Block\_assay\_statistical\_analyses

Ingrid Knapp

11/05/2020

**Set seed**

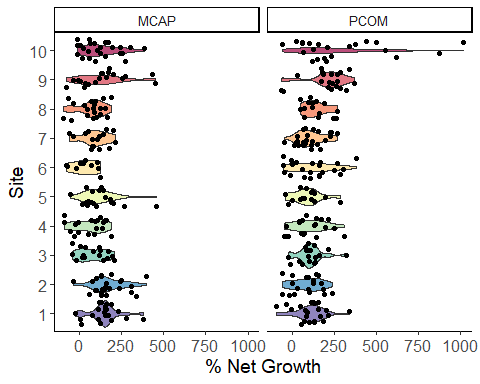
set.seed(1234)

**Load data**

## site mean median lower upper  
## 1 1 127.30170 130.37445 37.676936 216.9265  
## 2 2 135.42016 130.63332 34.006174 236.8342  
## 3 3 91.05749 93.95791 10.807228 171.3078  
## 4 4 80.68854 85.06870 -13.626991 175.0041  
## 5 5 106.29663 89.57705 6.275354 206.3179  
## 6 6 91.30222 87.45962 -26.430945 209.0354

**Plots\_Net\_growth**

#Boxplot-a more familiar output, but not in publication  
# All sites  
#boxplots\_all\_sites <- ggplot(data=df.g) +   
 # geom\_boxplot(aes(x=site, y=PercentNetGrowth, fill=site)) +   
 # facet\_wrap(vars(species)) +   
 # labs(x="Site", y="Percent net growth") +   
 # theme\_classic() +  
 # scale\_fill\_brewer(palette = "Spectral", direction = -1)+  
# geom\_jitter(aes(x=site, y=PercentNetGrowth))  
  
#boxplots\_all\_sites  
  
#violin plot  
  
# Flip axes  
  
violin\_all\_sites\_flipped <- ggplot(data = df.g, aes(y = site, x = PercentNetGrowth, fill = site, draw\_quantiles)) +  
geom\_violin(position = position\_nudge(x = 0, y = 0), alpha=0.7) +  
geom\_point(aes(x = PercentNetGrowth), position = position\_jitter(width = 0.15), size = 1.4) +  
expand\_limits(y = 5) +  
guides(fill = guide\_legend(reverse = TRUE)) +  
facet\_wrap(vars(species)) +   
labs(x="% Net Growth", y="Site") +   
scale\_color\_brewer(palette = "Spectral",direction = -1) +  
scale\_fill\_brewer(palette = "Spectral", direction = -1)+  
theme\_classic()+  
raincloud\_theme  
  
violin\_all\_sites\_flipped



**MCAP\_stats\_Net\_growth**

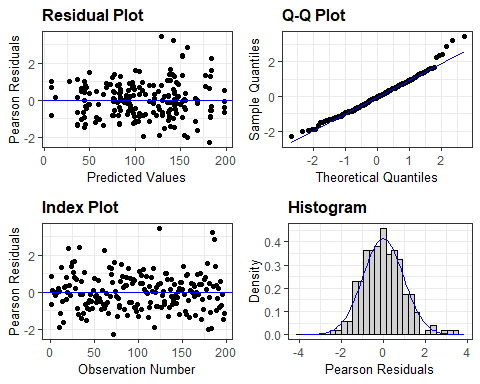
# Sites seperated (10 sites total)  
lm.growth.MCAP <- lmer(PercentNetGrowth ~ site + (1| genotype), data = subset(df.g,species=="MCAP"))  
summary(lm.growth.MCAP)

## Linear mixed model fit by REML ['lmerMod']  
## Formula: PercentNetGrowth ~ site + (1 | genotype)  
## Data: subset(df.g, species == "MCAP")  
##   
## REML criterion at convergence: 2271.5  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.2858 -0.6679 -0.0124 0.5877 3.4471   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## genotype (Intercept) 640.9 25.32   
## Residual 9071.8 95.25   
## Number of obs: 197, groups: genotype, 9  
##   
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 140.70 22.12 6.361  
## site2 29.28 27.67 1.058  
## site3 -70.87 30.41 -2.331  
## site4 -79.52 29.97 -2.653  
## site5 -25.01 29.92 -0.836  
## site6 -108.93 36.47 -2.987  
## site7 -60.15 30.86 -1.949  
## site8 -71.79 29.58 -2.427  
## site9 -11.53 29.46 -0.391  
## site10 -16.27 27.67 -0.588  
##   
## Correlation of Fixed Effects:  
## (Intr) site2 site3 site4 site5 site6 site7 site8 site9   
## site2 -0.679   
## site3 -0.615 0.494   
## site4 -0.630 0.502 0.454   
## site5 -0.626 0.503 0.456 0.461   
## site6 -0.510 0.411 0.372 0.379 0.381   
## site7 -0.605 0.485 0.438 0.445 0.448 0.367   
## site8 -0.637 0.510 0.460 0.471 0.472 0.388 0.453   
## site9 -0.637 0.509 0.461 0.471 0.469 0.385 0.455 0.477   
## site10 -0.680 0.543 0.490 0.502 0.501 0.411 0.486 0.511 0.509

Anova(lm.growth.MCAP, type = 3)

## Analysis of Deviance Table (Type III Wald chisquare tests)  
##   
## Response: PercentNetGrowth  
## Chisq Df Pr(>Chisq)   
## (Intercept) 40.459 1 2.008e-10 \*\*\*  
## site 33.986 9 8.983e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#normality/HOV  
resid\_panel(lm.growth.MCAP, plots = "default", type = NA, bins = 30,  
 smoother = FALSE, qqline = TRUE, qqbands = FALSE, scale = 1,  
 theme = "bw", axis.text.size = 10, title.text.size = 12,  
 title.opt = TRUE, nrow = NULL)

 **Porites\_compressa\_Net\_Growth**

# Sites seperated (10 sites total)  
lm.growth.PCOM <- lmer(sqrt(PercentNetGrowth) ~ site + (1| genotype), data = subset(df.g,species=="PCOM"))

## Warning in sqrt(PercentNetGrowth): NaNs produced  
  
## Warning in sqrt(PercentNetGrowth): NaNs produced  
  
## Warning in sqrt(PercentNetGrowth): NaNs produced

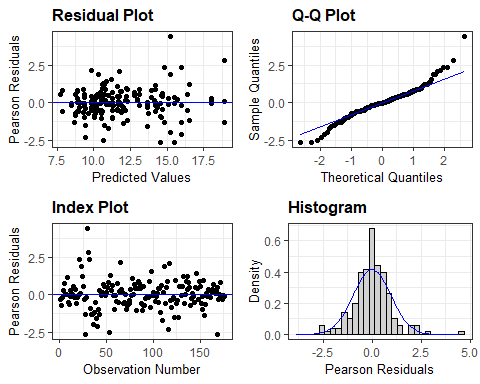
summary(lm.growth.PCOM)

## Linear mixed model fit by REML ['lmerMod']  
## Formula: sqrt(PercentNetGrowth) ~ site + (1 | genotype)  
## Data: subset(df.g, species == "PCOM")  
##   
## REML criterion at convergence: 951.9  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.6595 -0.5437 -0.0219 0.4929 4.4194   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## genotype (Intercept) 2.896 1.702   
## Residual 14.129 3.759   
## Number of obs: 176, groups: genotype, 9  
##   
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 11.0055 1.0411 10.571  
## site2 -1.2182 1.3069 -0.932  
## site3 -0.0462 1.2871 -0.036  
## site4 -0.0367 1.2645 -0.029  
## site5 -0.5096 1.3935 -0.366  
## site6 0.4623 1.2578 0.368  
## site7 -1.1221 1.1479 -0.978  
## site8 0.3725 1.3026 0.286  
## site9 3.8157 1.2238 3.118  
## site10 4.6992 1.1940 3.936  
##   
## Correlation of Fixed Effects:  
## (Intr) site2 site3 site4 site5 site6 site7 site8 site9   
## site2 -0.555   
## site3 -0.572 0.451   
## site4 -0.579 0.456 0.472   
## site5 -0.523 0.411 0.427 0.433   
## site6 -0.572 0.456 0.462 0.471 0.425   
## site7 -0.631 0.501 0.512 0.519 0.469 0.519   
## site8 -0.554 0.439 0.449 0.455 0.413 0.454 0.499   
## site9 -0.593 0.469 0.481 0.489 0.443 0.485 0.533 0.471   
## site10 -0.606 0.480 0.492 0.499 0.452 0.495 0.546 0.480 0.513

Anova(lm.growth.PCOM, type = 2)

## Analysis of Deviance Table (Type II Wald chisquare tests)  
##   
## Response: sqrt(PercentNetGrowth)  
## Chisq Df Pr(>Chisq)   
## site 49.543 9 1.313e-07 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#normality/HOV  
resid\_panel(lm.growth.PCOM, plots = "default", type = NA, bins = 30,  
 smoother = FALSE, qqline = TRUE, qqbands = FALSE, scale = 1,  
 theme = "bw", axis.text.size = 10, title.text.size = 12,  
 title.opt = TRUE, nrow = NULL)



**Survivorship**

**MCAP\_Survivorship**

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: alive\_2 ~ site + (1 | genotype)  
## Data: subset(df.survivorship.outplantalive, species == "MCAP")  
## Control: glmerControl(tolPwrss = 0.001, optimizer = "nloptwrap")  
##   
## AIC BIC logLik deviance df.resid   
## 281.6 321.1 -129.8 259.6 256   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -4.4745 -0.5518 0.3233 0.5951 1.5229   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## genotype (Intercept) 0.3641 0.6034   
## Number of obs: 267, groups: genotype, 9  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 2.0904 0.6599 3.168 0.001536 \*\*   
## site2 1.2099 1.1970 1.011 0.312120   
## site3 -1.8106 0.7352 -2.463 0.013791 \*   
## site4 -0.4987 0.8427 -0.592 0.554023   
## site5 -0.9201 0.7904 -1.164 0.244410   
## site6 -2.6281 0.7672 -3.425 0.000614 \*\*\*  
## site7 -1.5003 0.7513 -1.997 0.045823 \*   
## site8 -1.5860 0.7336 -2.162 0.030628 \*   
## site9 -0.4121 0.8390 -0.491 0.623359   
## site10 0.5136 0.9683 0.530 0.595801   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) site2 site3 site4 site5 site6 site7 site8 site9   
## site2 -0.495   
## site3 -0.816 0.445   
## site4 -0.706 0.388 0.635   
## site5 -0.754 0.414 0.679 0.589   
## site6 -0.788 0.426 0.710 0.610 0.652   
## site7 -0.792 0.434 0.712 0.618 0.660 0.686   
## site8 -0.815 0.446 0.734 0.635 0.679 0.707 0.712   
## site9 -0.707 0.389 0.634 0.552 0.589 0.610 0.620 0.635   
## site10 -0.613 0.337 0.551 0.480 0.512 0.529 0.538 0.551 0.481

## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.

## Warning: The null model is correct only if all variables used by the original  
## model remain unchanged.

## R2m R2c  
## theoretical 0.2521079 0.3266327  
## delta 0.1855130 0.2403519

**PCOM\_Survivorship**

glm1.survival.PCOM <- glmer(alive\_2 ~   
 site + (1|genotype),  
 data = subset(df.survivorship.outplantalive, species=="PCOM"),  
 family = binomial (link = "logit"),   
 control = glmerControl(tolPwrss=1e-3, optimizer = "nloptwrap"))

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  
## Model failed to converge with max|grad| = 0.02784 (tol = 0.002, component 1)

summary(glm1.survival.PCOM)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: alive\_2 ~ site + (1 | genotype)  
## Data: subset(df.survivorship.outplantalive, species == "PCOM")  
## Control: glmerControl(tolPwrss = 0.001, optimizer = "nloptwrap")  
##   
## AIC BIC logLik deviance df.resid   
## 216.8 255.0 -97.4 194.8 226   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -4.1660 0.2778 0.3567 0.4169 0.8544   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## genotype (Intercept) 0.1236 0.3516   
## Number of obs: 237, groups: genotype, 9  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.97012 0.62621 3.146 0.00165 \*\*  
## site2 -0.04324 0.88561 -0.049 0.96106   
## site3 -1.01188 0.76251 -1.327 0.18450   
## site4 -0.27744 0.82696 -0.335 0.73725   
## site5 -1.21787 0.76952 -1.583 0.11351   
## site6 0.39643 0.96397 0.411 0.68089   
## site7 -0.28566 0.78939 -0.362 0.71745   
## site8 0.72801 1.20144 0.606 0.54455   
## site9 0.04981 0.88075 0.057 0.95490   
## site10 0.50014 0.97031 0.515 0.60624   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) site2 site3 site4 site5 site6 site7 site8 site9   
## site2 -0.683   
## site3 -0.792 0.565   
## site4 -0.731 0.526 0.602   
## site5 -0.784 0.554 0.644 0.593   
## site6 -0.626 0.447 0.515 0.477 0.508   
## site7 -0.765 0.552 0.631 0.585 0.621 0.499   
## site8 -0.502 0.354 0.412 0.379 0.409 0.326 0.398   
## site9 -0.687 0.501 0.567 0.528 0.557 0.450 0.553 0.357   
## site10 -0.624 0.457 0.515 0.481 0.505 0.409 0.503 0.323 0.457  
## optimizer (nloptwrap) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.02784 (tol = 0.002, component 1)

r.squaredGLMM(glm1.survival.PCOM)

## Warning: The null model is correct only if all variables used by the original  
## model remain unchanged.

## R2m R2c  
## theoretical 0.08595059 0.11905087  
## delta 0.04017875 0.05565191