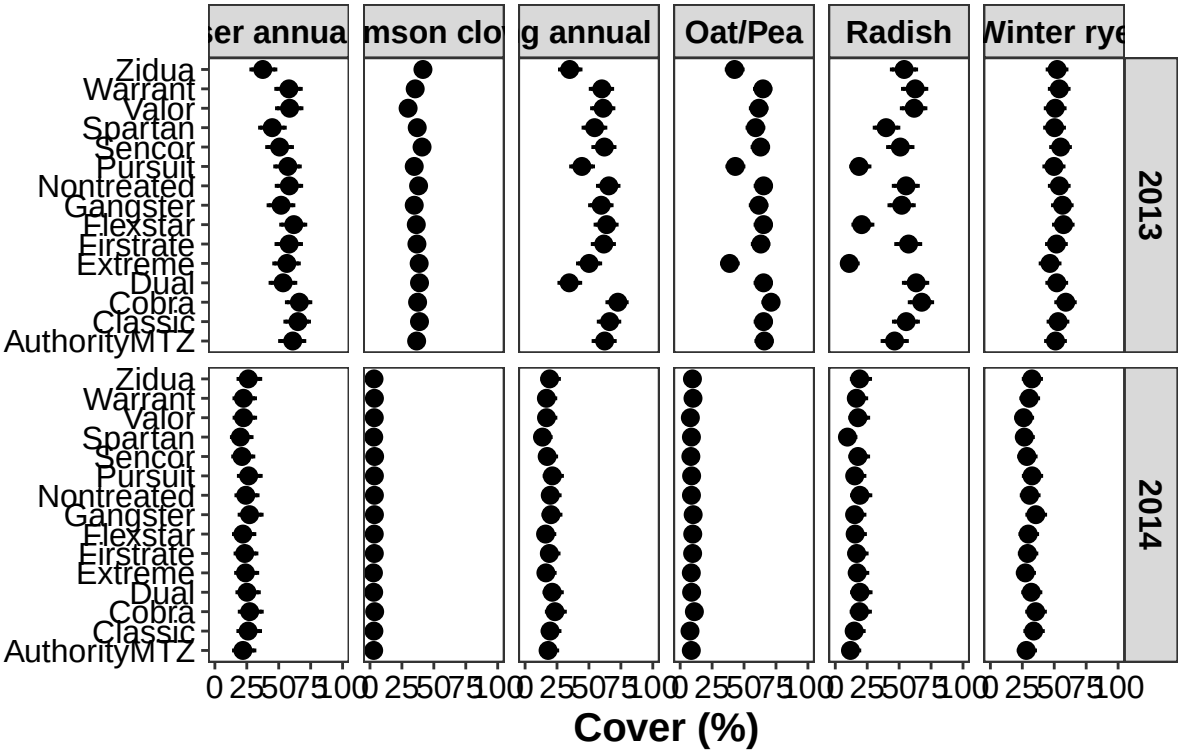
```
crop <- c("Crimson clover","Crimson clover","Crimson clover","Crimson clover","Crimson clover","Crimson
year <- c("2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013", "2013

lsm12 <- as.data.frame(lsm12$emmeans)
Cri <- data.frame(crop, lsm12)
```

```
New <- bind_rows(Bru, Cri, Kin, Ots, Rad, Win)
```

```
## Warning in bind_rows_(x, .id): Unequal factor levels: coercing to character
```

```
## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector
```

```
ggplot(New, aes(x = herbicide, y=prop*100)) + facet_grid(year~crop) +
  geom_point(shape = 16, size = 3) + coord_flip() + ylim(0, 100) + labs(y="Cover (%)", x="") +
  geom_errorbar(aes(ymin  =  lower.CL*100, ymax  =  upper.CL*100), width =  0.2, size  =  0.7) +
  theme_bw() + theme(axis.title   = element_text(face = "bold", size=15), panel.grid = element_blank(),
                     axis.text = element_text(size=12, color="black"), strip.text = element_text(size=12,
                     plot.caption = element_text(hjust = 0)) +
  ggtitle ("", subtitle = "")
```




```
#ggsave("Soy13.pdf", height=6, width=15)
```