|  |
| --- |
| 2015-06-12 2 0  2015-06-13 1 0  2016-06-05 0 17  2016-06-06 0 31  2016-06-07 0 41  2016-06-08 0 56  2016-06-16 0 6  > modBRIX2 <- lmer(BRIX ~ treatment \* year + (1|plot/plant) + (1|year/date), data = balssugboth)  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Hessian is numerically singular: parameters are not uniquely determined  > modBRIX2 <- lmer(BRIX ~ treatment \* year +(1|year/date), data = balssugboth)  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Hessian is numerically singular: parameters are not uniquely determined  > modBRIX2 <- lmer(BRIX ~ (1|year/date), data = balssugboth)  > summary(modBRIX2)  Linear mixed model fit by REML ['lmerMod']  Formula: BRIX ~ (1 | year/date)  Data: balssugboth  REML criterion at convergence: 1717.6  Scaled residuals:  Min 1Q Median 3Q Max  -2.7713 -0.6874 -0.0649 0.8138 3.5056  Random effects:  Groups Name Variance Std.Dev.  date:year (Intercept) 38.260 6.185  year (Intercept) 4.581 2.140  Residual 74.766 8.647  Number of obs: 237, groups: date:year, 13; year, 2  Fixed effects:  Estimate Std. Error t value  (Intercept) 25.729 2.442 10.54  > modBRIX2 <- lmer(BRIX ~ treatment \* year + (1|plot/plant) + (1|year/date), data = balssugboth)  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Hessian is numerically singular: parameters are not uniquely determined  > modBRIX2 <- lmer(BRIX ~ treatment + (1|plot/plant) + (1|year/date), data = balssugboth)  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year/date), data = balssugboth)  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Hessian is numerically singular: parameters are not uniquely determined  > balssugboth$TY <- with(balssugboth, paste(treatment, year))  > with(balssugboth, table(date, TY))  TY  date C 2015 C 2016 H 2015 H 2016  2015-06-02 4 0 2 0  2015-06-03 5 0 12 0  2015-06-06 3 0 9 0  2015-06-08 8 0 12 0  2015-06-10 3 0 5 0  2015-06-11 7 0 13 0  2015-06-12 0 0 2 0  2015-06-13 0 0 1 0  2016-06-05 0 5 0 12  2016-06-06 0 23 0 8  2016-06-07 0 22 0 19  2016-06-08 0 30 0 26  2016-06-16 0 0 0 6  > with(balssugboth, table(date, treatment))  treatment  date C H  2015-06-02 4 2  2015-06-03 5 12  2015-06-06 3 9  2015-06-08 8 12  2015-06-10 3 5  2015-06-11 7 13  2015-06-12 0 2  2015-06-13 0 1  2016-06-05 5 12  2016-06-06 23 8  2016-06-07 22 19  2016-06-08 30 26  2016-06-16 0 6  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year/date), data = balssugboth)  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Hessian is numerically singular: parameters are not uniquely determined  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year/date), data = subset(balssugboth, date != "2015-06-13"))  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Model failed to converge: degenerate Hessian with 1 negative eigenvalues  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year/date), data = subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13")))  Warning messages:  1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  unable to evaluate scaled gradient  2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Hessian is numerically singular: parameters are not uniquely determined  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year/date), data = subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13", "2016-06-16")))  Warning message:  In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Model is nearly unidentifiable: large eigenvalue ratio  - Rescale variables?  > modBRIX2 <- lmer(BRIX ~ treatment + (1|plot/plant) + (1|year/date), data = subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13", "2016-06-16")))  > summary(modBRIX2)  Linear mixed model fit by REML ['lmerMod']  Formula: BRIX ~ treatment + (1 | plot/plant) + (1 | year/date)  Data: subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13",  "2016-06-16"))  REML criterion at convergence: 1612.7  Scaled residuals:  Min 1Q Median 3Q Max  -3.2245 -0.6864 -0.0622 0.6282 4.0348  Random effects:  Groups Name Variance Std.Dev.  plant:plot (Intercept) 8.351 2.890  plot (Intercept) 7.394 2.719  date:year (Intercept) 19.607 4.428  year (Intercept) 13.134 3.624  Residual 56.727 7.532  Number of obs: 228, groups: plant:plot, 51; plot, 11; date:year, 10; year, 2  Fixed effects:  Estimate Std. Error t value  (Intercept) 22.053 3.306 6.670  treatmentH 3.050 2.159 1.413  Correlation of Fixed Effects:  (Intr)  treatmentH -0.318  > summary(balssugboth$BRIX)  Min. 1st Qu. Median Mean 3rd Qu. Max.  1.00 18.00 24.00 24.82 31.00 49.00  > modBRIX2 <- lmer(BRIX ~ treatment + (1|plot/plant) + (1|year/date), data = subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13", "2016-06-16")))  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year/date), data = subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13", "2016-06-16")))  Warning message:  In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  Model is nearly unidentifiable: large eigenvalue ratio  - Rescale variables?  > summary(modBRIX2)  Linear mixed model fit by REML ['lmerMod']  Formula: BRIX ~ treatment \* year + (1 | plot/plant) + (1 | year/date)  Data: subset(balssugboth, !date %in% c("2015-06-12", "2015-06-13",  "2016-06-16"))  REML criterion at convergence: 1600.4  Scaled residuals:  Min 1Q Median 3Q Max  -3.3238 -0.7042 -0.0449 0.6481 3.9836  Random effects:  Groups Name Variance Std.Dev.  plant:plot (Intercept) 7.885 2.808  plot (Intercept) 7.508 2.740  date:year (Intercept) 19.288 4.392  year (Intercept) 35.229 5.935  Residual 56.644 7.526  Number of obs: 228, groups: plant:plot, 51; plot, 11; date:year, 10; year, 2  Fixed effects:  Estimate Std. Error t value  (Intercept) 17.479 6.537 2.674  treatmentH 5.594 2.753 2.032  year2016 8.264 9.076 0.910  treatmentH:year2016 -3.718 2.520 -1.475  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.236  year2016 -0.695 0.111  trtmnH:2016 0.170 -0.621 -0.167  convergence code: 0  Model is nearly unidentifiable: large eigenvalue ratio  - Rescale variables?  > ranef(modBRIX2)  $`plant:plot`  (Intercept)  CC6-10:CC6 2.98694825  CC6-5:CC6 0.41662209  CC6-9:CC6 -0.97853442  CH5-2:CH5 0.55626100  CH5-5:CH5 -0.76942436  CH5-6:CH5 -2.53311710  CH5-7:CH5 0.18836502  CHSR8-2:CHSR8 1.39764586  CHSR8-4:CHSR8 -1.24227396  CHSR8-6:CHSR8 3.30194038  CSR7-9:CSR7 -0.09179030  EC3-3:EC3 -2.09131646  EC3-8:EC3 1.51690722  EH4-3:EH4 0.95582109  EH4-5:EH4 -2.24328493  EH4-6:EH4 -2.04956942  EH4-7:EH4 3.08278801  EHSR1-2:EHSR1 0.98534053  ESR2-2:ESR2 0.72640854  ESR2-8:ESR2 1.00250709  WC11-3:WC11 1.41185294  WC11-4:WC11 -1.15032580  WHSR9-1:WHSR9 0.53899643  WHSR9-2:WHSR9 -2.85854782  WHSR9-3:WHSR9 0.91752561  WHSR9-4:WHSR9 -0.42510135  WSR10-1:WSR10 -0.62775139  WSR10-9:WSR10 -1.34908117  CC6-1:CC6 -1.38828381  CC6-6:CC6 -0.95884122  CC6-7:CC6 -1.16414156  CH5-3:CH5 -0.10052794  CH5-4:CH5 1.07325531  CHSR8-1:CHSR8 0.13368478  CHSR8-5:CHSR8 1.36745377  CSR7-1:CSR7 0.47467237  CSR7-3:CSR7 0.78403984  CSR7-5:CSR7 -1.99646857  CSR7-8:CSR7 0.64709566  EC3-1:EC3 0.44326244  EH4-4:EH4 0.60816125  EH4-8:EH4 0.49927352  EH4-9:EH4 -0.10993074  EHSR1-1:EHSR1 -2.11771404  EHSR1-5:EHSR1 -1.15702090  ESR2-6:ESR2 0.12706195  WC11-2:WC11 0.57116049  WC11-5:WC11 -3.06715930  WC11-7:WC11 0.96291247  WSR10-3:WSR10 2.87533396  WSR10-7:WSR10 -0.08309133  $plot  (Intercept)  CC6 -1.0342340  CH5 -1.5093069  CHSR8 4.7210955  CSR7 -0.1737173  EC3 -0.1248690  EH4 0.7076798  EHSR1 -2.1798037  ESR2 1.7671341  WC11 -1.2106911  WHSR9 -1.7396646  WSR10 0.7763773  $`date:year`  (Intercept)  2015-06-02:2015 -2.0606618  2015-06-03:2015 4.0065555  2015-06-06:2015 0.4101130  2015-06-08:2015 1.1455834  2015-06-10:2015 3.2317366  2015-06-11:2015 -6.7333267  2016-06-05:2016 -0.6223493  2016-06-06:2016 -0.1382920  2016-06-07:2016 5.2149946  2016-06-08:2016 -4.4543533  $year  (Intercept)  2015 1.277097e-14  2016 -6.503656e-12  > fixef(modBRIX2)  (Intercept) treatmentH year2016 treatmentH:year2016  17.479111 5.593903 8.264350 -3.717971  > modBRIX2 <- lmer(BRIX ~ treatment\*year + (1|plot/plant) + (1|year:date), data = balssugboth)  > summary(modBRIX2)  Linear mixed model fit by REML ['lmerMod']  Formula: BRIX ~ treatment \* year + (1 | plot/plant) + (1 | year:date)  Data: balssugboth  REML criterion at convergence: 1674.6  Scaled residuals:  Min 1Q Median 3Q Max  -3.2631 -0.6907 -0.0105 0.6510 3.9563  Random effects:  Groups Name Variance Std.Dev.  plant:plot (Intercept) 5.046 2.246  year:date (Intercept) 39.732 6.303  plot (Intercept) 7.617 2.760  Residual 59.121 7.689  Number of obs: 237, groups: plant:plot, 51; year:date, 13; plot, 11  Fixed effects:  Estimate Std. Error t value  (Intercept) 19.702 3.140 6.274  treatmentH 5.968 2.694 2.215  year2016 8.089 4.220 1.917  treatmentH:year2016 -3.975 2.474 -1.607  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.504  year2016 -0.637 0.253  trtmnH:2016 0.367 -0.619 -0.387  > with(balssugboth, plot(as.factor(date), BRIX.grid))  Error in xy.coords(x, y, xlabel, ylabel, log) :  'x' and 'y' lengths differ  > with(balssugboth, plot(as.factor(date), BRIX))  > anova(modBRIX2)  Analysis of Variance Table  Df Sum Sq Mean Sq F value  treatment 1 138.04 138.04 2.3350  year 1 116.50 116.50 1.9706  treatment:year 1 152.64 152.64 2.5819  > modBRIX <- lmer(BRIX ~ treatment \* year + (1|plot/plant) +(1|year:date), data = balssugboth)  > BRIX.grid <- ref.grid(modBRIX)  > summary(BRIX.grid)  treatment year prediction SE df  C 2015 19.70205 3.177432 23.19  H 2015 25.67008 2.952513 17.71  C 2016 27.79060 3.297378 13.57  H 2016 29.78385 3.284991 13.31  > lsmeans(BRIX.grid, "treatment")  NOTE: Results may be misleading due to involvement in interactions  treatment lsmean SE df lower.CL upper.CL  C 23.74632 2.440252 17.96 18.61863 28.87401  H 27.72696 2.399948 15.70 22.63149 32.82243  Results are averaged over the levels of: year  Confidence level used: 0.95  > lsmeans(BRIX.grid, "year")  NOTE: Results may be misleading due to involvement in interactions  year lsmean SE df lower.CL upper.CL  2015 22.68606 2.745218 15.14 16.83932 28.53280  2016 28.78722 3.088389 11.17 22.00211 35.57234  Results are averaged over the levels of: treatment  Confidence level used: 0.95  > BRIX.treat <- lsmeans(BRIX.grid, "treatment")  NOTE: Results may be misleading due to involvement in interactions  > pairs(BRIX.treat)  contrast estimate SE df t.ratio p.value  C - H -3.980639 2.174109 10.75 -1.831 0.0949  Results are averaged over the levels of: year  > library(lubridate)  >  > # Read and minor munging of dataframes  >  > balsam15 <- read.csv("nectar analysis/data files/balsam15.csv", header = T, as.is = T)  > balsam16 <- read.csv("nectar analysis/data files/balsam16.csv", header = T, as.is = T)  > buckwt15 <- read.csv("nectar analysis/data files/buckwt15.csv", header = T, as.is = T)  > buckwt16 <- read.csv("nectar analysis/data files/buckwt16.csv", header = T, as.is = T)  >  > balsam <- rbind(balsam15, balsam16)  > buckwt <- rbind(buckwt15, buckwt16)  >  > rm(balsam15)  > rm(balsam16)  > rm(buckwt15)  > rm(buckwt16)  >  > balsam$date <- ymd(balsam$date)  > balsam$plot <- as.factor(balsam$plot)  > balsam$treatment <- as.factor(balsam$treatment)  > balsam$plant <- as.factor(balsam$plant)  >  > buckwt$date <- ymd(buckwt$date)  > buckwt$plot <- as.factor(buckwt$plot)  > buckwt$treatment <- as.factor(buckwt$treatment)  > buckwt$quad <- as.factor(buckwt$quad)  >  > # Calculate percentage of flowers that are/aren't producing nectar  >  > balscontrol <- subset(balsam, treatment == "C")  > pz.bac <- sum(balscontrol$volume == "0")/nrow(balscontrol)  > pnz.bac <- sum(balscontrol$volume != "0")/nrow(balscontrol)  >  > balsheat <- subset(balsam, treatment == "H")  > pz.bah <- sum(balsheat$volume == "0")/nrow(balsheat)  > pnz.bah <- sum(balsheat$volume != "0")/nrow(balsheat)  >  > buckcontrol <- subset(buckwt, treatment == "C")  > pz.buc <- sum(buckcontrol$volume == "0")/nrow(buckcontrol)  > pnz.buc <- sum(buckcontrol$volume != "0")/nrow(buckcontrol)  >  > buckheat <- subset(buckwt, treatment == "H")  > pz.buh <- sum(buckheat$volume == "0")/nrow(buckheat)  > pnz.buh <- sum(buckheat$volume != "0")/nrow(buckheat)  >  > rm(balscontrol)  > rm(balsheat)  > rm(buckcontrol)  > rm(buckheat)  >  > # Create dataframes for linear analysis  >  > balsam$necpres[balsam$volume != "0"] <- "1"  > balsam$necpres[balsam$volume == "0"] <- "0"  > balsam$necpres <- as.factor(balsam$necpres)  > balsam <- balsam[,-c(5:7)]  >  > buckwt$necpres[buckwt$volume != "0"] <- "1"  > buckwt$necpres[buckwt$volume == "0"] <- "0"  > buckwt$necpres <- as.factor(buckwt$necpres)  > buckwt <- buckwt[,-c(5:7)]  >  > # Models  >  > modbals <- glm(necpres ~ treatment, data = balsam, family = binomial)  > modbuck <- glm(necpres ~ treatment, data = buckwt, family = binomial)  >  > summary(modbals)  Call:  glm(formula = necpres ~ treatment, family = binomial, data = balsam)  Deviance Residuals:  Min 1Q Median 3Q Max  -1.3980 -1.3874 0.9718 0.9810 0.9810  Coefficients:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 0.50509 0.15135 3.337 0.000846 \*\*\*  treatmentH -0.02392 0.20270 -0.118 0.906069  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  (Dispersion parameter for binomial family taken to be 1)  Null deviance: 556.27 on 418 degrees of freedom  Residual deviance: 556.26 on 417 degrees of freedom  AIC: 560.26  Number of Fisher Scoring iterations: 4  > summary(modbuck)  Call:  glm(formula = necpres ~ treatment, family = binomial, data = buckwt)  Deviance Residuals:  Min 1Q Median 3Q Max  -1.9781 0.5521 0.5521 0.6544 0.6544  Coefficients:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 1.4323 0.1107 12.933 <2e-16 \*\*\*  treatmentH 0.3717 0.1714 2.168 0.0302 \*  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  (Dispersion parameter for binomial family taken to be 1)  Null deviance: 910.44 on 1004 degrees of freedom  Residual deviance: 905.68 on 1003 degrees of freedom  AIC: 909.68  Number of Fisher Scoring iterations: 4  > modbals2 <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  Error in model.frame.default(data = balsam, drop.unused.levels = TRUE, :  invalid type (closure) for variable 'year'  > balsam$date <- as.factor(balsam$date)  > modbals2 <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  Error in model.frame.default(data = balsam, drop.unused.levels = TRUE, :  invalid type (closure) for variable 'year'  > balsam$date <- ymd(balsam$date)  > balsam$year <- as.factor(y((balsam$date))  +  +  + buckwt$date <- ymd(buckwt$date)  Error: unexpected symbol in:  "  buckwt"  > buckwt$plot <- as.factor(buckwt$plot)  > buckwt$treatment <- as.factor(buckwt$treatment)  > buckwt$quad <- as.factor(buckwt$quad)  >  > # Calculate percentage of flowers that are/aren't producing nectar  >  > balscontrol <- subset(balsam, treatment == "C")  > pz.bac <- sum(balscontrol$volume == "0")/nrow(balscontrol)  > pnz.bac <- sum(balscontrol$volume != "0")/nrow(balscontrol)  >  > balsheat <- subset(balsam, treatment == "H")  > pz.bah <- sum(balsheat$volume == "0")/nrow(balsheat)  > pnz.bah <- sum(balsheat$volume != "0")/nrow(balsheat)  >  > buckcontrol <- subset(buckwt, treatment == "C")  > pz.buc <- sum(buckcontrol$volume == "0")/nrow(buckcontrol)  > pnz.buc <- sum(buckcontrol$volume != "0")/nrow(buckcontrol)  >  > buckheat <- subset(buckwt, treatment == "H")  > pz.buh <- sum(buckheat$volume == "0")/nrow(buckheat)  > pnz.buh <- sum(buckheat$volume != "0")/nrow(buckheat)  >  > rm(balscontrol)  > rm(balsheat)  > rm(buckcontrol)  > rm(buckheat)  >  > # Create dataframes for linear analysis  >  > balsam$necpres[balsam$volume != "0"] <- "1"  > balsam$necpres[balsam$volume == "0"] <- "0"  > balsam$necpres <- as.factor(balsam$necpres)  > balsam <- balsam[,-c(5:7)]  >  > buckwt$necpres[buckwt$volume != "0"] <- "1"  > buckwt$necpres[buckwt$volume == "0"] <- "0"  > buckwt$necpres <- as.factor(buckwt$necpres)  > buckwt <- buckwt[,-c(5:7)]  >  > # Models  >  > modbals <- glm(necpres ~ treatment, data = balsam, family = binomial)  Error in eval(expr, envir, enclos) : object 'necpres' not found  > modbuck <- glm(necpres ~ treatment, data = buckwt, family = binomial)  Error in eval(expr, envir, enclos) : object 'necpres' not found  >  > modbals2 <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  Error in eval(expr, envir, enclos) : object 'necpres' not found  > balsam$year <- as.factor(y((balsam$date)))  Error in is.factor(x) : could not find function "y"  > balsam$year <- as.factor(year((balsam$date)))  > modbals2 <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  Error in eval(expr, envir, enclos) : object 'necpres' not found  > library(lubridate)  >  > # Read and minor munging of dataframes  >  > balsam15 <- read.csv("nectar analysis/data files/balsam15.csv", header = T, as.is = T)  > balsam16 <- read.csv("nectar analysis/data files/balsam16.csv", header = T, as.is = T)  > buckwt15 <- read.csv("nectar analysis/data files/buckwt15.csv", header = T, as.is = T)  > buckwt16 <- read.csv("nectar analysis/data files/buckwt16.csv", header = T, as.is = T)  >  > balsam <- rbind(balsam15, balsam16)  > buckwt <- rbind(buckwt15, buckwt16)  >  > rm(balsam15)  > rm(balsam16)  > rm(buckwt15)  > rm(buckwt16)  >  > balsam$date <- ymd(balsam$date)  > balsam$plot <- as.factor(balsam$plot)  > balsam$treatment <- as.factor(balsam$treatment)  > balsam$plant <- as.factor(balsam$plant)  > balsam$year <- as.factor(year((balsam$date)))  >  >  > buckwt$date <- ymd(buckwt$date)  > buckwt$plot <- as.factor(buckwt$plot)  > buckwt$treatment <- as.factor(buckwt$treatment)  > buckwt$quad <- as.factor(buckwt$quad)  >  > # Calculate percentage of flowers that are/aren't producing nectar  >  > balscontrol <- subset(balsam, treatment == "C")  > pz.bac <- sum(balscontrol$volume == "0")/nrow(balscontrol)  > pnz.bac <- sum(balscontrol$volume != "0")/nrow(balscontrol)  >  > balsheat <- subset(balsam, treatment == "H")  > pz.bah <- sum(balsheat$volume == "0")/nrow(balsheat)  > pnz.bah <- sum(balsheat$volume != "0")/nrow(balsheat)  >  > buckcontrol <- subset(buckwt, treatment == "C")  > pz.buc <- sum(buckcontrol$volume == "0")/nrow(buckcontrol)  > pnz.buc <- sum(buckcontrol$volume != "0")/nrow(buckcontrol)  >  > buckheat <- subset(buckwt, treatment == "H")  > pz.buh <- sum(buckheat$volume == "0")/nrow(buckheat)  > pnz.buh <- sum(buckheat$volume != "0")/nrow(buckheat)  >  > rm(balscontrol)  > rm(balsheat)  > rm(buckcontrol)  > rm(buckheat)  >  > # Create dataframes for linear analysis  >  > balsam$necpres[balsam$volume != "0"] <- "1"  > balsam$necpres[balsam$volume == "0"] <- "0"  > balsam$necpres <- as.factor(balsam$necpres)  > balsam <- balsam[,-c(5:7)]  >  > buckwt$necpres[buckwt$volume != "0"] <- "1"  > buckwt$necpres[buckwt$volume == "0"] <- "0"  > buckwt$necpres <- as.factor(buckwt$necpres)  > buckwt <- buckwt[,-c(5:7)]  >  > # Models  >  > modbals <- glm(necpres ~ treatment, data = balsam, family = binomial)  > modbuck <- glm(necpres ~ treatment, data = buckwt, family = binomial)  >  > modbals2 <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  > summary(modbals2)  Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [  glmerMod]  Family: binomial ( logit )  Formula: necpres ~ treatment \* year + (1 | plot/plant) + (1 | year:date)  Data: balsam  AIC BIC logLik deviance df.resid  513.6 541.8 -249.8 499.6 412  Scaled residuals:  Min 1Q Median 3Q Max  -2.2901 -0.8135 0.4517 0.6754 2.2653  Random effects:  Groups Name Variance Std.Dev.  plant:plot (Intercept) 0.1692 0.4113  year:date (Intercept) 2.0089 1.4173  plot (Intercept) 0.0000 0.0000  Number of obs: 419, groups: plant:plot, 56; year:date, 13; plot, 11  Fixed effects:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 0.2996 0.6254 0.479 0.6319  treatmentH 0.8095 0.4564 1.774 0.0761 .  year2016 0.1278 0.9153 0.140 0.8890  treatmentH:year2016 -0.7051 0.5305 -1.329 0.1838  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.405  year2016 -0.675 0.264  trtmnH:2016 0.334 -0.810 -0.326  > buckwt$year <- as.factor(year((buckwt$date)))  > modbuck2 <- glmer(necpres ~ treatment \* year + (1|plot) + (1| year:date), data = balsam, family = binomial)  > modbuck2 <- glmer(necpres ~ treatment \* year + (1|plot) + (1| year:date), data = buckwt, family = binomial)  > summary(modbuck2)  Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [  glmerMod]  Family: binomial ( logit )  Formula: necpres ~ treatment \* year + (1 | plot) + (1 | year:date)  Data: buckwt  AIC BIC logLik deviance df.resid  714.6 744.1 -351.3 702.6 999  Scaled residuals:  Min 1Q Median 3Q Max  -9.5158 0.1042 0.1474 0.4449 1.5165  Random effects:  Groups Name Variance Std.Dev.  year:date (Intercept) 0.7917 0.8897  plot (Intercept) 0.3620 0.6016  Number of obs: 1005, groups: year:date, 20; plot, 12  Fixed effects:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 4.3451 0.6325 6.870 6.42e-12 \*\*\*  treatmentH -0.2862 0.7245 -0.395 0.693  year2016 -3.5682 0.6828 -5.226 1.73e-07 \*\*\*  treatmentH:year2016 0.6802 0.6659 1.022 0.307  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.604  year2016 -0.778 0.434  trtmnH:2016 0.509 -0.831 -0.513  > library(lubridate)  >  > # Read and minor munging of dataframes  >  > balsam15 <- read.csv("nectar analysis/data files/balsam15.csv", header = T, as.is = T)  > balsam16 <- read.csv("nectar analysis/data files/balsam16.csv", header = T, as.is = T)  > buckwt15 <- read.csv("nectar analysis/data files/buckwt15.csv", header = T, as.is = T)  > buckwt16 <- read.csv("nectar analysis/data files/buckwt16.csv", header = T, as.is = T)  >  > balsam <- rbind(balsam15, balsam16)  > buckwt <- rbind(buckwt15, buckwt16)  >  > rm(balsam15)  > rm(balsam16)  > rm(buckwt15)  > rm(buckwt16)  >  > balsam$date <- ymd(balsam$date)  > balsam$plot <- as.factor(balsam$plot)  > balsam$treatment <- as.factor(balsam$treatment)  > balsam$plant <- as.factor(balsam$plant)  > balsam$year <- as.factor(year((balsam$date)))  >  >  > buckwt$date <- ymd(buckwt$date)  > buckwt$plot <- as.factor(buckwt$plot)  > buckwt$treatment <- as.factor(buckwt$treatment)  > buckwt$quad <- as.factor(buckwt$quad)  > buckwt$year <- as.factor(year((buckwt$date)))  >  > # Calculate percentage of flowers that are/aren't producing nectar  >  > balscontrol <- subset(balsam, treatment == "C")  > pz.bac <- sum(balscontrol$volume == "0")/nrow(balscontrol)  > pnz.bac <- sum(balscontrol$volume != "0")/nrow(balscontrol)  >  > balsheat <- subset(balsam, treatment == "H")  > pz.bah <- sum(balsheat$volume == "0")/nrow(balsheat)  > pnz.bah <- sum(balsheat$volume != "0")/nrow(balsheat)  >  > buckcontrol <- subset(buckwt, treatment == "C")  > pz.buc <- sum(buckcontrol$volume == "0")/nrow(buckcontrol)  > pnz.buc <- sum(buckcontrol$volume != "0")/nrow(buckcontrol)  >  > buckheat <- subset(buckwt, treatment == "H")  > pz.buh <- sum(buckheat$volume == "0")/nrow(buckheat)  > pnz.buh <- sum(buckheat$volume != "0")/nrow(buckheat)  >  > rm(balscontrol)  > rm(balsheat)  > rm(buckcontrol)  > rm(buckheat)  >  > # Create dataframes for linear analysis  >  > balsam$necpres[balsam$volume != "0"] <- "1"  > balsam$necpres[balsam$volume == "0"] <- "0"  > balsam$necpres <- as.factor(balsam$necpres)  > balsam <- balsam[,-c(5:7)]  >  > buckwt$necpres[buckwt$volume != "0"] <- "1"  > buckwt$necpres[buckwt$volume == "0"] <- "0"  > buckwt$necpres <- as.factor(buckwt$necpres)  > buckwt <- buckwt[,-c(5:7)]  >  > # Models  >  > modbals <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  >  > modbuck <- glmer(necpres ~ treatment \* year + (1|plot) + (1| year:date), data = buckwt, family = binomial)  > modbals <- glmer(necpres ~ treatment \* year + (1|plot) + (1| year:date), data = balsam, family = binomial)  > modbals <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  > summary(modbals)  Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [  glmerMod]  Family: binomial ( logit )  Formula: necpres ~ treatment \* year + (1 | plot/plant) + (1 | year:date)  Data: balsam  AIC BIC logLik deviance df.resid  513.6 541.8 -249.8 499.6 412  Scaled residuals:  Min 1Q Median 3Q Max  -2.2901 -0.8135 0.4517 0.6754 2.2653  Random effects:  Groups Name Variance Std.Dev.  plant:plot (Intercept) 0.1692 0.4113  year:date (Intercept) 2.0089 1.4173  plot (Intercept) 0.0000 0.0000  Number of obs: 419, groups: plant:plot, 56; year:date, 13; plot, 11  Fixed effects:  Estimate Std. 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Error z value Pr(>|z|)  (Intercept) 4.3451 0.6325 6.870 6.42e-12 \*\*\*  treatmentH -0.2862 0.7245 -0.395 0.693  year2016 -3.5682 0.6828 -5.226 1.73e-07 \*\*\*  treatmentH:year2016 0.6802 0.6659 1.022 0.307  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.604  year2016 -0.778 0.434  trtmnH:2016 0.509 -0.831 -0.513  > library(lubridate)  >  > # Read and minor munging of dataframes  >  > balsam15 <- read.csv("nectar analysis/data files/balsam15.csv", header = T, as.is = T)  > balsam16 <- read.csv("nectar analysis/data files/balsam16.csv", header = T, as.is = T)  > buckwt15 <- read.csv("nectar analysis/data files/buckwt15.csv", header = T, as.is = T)  > buckwt16 <- read.csv("nectar analysis/data files/buckwt16.csv", header = T, as.is = T)  >  > balsam <- rbind(balsam15, balsam16)  > buckwt <- rbind(buckwt15, buckwt16)  >  > rm(balsam15)  > rm(balsam16)  > rm(buckwt15)  > rm(buckwt16)  >  > balsam$date <- ymd(balsam$date)  > balsam$plot <- as.factor(balsam$plot)  > balsam$treatment <- as.factor(balsam$treatment)  > balsam$plant <- as.factor(balsam$plant)  > balsam$year <- as.factor(year((balsam$date)))  >  >  > buckwt$date <- ymd(buckwt$date)  > buckwt$plot <- as.factor(buckwt$plot)  > buckwt$treatment <- as.factor(buckwt$treatment)  > buckwt$quad <- as.factor(buckwt$quad)  > buckwt$year <- as.factor(year((buckwt$date)))  >  > # Calculate percentage of flowers that are/aren't producing nectar  >  > balscontrol <- subset(balsam, treatment == "C")  > pz.bac <- sum(balscontrol$volume == "0")/nrow(balscontrol)  > pnz.bac <- sum(balscontrol$volume != "0")/nrow(balscontrol)  >  > balsheat <- subset(balsam, treatment == "H")  > pz.bah <- sum(balsheat$volume == "0")/nrow(balsheat)  > pnz.bah <- sum(balsheat$volume != "0")/nrow(balsheat)  >  > buckcontrol <- subset(buckwt, treatment == "C")  > pz.buc <- sum(buckcontrol$volume == "0")/nrow(buckcontrol)  > pnz.buc <- sum(buckcontrol$volume != "0")/nrow(buckcontrol)  >  > buckheat <- subset(buckwt, treatment == "H")  > pz.buh <- sum(buckheat$volume == "0")/nrow(buckheat)  > pnz.buh <- sum(buckheat$volume != "0")/nrow(buckheat)  >  > rm(balscontrol)  > rm(balsheat)  > rm(buckcontrol)  > rm(buckheat)  >  > # Create dataframes for linear analysis  >  > balsam$necpres[balsam$volume != "0"] <- "1"  > balsam$necpres[balsam$volume == "0"] <- "0"  > balsam$necpres <- as.factor(balsam$necpres)  > balsam <- balsam[,-c(5:7)]  >  > buckwt$necpres[buckwt$volume != "0"] <- "1"  > buckwt$necpres[buckwt$volume == "0"] <- "0"  > buckwt$necpres <- as.factor(buckwt$necpres)  > buckwt <- buckwt[,-c(5:7)]  >  > # Models  >  > modbals <- glmer(necpres ~ treatment \* year + (1|plot/plant) + (1| year:date), data = balsam, family = binomial)  > summary(modbals)  Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [  glmerMod]  Family: binomial ( logit )  Formula: necpres ~ treatment \* year + (1 | plot/plant) + (1 | year:date)  Data: balsam  AIC BIC logLik deviance df.resid  513.6 541.8 -249.8 499.6 412  Scaled residuals:  Min 1Q Median 3Q Max  -2.2901 -0.8135 0.4517 0.6754 2.2653  Random effects:  Groups Name Variance Std.Dev.  plant:plot (Intercept) 0.1692 0.4113  year:date (Intercept) 2.0089 1.4173  plot (Intercept) 0.0000 0.0000  Number of obs: 419, groups: plant:plot, 56; year:date, 13; plot, 11  Fixed effects:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 0.2996 0.6254 0.479 0.6319  treatmentH 0.8095 0.4564 1.774 0.0761 .  year2016 0.1278 0.9153 0.140 0.8890  treatmentH:year2016 -0.7051 0.5305 -1.329 0.1838  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.405  year2016 -0.675 0.264  trtmnH:2016 0.334 -0.810 -0.326  >  > modbuck <- glmer(necpres ~ treatment \* year + (1|plot) + (1| year:date), data = buckwt, family = binomial)  > summary(modbuck)  Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [  glmerMod]  Family: binomial ( logit )  Formula: necpres ~ treatment \* year + (1 | plot) + (1 | year:date)  Data: buckwt  AIC BIC logLik deviance df.resid  714.6 744.1 -351.3 702.6 999  Scaled residuals:  Min 1Q Median 3Q Max  -9.5158 0.1042 0.1474 0.4449 1.5165  Random effects:  Groups Name Variance Std.Dev.  year:date (Intercept) 0.7917 0.8897  plot (Intercept) 0.3620 0.6016  Number of obs: 1005, groups: year:date, 20; plot, 12  Fixed effects:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 4.3451 0.6325 6.870 6.42e-12 \*\*\*  treatmentH -0.2862 0.7245 -0.395 0.693  year2016 -3.5682 0.6828 -5.226 1.73e-07 \*\*\*  treatmentH:year2016 0.6802 0.6659 1.022 0.307  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Correlation of Fixed Effects:  (Intr) trtmnH yr2016  treatmentH -0.604  year2016 -0.778 0.434  trtmnH:2016 0.509 -0.831 -0.513  > plot(as.factor(balsam$date), balsam$BRIX)  > balsam15 <- read.csv("nectar analysis/data files/balsam15.csv", header = T, as.is = T)  > balsam16 <- read.csv("nectar analysis/data files/balsam16.csv", header = T, as.is = T)  > buckwt15 <- read.csv("nectar analysis/data files/buckwt15.csv", header = T, as.is = T)  > buckwt16 <- read.csv("nectar analysis/data files/buckwt16.csv", header = T, as.is = T)  >  > balsam <- rbind(balsam15, balsam16)  > buckwt <- rbind(buckwt15, buckwt16)  >  > rm(balsam15)  > rm(balsam16)  > rm(buckwt15)  > rm(buckwt16)  >  > balsam$date <- ymd(balsam$date)  > balsam$plot <- as.factor(balsam$plot)  > balsam$treatment <- as.factor(balsam$treatment)  > balsam$plant <- as.factor(balsam$plant)  > balsam$year <- as.factor(year((balsam$date)))  >  >  > buckwt$date <- ymd(buckwt$date)  > buckwt$plot <- as.factor(buckwt$plot)  > buckwt$treatment <- as.factor(buckwt$treatment)  > buckwt$quad <- as.factor(buckwt$quad)  > buckwt$year <- as.factor(year((buckwt$date)))  > plot(as.factor(balsam$date), balsam$BRIX)  > plot(as.factor(buckwt$date), buckwt$BRIX)  > with(balsam, table(date, treatment))  treatment  date C H  2015-06-02 4 2  2015-06-03 5 12  2015-06-06 6 9  2015-06-08 13 18  2015-06-10 10 11  2015-06-11 9 16  2015-06-12 3 9  2015-06-13 6 23  2016-06-05 10 22  2016-06-06 32 16  2016-06-07 40 40  2016-06-08 41 33  2016-06-16 7 22 |
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