GlasshouseTrials\_Pcontorta

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## R Markdown

GlasshouseTrial\_Pcontorta <- read.delim("GlasshouseTrial\_Pcontorta.txt")  
  
GlasshouseTrial\_Pcontorta$Adjusted.Height..mm. <- as.numeric(GlasshouseTrial\_Pcontorta$Adjusted.Height..mm.)  
  
GlasshouseTrial\_Pcontorta$DBB..mm. <- as.numeric(GlasshouseTrial\_Pcontorta$DBB..mm.)

## Warning: NAs introduced by coercion

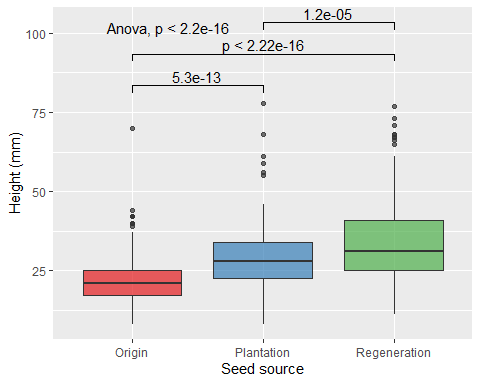
GlasshouseTrial\_Pcontorta$Type <- as.factor(GlasshouseTrial\_Pcontorta$Type)  
  
GlasshouseTrial\_Pcontorta$Provenance <- as.factor(GlasshouseTrial\_Pcontorta$Provenance)  
  
GlasshouseTrial\_Pcontorta$Collection.site..UK. <- as.factor(GlasshouseTrial\_Pcontorta$Collection.site..UK.)

my\_comparisons <- list( c("Origin", "Plantation"), c("Origin", "Regeneration"), c("Plantation", "Regeneration") )  
  
  
###Height   
  
TypePlot\_Height <- ggplot(GlasshouseTrial\_Pcontorta, aes(x=Type, y=Adjusted.Height..mm., fill=Type)) +  
 geom\_boxplot(alpha=0.7) +  
 theme(legend.position="none") +  
 scale\_fill\_brewer(palette="Set1") +  
 xlab("Seed source") + ylab("Height (mm)") +  
 stat\_compare\_means(method= "t.test", comparisons = my\_comparisons, label.y = c(80, 90, 100), hide.ns = TRUE) +  
 stat\_compare\_means(method= "anova", label.y = 100)  
TypePlot\_Height

## Warning: Removed 125 rows containing non-finite values (`stat\_boxplot()`).

## Warning: Removed 125 rows containing non-finite values (`stat\_signif()`).

## Warning: Removed 125 rows containing non-finite values  
## (`stat\_compare\_means()`).

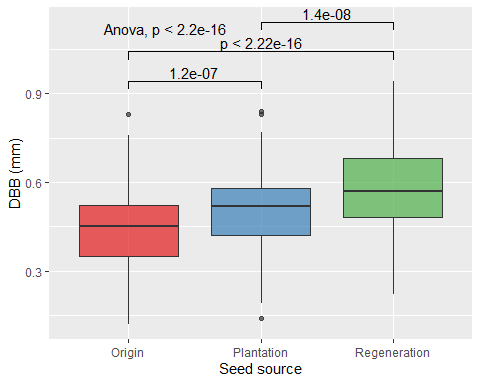


##DBB  
TypePlot\_DBB <- ggplot(GlasshouseTrial\_Pcontorta, aes(x=Type, y=DBB..mm., fill=Type)) +  
 geom\_boxplot(alpha=0.7) +  
 theme(legend.position="none") +  
 scale\_fill\_brewer(palette="Set1") +  
 xlab("Seed source") + ylab("DBB (mm)") +  
 stat\_compare\_means(method= "t.test", comparisons = my\_comparisons, label.y = c(0.90, 1, 1.1), hide.ns = TRUE) +  
 stat\_compare\_means(method= "anova", label.y = 1.1)  
TypePlot\_DBB

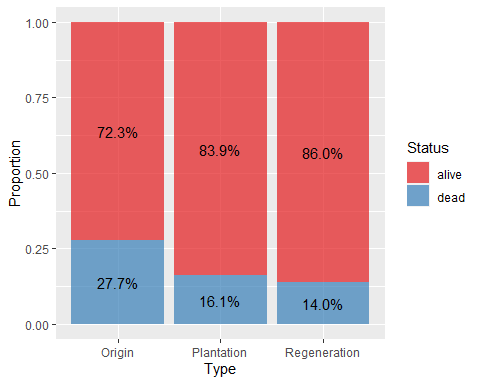
## Warning: Removed 27 rows containing non-finite values (`stat\_boxplot()`).

## Warning: Removed 27 rows containing non-finite values (`stat\_signif()`).

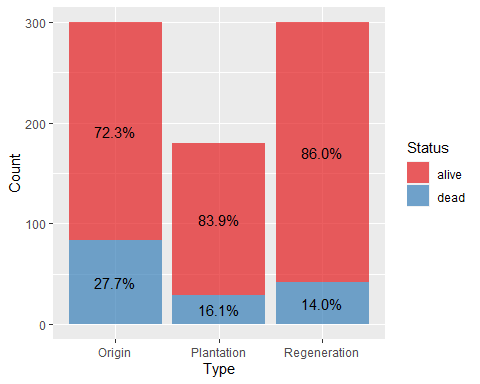
## Warning: Removed 27 rows containing non-finite values (`stat\_compare\_means()`).



TypePlot\_ProportionMortality <- ggplot(GlasshouseTrial\_Pcontorta) +  
 aes(x = Type, fill = Status, by = Type) +  
 geom\_bar(position = "fill", alpha=0.7) +  
 geom\_text(stat = "prop", position = position\_fill(.5)) +  
 xlab("Type") + ylab("Proportion") +  
 scale\_fill\_brewer(palette = "Set1", name="Status")  
TypePlot\_ProportionMortality

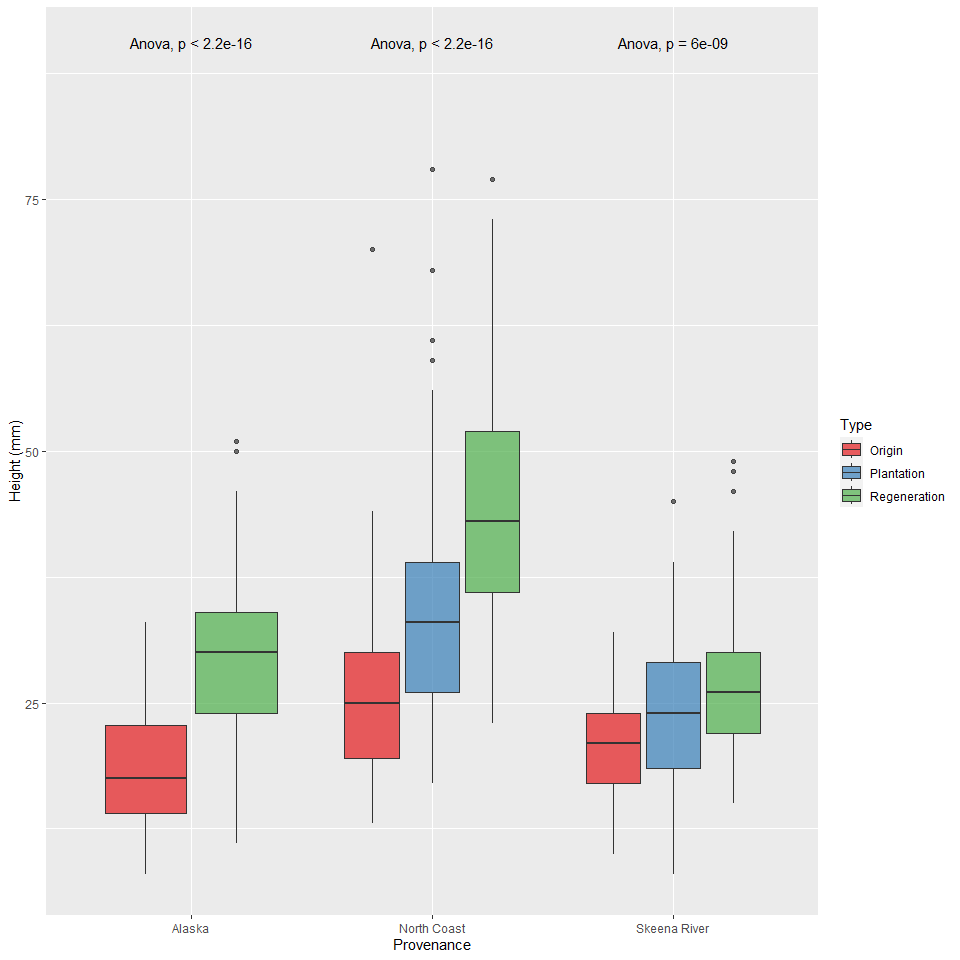


TypePlot\_CountMortality <- ggplot(GlasshouseTrial\_Pcontorta) +  
 aes(x = Type, fill = Status, by = Type) +  
 geom\_bar(alpha=0.7) +  
 geom\_text(stat = "prop", position = position\_stack(.5)) +  
 xlab("Type") + ylab("Count") +  
 scale\_fill\_brewer(palette = "Set1", name="Status")  
TypePlot\_CountMortality



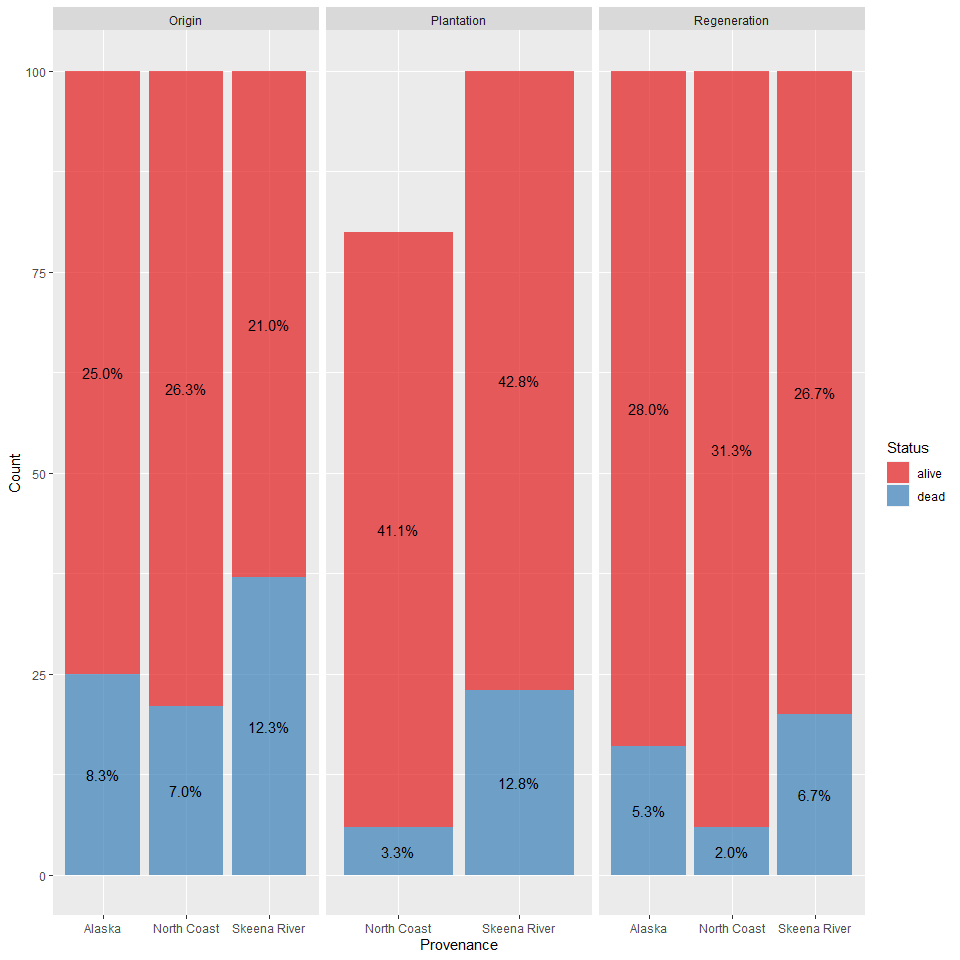
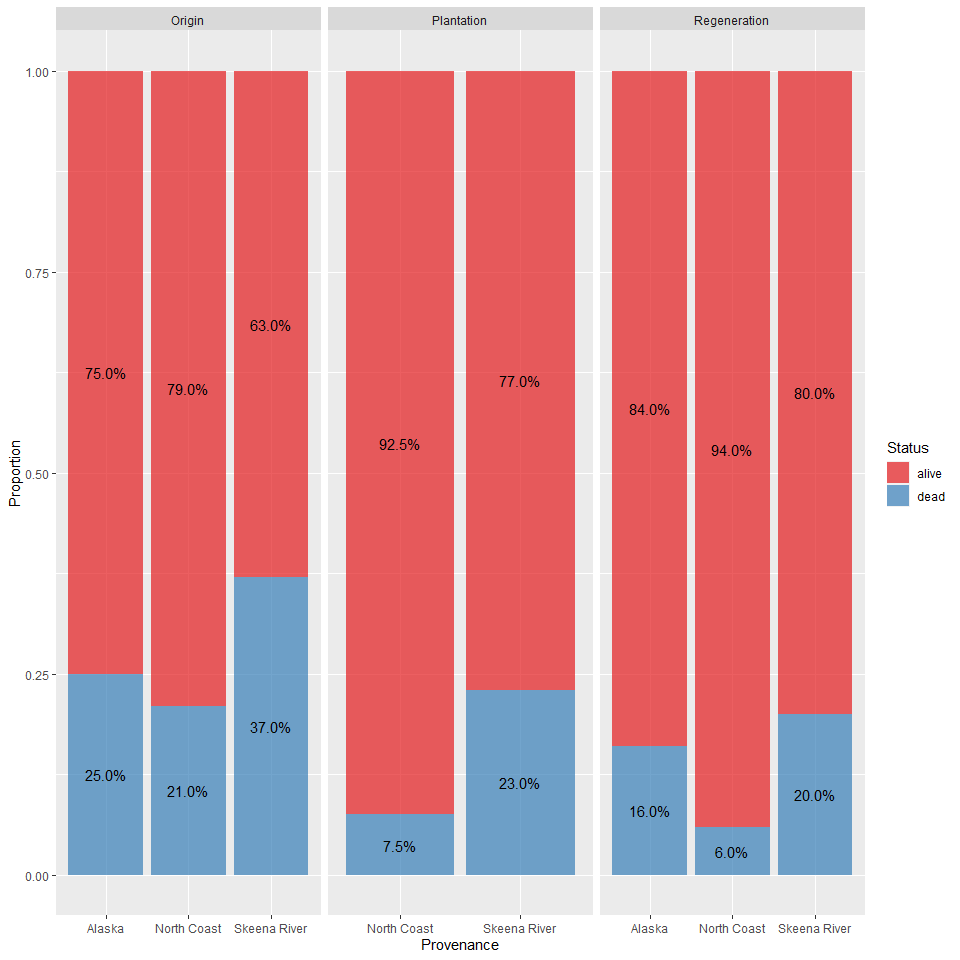
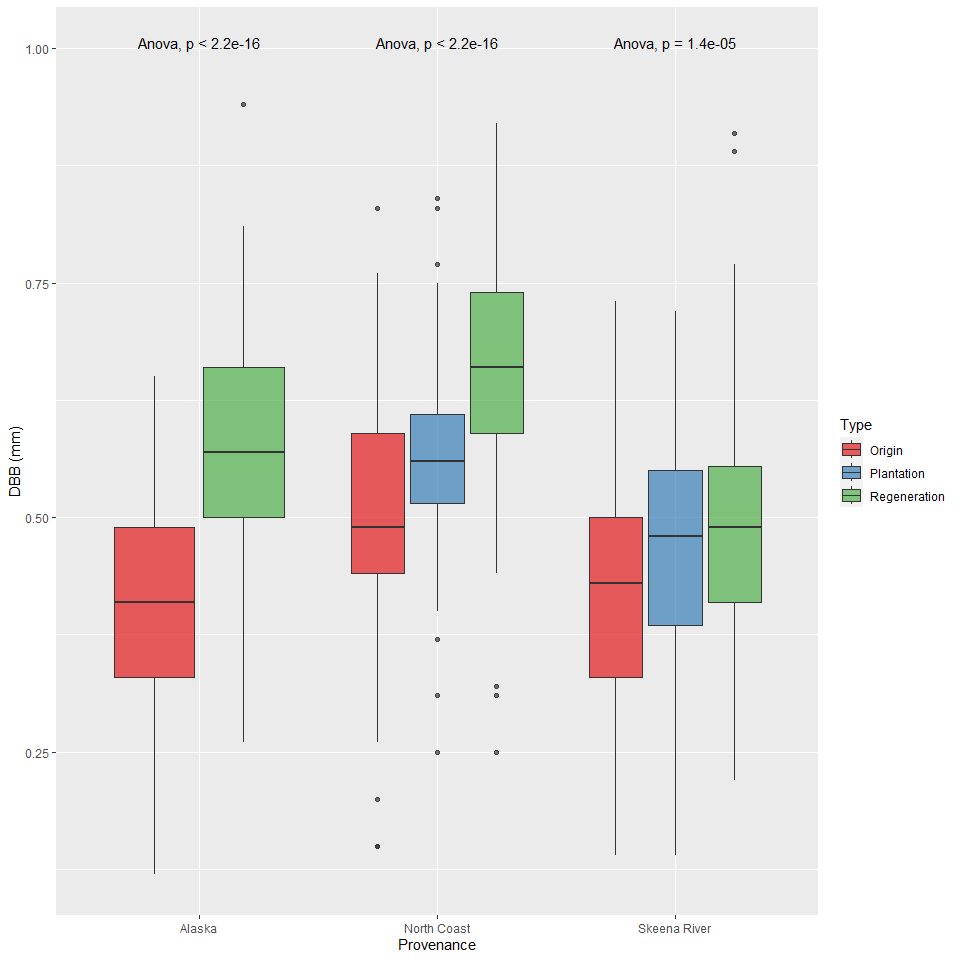
## Warning: Removed 125 rows containing non-finite values (`stat\_boxplot()`).

## Warning: Removed 125 rows containing non-finite values  
## (`stat\_compare\_means()`).



## Warning: Removed 27 rows containing non-finite values (`stat\_boxplot()`).

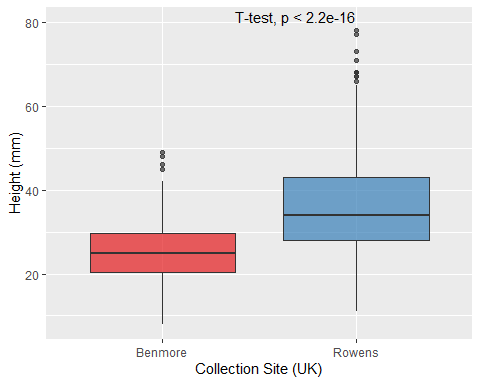
## Warning: Removed 27 rows containing non-finite values (`stat\_compare\_means()`).



###Height   
  
GlasshouseTrial\_Pcontorta\_UKCollections <- GlasshouseTrial\_Pcontorta[which(GlasshouseTrial\_Pcontorta$Type %in% c("Plantation", "Regeneration")), ]  
  
CollectionSitePlot\_Height <- ggplot(GlasshouseTrial\_Pcontorta\_UKCollections, aes(x=Collection.site..UK., y=Adjusted.Height..mm., fill=Collection.site..UK.)) +  
 geom\_boxplot(alpha=0.7) +  
 theme(legend.position="none") +  
 scale\_fill\_brewer(palette="Set1") +  
 xlab("Collection Site (UK)") + ylab("Height (mm)") +  
 stat\_compare\_means(method = "t.test",label.x = 1.5, label.y = 80)   
CollectionSitePlot\_Height

## Warning: Removed 51 rows containing non-finite values (`stat\_boxplot()`).

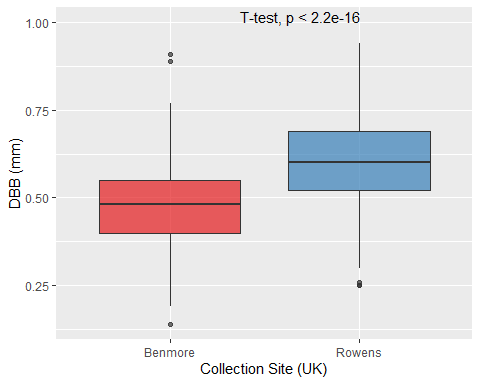
## Warning: Removed 51 rows containing non-finite values (`stat\_compare\_means()`).



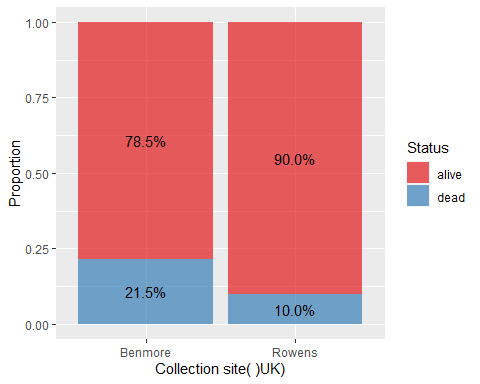
##DBB  
  
CollectionSitePlot\_DBB <- ggplot(GlasshouseTrial\_Pcontorta\_UKCollections, aes(x=Collection.site..UK., y=DBB..mm., fill=Collection.site..UK.)) +  
 geom\_boxplot(alpha=0.7) +  
 theme(legend.position="none") +  
 scale\_fill\_brewer(palette="Set1") +  
 xlab("Collection Site (UK)") + ylab("DBB (mm)") +  
 stat\_compare\_means(method = "t.test",label.x = 1.5, label.y = 1)   
CollectionSitePlot\_DBB

## Warning: Removed 7 rows containing non-finite values (`stat\_boxplot()`).

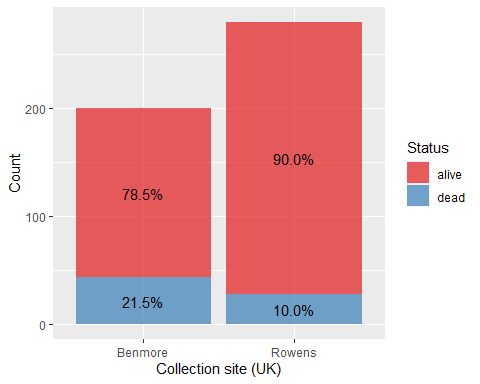
## Warning: Removed 7 rows containing non-finite values (`stat\_compare\_means()`).



CollectionSitePlot\_ProportionMortality <- ggplot(GlasshouseTrial\_Pcontorta\_UKCollections) +  
 aes(x = Collection.site..UK., fill = Status, by = Collection.site..UK.) +  
 geom\_bar(position = "fill", alpha=0.7) +  
 geom\_text(stat = "prop", position = position\_fill(.5)) +  
 xlab("Collection site( )UK)") + ylab("Proportion") +  
 scale\_fill\_brewer(palette = "Set1", name="Status")  
CollectionSitePlot\_ProportionMortality



CollectionSitePlot\_CountMortality <- ggplot(GlasshouseTrial\_Pcontorta\_UKCollections) +  
 aes(x = Collection.site..UK., fill = Status, by = Collection.site..UK.) +  
 geom\_bar(alpha=0.7) +  
 geom\_text(stat = "prop", position = position\_stack(.5)) +  
 xlab("Collection site (UK)") + ylab("Count") +  
 scale\_fill\_brewer(palette = "Set1", name="Status")  
CollectionSitePlot\_CountMortality



Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.