Eradication Effectiveness Binary

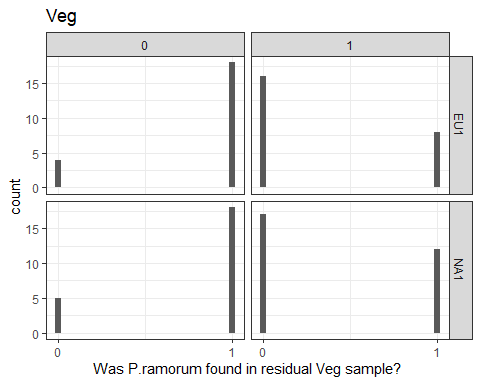
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15 Jan 2021

#Visualizing raw site data

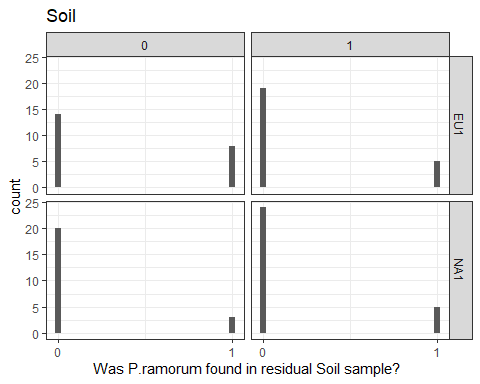
ggplot(AllSites, aes(x=x)) +  
 geom\_histogram( aes(x = VegBin, y = stat(count))) +  
 scale\_x\_continuous(name = "Was P.ramorum found in residual Veg sample?", breaks = seq(0, 1)) +  
 facet\_grid(Lineage ~ TrtBin) +  
 labs(title = "Veg") +  
 theme\_bw()

## `stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.



ggplot(AllSites, aes(x=x)) +  
 geom\_histogram( aes(x = SoilBin, y = stat(count))) +  
 scale\_x\_continuous(name = "Was P.ramorum found in residual Soil sample?", breaks = seq(0, 1)) +  
 facet\_grid(Lineage ~ TrtBin) +  
 labs(title = "Soil") +  
 theme\_bw()

## `stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.

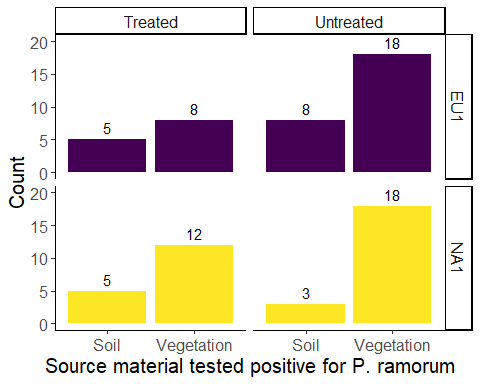


Trt <- c(rep("Untreated", 4), rep("Treated", 4))  
Lin <- c("EU1","EU1","NA1","NA1","EU1","EU1","NA1","NA1")  
Tis <- c("Vegetation","Soil","Vegetation","Soil","Vegetation","Soil","Vegetation","Soil")  
Count <- c(18,8,18,3,8,5,12,5)  
df <- data.frame(Trt,Lin,Tis,Count)  
df

## Trt Lin Tis Count  
## 1 Untreated EU1 Vegetation 18  
## 2 Untreated EU1 Soil 8  
## 3 Untreated NA1 Vegetation 18  
## 4 Untreated NA1 Soil 3  
## 5 Treated EU1 Vegetation 8  
## 6 Treated EU1 Soil 5  
## 7 Treated NA1 Vegetation 12  
## 8 Treated NA1 Soil 5

ggplot(df,aes(x=Tis,y=Count,fill=Lin))+  
 geom\_bar(stat="identity",position="dodge")+  
 scale\_fill\_discrete(name="Lineage",labels=c("EU1", "NA1"))+  
 scale\_fill\_viridis\_d() +  
 theme\_classic()+  
 theme(legend.position="none", text = element\_text(size=15))+  
 xlab("Source material tested positive for P. ramorum")+  
 ylab("Count")+  
 ylim(0, 20)+  
 geom\_text(aes(label = Count), vjust = -0.5)+  
 facet\_grid(Lin~Trt)

## Scale for 'fill' is already present. Adding another scale for 'fill', which  
## will replace the existing scale.



#Raw vegetation data seems to show that, for untreated sites (0 column) many were positive for P.ramorum (both NA1 and EU1). For treated sites (1 column) fewer sites tested positive than negative.  
  
#Raw soil data seems to show that, regardless of treatment, fewer sites tested positive for P.ramorum than negative.

# Binomial Vegetation

## Generally

#Fitting a binomial model  
veg\_null = glm(VegBin~1, family = binomial, data=AllSites)  
veg\_full = glm(VegBin~Lineage \* WFBin \* TrtBin \* SoilBin, family=binomial, data=AllSites)  
step(veg\_null, scope = list(upper=veg\_full), direction="both", test="Chisq", data=AllSites)

## Start: AIC=135.85  
## VegBin ~ 1  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + TrtBin 1 115.29 119.29 18.5616 1.645e-05 \*\*\*  
## + SoilBin 1 119.84 123.84 14.0136 0.0001815 \*\*\*  
## + WFBin 1 130.81 134.81 3.0393 0.0812711 .   
## <none> 133.85 135.85   
## + Lineage 1 133.84 137.84 0.0137 0.9069750   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=119.29  
## VegBin ~ TrtBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + SoilBin 1 100.88 106.88 14.4066 0.0001473 \*\*\*  
## <none> 115.29 119.29   
## + Lineage 1 115.20 121.20 0.0883 0.7663156   
## + WFBin 1 115.25 121.25 0.0333 0.8553100   
## - TrtBin 1 133.85 135.85 18.5616 1.645e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=106.88  
## VegBin ~ TrtBin + SoilBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## <none> 100.882 106.88   
## + TrtBin:SoilBin 1 99.207 107.21 1.6753 0.1955494   
## + Lineage 1 100.314 108.31 0.5681 0.4510246   
## + WFBin 1 100.759 108.76 0.1227 0.7260722   
## - SoilBin 1 115.288 119.29 14.4066 0.0001473 \*\*\*  
## - TrtBin 1 119.836 123.84 18.9546 1.339e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = VegBin ~ TrtBin + SoilBin, family = binomial, data = AllSites)  
##   
## Coefficients:  
## (Intercept) TrtBin SoilBin   
## 1.065 -2.048 2.558   
##   
## Degrees of Freedom: 97 Total (i.e. Null); 95 Residual  
## Null Deviance: 133.8   
## Residual Deviance: 100.9 AIC: 106.9

#VegBin ~ TrtBin + SoilBin  
  
#Is positive veg predicted by treatment and positive soil? (model from stepwise fit)  
LRVeg\_Gen <- glm(VegBin ~ TrtBin + SoilBin, family=binomial, data=AllSites)  
summary(LRVeg\_Gen)

##   
## Call:  
## glm(formula = VegBin ~ TrtBin + SoilBin, family = binomial, data = AllSites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.7018 -0.7975 0.2295 0.7696 1.6127   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.0653 0.3861 2.759 0.00580 \*\*   
## TrtBin -2.0477 0.5054 -4.051 5.09e-05 \*\*\*  
## SoilBin 2.5581 0.8208 3.117 0.00183 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 133.85 on 97 degrees of freedom  
## Residual deviance: 100.88 on 95 degrees of freedom  
## AIC: 106.88  
##   
## Number of Fisher Scoring iterations: 5

summ(LRVeg\_Gen)

## MODEL INFO:  
## Observations: 98  
## Dependent Variable: VegBin  
## Type: Generalized linear model  
## Family: binomial   
## Link function: logit   
##   
## MODEL FIT:  
## <U+03C7>²(2) = 32.97, p = 0.00  
## Pseudo-R² (Cragg-Uhler) = 0.38  
## Pseudo-R² (McFadden) = 0.25  
## AIC = 106.88, BIC = 114.64   
##   
## Standard errors: MLE  
## ------------------------------------------------  
## Est. S.E. z val. p  
## ----------------- ------- ------ -------- ------  
## (Intercept) 1.07 0.39 2.76 0.01  
## TrtBin -2.05 0.51 -4.05 0.00  
## SoilBin 2.56 0.82 3.12 0.00  
## ------------------------------------------------

1-pchisq(133.85-100.88, 97-95)

## [1] 6.928759e-08

export\_summs(LRVeg\_Gen, veg\_null, scale = TRUE)

## Registered S3 methods overwritten by 'broom':  
## method from   
## tidy.glht jtools  
## tidy.summary.glht jtools

|  |  |  |
| --- | --- | --- |
|  | Model 1 | Model 2 |
| (Intercept) | 1.07 \*\* | 0.29 |
|  | (0.39) | (0.20) |
| TrtBin | -2.05 \*\*\* |  |
|  | (0.51) |  |
| SoilBin | 2.56 \*\* |  |
|  | (0.82) |  |
| N | 98 | 98 |
| AIC | 106.88 | 135.85 |
| BIC | 114.64 | 138.43 |
| Pseudo R2 | 0.38 | 0.00 |
| All continuous predictors are mean-centered and scaled by 1 standard deviation. \*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05. | | |

## Interpretation

For a given site, any treatment changes the log odds of there being positive vegetation by -2.05. For a given site, SOD being found in soil changes the log odds of there being SOD-positive vegetation by 2.56.

Intercept = 1 (pos veg on plot). It looks like there’s a significant predictive quality for whether a site has been treated as to whether there is positive veg. In other words, a treated site has a negative association with positive veg (is less likely to have positive veg than an untreated site).

It is plausible that the data emanate from a logistic model that includes these variables. We can reject the null hypothesis that the deviance of the model with these variables is the same as the deviance of the model with only the constant. Given a 1 unit increase in TrtBin, we expect a loss of 2 in VegBin (e.g. when Treatment is applied, we expect positive veg to decrease from “present” to “not present”).

chi square 0.00000006928759

## NA1

#Subsetting data  
NA1Sites <- subset(AllSites, AllSites$Lineage == "NA1")  
  
NAV\_null = glm(VegBin~1, family = binomial, data=NA1Sites)  
NAV\_full = glm(VegBin~WFBin \* TrtBin \* SoilBin, family=binomial, data=NA1Sites)  
step(NAV\_null, scope = list(upper=NAV\_full), direction="both", test="Chisq", data=NA1Sites)

## Start: AIC=72.85  
## VegBin ~ 1  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + SoilBin 1 60.997 64.997 9.8547 0.001694 \*\*  
## + TrtBin 1 63.421 67.421 7.4305 0.006413 \*\*  
## + WFBin 1 67.073 71.073 3.7784 0.051919 .   
## <none> 70.852 72.852   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=65  
## VegBin ~ SoilBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + TrtBin 1 51.468 57.468 9.5290 0.002023 \*\*  
## + WFBin 1 54.683 60.683 6.3144 0.011976 \*   
## <none> 60.997 64.997   
## - SoilBin 1 70.852 72.852 9.8547 0.001694 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=57.47  
## VegBin ~ SoilBin + TrtBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## <none> 51.468 57.468   
## + WFBin 1 50.248 58.248 1.2203 0.2693050   
## + TrtBin:SoilBin 1 51.468 59.468 0.0000 0.9998525   
## - TrtBin 1 60.997 64.997 9.5290 0.0020225 \*\*   
## - SoilBin 1 63.421 67.421 11.9531 0.0005456 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = VegBin ~ SoilBin + TrtBin, family = binomial, data = NA1Sites)  
##   
## Coefficients:  
## (Intercept) SoilBin TrtBin   
## 1.099 18.842 -1.986   
##   
## Degrees of Freedom: 51 Total (i.e. Null); 49 Residual  
## Null Deviance: 70.85   
## Residual Deviance: 51.47 AIC: 57.47

#VegBin ~ SoilBin + TrtBin  
  
#Is NA1 Positive veg predicted by treatment and positive soil? (model from stepwise fit)  
LRVeg\_NA1 <- glm(VegBin~SoilBin + TrtBin, family=binomial, data=NA1Sites)  
summary(LRVeg\_NA1)

##   
## Call:  
## glm(formula = VegBin ~ SoilBin + TrtBin, family = binomial, data = NA1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.66511 -0.83047 0.00018 0.75853 1.56980   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.0986 0.5164 2.127 0.03338 \*   
## SoilBin 18.8417 2065.0941 0.009 0.99272   
## TrtBin -1.9859 0.6844 -2.902 0.00371 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 70.852 on 51 degrees of freedom  
## Residual deviance: 51.468 on 49 degrees of freedom  
## AIC: 57.468  
##   
## Number of Fisher Scoring iterations: 17

summ(LRVeg\_NA1, exp = TRUE)

## MODEL INFO:  
## Observations: 52  
## Dependent Variable: VegBin  
## Type: Generalized linear model  
## Family: binomial   
## Link function: logit   
##   
## MODEL FIT:  
## <U+03C7>²(2) = 19.38, p = 0.00  
## Pseudo-R² (Cragg-Uhler) = 0.42  
## Pseudo-R² (McFadden) = 0.27  
## AIC = 57.47, BIC = 63.32   
##   
## Standard errors: MLE  
## ---------------------------------------------------------------  
## exp(Est.) 2.5% 97.5% z val. p  
## ----------------- -------------- ------ ------- -------- ------  
## (Intercept) 3.00 1.09 8.25 2.13 0.03  
## SoilBin 152357525.27 0.00 Inf 0.01 0.99  
## TrtBin 0.14 0.04 0.52 -2.90 0.00  
## ---------------------------------------------------------------

1-pchisq(70.852-51.468, 51-49)

## [1] 6.177573e-05

export\_summs(LRVeg\_NA1, NAV\_null, scale = TRUE)

|  |  |  |
| --- | --- | --- |
|  | Model 1 | Model 2 |
| (Intercept) | 1.10 \* | 0.31 |
|  | (0.52) | (0.28) |
| SoilBin | 18.84 |  |
|  | (2065.09) |  |
| TrtBin | -1.99 \*\* |  |
|  | (0.68) |  |
| N | 52 | 52 |
| AIC | 57.47 | 72.85 |
| BIC | 63.32 | 74.80 |
| Pseudo R2 | 0.42 | 0.00 |
| All continuous predictors are mean-centered and scaled by 1 standard deviation. \*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05. | | |

## Interpretation

For a given NA1 site, any treatment changes the log odds of there being positive vegetation by -1.99.

Intercept = 1 (as in, yes there’s pos veg on plot), it looks like there’s a significant predictive quality for whether a site has been treated as to whether there is positive veg. In other words, a treated site has a negative association with positive veg (is less likely to have positive veg than an untreated site).

It is plausible that the data emanate from a logistic model that includes these variables. We can reject the null hypothesis that the deviance of the model with these variables is the same as the deviance of the model with only the constant.

chi square 0.00006177573

## EU1

#Subsetting data  
EU1Sites <- subset(AllSites, AllSites$Lineage == "EU1")  
  
EUV\_null = glm(VegBin~1, family = binomial, data=EU1Sites)  
EUV\_full = glm(VegBin~WFBin \* TrtBin \* SoilBin, family=binomial, data=EU1Sites)  
step(EUV\_null, scope = list(upper=EUV\_full), direction="both", test="Chisq", data=EU1Sites)

## Start: AIC=64.98  
## VegBin ~ 1  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + TrtBin 1 51.415 55.415 11.5699 0.0006703 \*\*\*  
## + SoilBin 1 56.637 60.637 6.3477 0.0117534 \*   
## <none> 62.985 64.985   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=55.41  
## VegBin ~ TrtBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + SoilBin 1 46.439 52.439 4.9757 0.0257054 \*   
## <none> 51.415 55.415   
## - TrtBin 1 62.985 64.985 11.5699 0.0006703 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=52.44  
## VegBin ~ TrtBin + SoilBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## <none> 46.439 52.439   
## + TrtBin:SoilBin 1 45.137 53.137 1.3017 0.253907   
## - SoilBin 1 51.415 55.415 4.9757 0.025705 \*   
## - TrtBin 1 56.637 60.637 10.1979 0.001406 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = VegBin ~ TrtBin + SoilBin, family = binomial, data = EU1Sites)  
##   
## Coefficients:  
## (Intercept) TrtBin SoilBin   
## 1.060 -2.200 1.892   
##   
## Degrees of Freedom: 45 Total (i.e. Null); 43 Residual  
## Null Deviance: 62.98   
## Residual Deviance: 46.44 AIC: 52.44

#VegBin ~ SoilBin + TrtBin  
  
#Is EU1 Positive veg predicted by treatment and positive soil? (model from stepwise fit)  
LRVeg\_EU1 <- glm(VegBin~SoilBin \* TrtBin, family=binomial, data=EU1Sites)  
summary(LRVeg\_EU1)

##   
## Call:  
## glm(formula = VegBin ~ SoilBin \* TrtBin, family = binomial, data = EU1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.0393 -0.6876 0.5168 0.6945 1.7653   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.2993 0.6513 1.995 0.04607 \*   
## SoilBin 0.6466 1.2518 0.517 0.60547   
## TrtBin -2.6210 0.8608 -3.045 0.00233 \*\*  
## SoilBin:TrtBin 2.0614 1.7702 1.164 0.24423   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 62.985 on 45 degrees of freedom  
## Residual deviance: 45.137 on 42 degrees of freedom  
## AIC: 53.137  
##   
## Number of Fisher Scoring iterations: 4

summ(LRVeg\_EU1, exp = TRUE)

## MODEL INFO:  
## Observations: 46  
## Dependent Variable: VegBin  
## Type: Generalized linear model  
## Family: binomial   
## Link function: logit   
##   
## MODEL FIT:  
## <U+03C7>²(3) = 17.85, p = 0.00  
## Pseudo-R² (Cragg-Uhler) = 0.43  
## Pseudo-R² (McFadden) = 0.28  
## AIC = 53.14, BIC = 60.45   
##   
## Standard errors: MLE  
## ----------------------------------------------------------------  
## exp(Est.) 2.5% 97.5% z val. p  
## -------------------- ----------- ------ -------- -------- ------  
## (Intercept) 3.67 1.02 13.14 1.99 0.05  
## SoilBin 1.91 0.16 22.20 0.52 0.61  
## TrtBin 0.07 0.01 0.39 -3.05 0.00  
## SoilBin:TrtBin 7.86 0.24 252.40 1.16 0.24  
## ----------------------------------------------------------------

1-pchisq(62.985-45.137, 45-42)

## [1] 0.0004727664

export\_summs(LRVeg\_EU1, EUV\_null, scale = TRUE)

|  |  |  |
| --- | --- | --- |
|  | Model 1 | Model 2 |
| (Intercept) | 1.30 \* | 0.26 |
|  | (0.65) | (0.30) |
| SoilBin | 0.65 |  |
|  | (1.25) |  |
| TrtBin | -2.62 \*\* |  |
|  | (0.86) |  |
| SoilBin:TrtBin | 2.06 |  |
|  | (1.77) |  |
| N | 46 | 46 |
| AIC | 53.14 | 64.98 |
| BIC | 60.45 | 66.81 |
| Pseudo R2 | 0.43 | 0.00 |
| All continuous predictors are mean-centered and scaled by 1 standard deviation. \*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05. | | |

## Interpretation

For a given EU1 site, any treatment changes the log odds of there being positive vegetation by -2.6.

Intercept = 1 (as in, yes there’s pos veg on plot), it looks like there’s a significant predictive quality for whether a site has been treated as to whether there is positive veg. In other words, a treated site has a negative association with positive veg (is less likely to have positive veg than an untreated site).

It is plausible that the data emanate from a logistic model that includes these variables. We can reject the null hypothesis that the deviance of the model with these variables is the same as the deviance of the model with only the constant.

chi square 0.0004727664

# Binomial Soil

## Generally

soil\_null = glm(SoilBin~1, family = binomial, data=AllSites)  
soil\_full = glm(SoilBin~WFBin \* Lineage \* TrtBin \* VegBin, family=binomial, data=AllSites)  
step(soil\_null, scope = list(upper=soil\_full), direction="both", test="Chisq", data=AllSItess)

## Start: AIC=103.84  
## SoilBin ~ 1  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + VegBin 1 87.824 91.824 14.0136 0.0001815 \*\*\*  
## + Lineage 1 99.426 103.426 2.4112 0.1204678   
## <none> 101.838 103.838   
## + TrtBin 1 101.389 105.389 0.4482 0.5031886   
## + WFBin 1 101.838 105.838 0.0000 0.9999999   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=91.82  
## SoilBin ~ VegBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + Lineage 1 84.914 90.914 2.9099 0.0880351 .   
## <none> 87.824 91.824   
## + TrtBin 1 86.983 92.983 0.8412 0.3590519   
## + WFBin 1 87.284 93.284 0.5396 0.4625808   
## - VegBin 1 101.838 103.838 14.0136 0.0001815 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=90.91  
## SoilBin ~ VegBin + Lineage  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + WFBin 1 82.759 90.759 2.1550 0.1421039   
## <none> 84.914 90.914   
## + Lineage:VegBin 1 83.224 91.224 1.6901 0.1935882   
## + TrtBin 1 83.727 91.727 1.1874 0.2758587   
## - Lineage 1 87.824 91.824 2.9099 0.0880351 .   
## - VegBin 1 99.426 103.426 14.5123 0.0001392 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=90.76  
## SoilBin ~ VegBin + Lineage + WFBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + Lineage:VegBin 1 80.179 90.179 2.5797 0.1082   
## <none> 82.759 90.759   
## - WFBin 1 84.914 90.914 2.1550 0.1421   
## + WFBin:VegBin 1 80.987 90.987 1.7722 0.1831   
## + TrtBin 1 82.400 92.400 0.3592 0.5490   
## - Lineage 1 87.284 93.284 4.5253 0.0334 \*   
## - VegBin 1 98.918 104.918 16.1586 5.825e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=90.18  
## SoilBin ~ VegBin + Lineage + WFBin + VegBin:Lineage  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## <none> 80.179 90.179   
## - VegBin:Lineage 1 82.759 90.759 2.57974 0.1082   
## - WFBin 1 83.224 91.224 3.04467 0.0810 .  
## + TrtBin 1 80.025 92.025 0.15414 0.6946   
## + WFBin:VegBin 1 80.179 92.179 0.00000 0.9998   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = SoilBin ~ VegBin + Lineage + WFBin + VegBin:Lineage,   
## family = binomial, data = AllSites)  
##   
## Coefficients:  
## (Intercept) VegBin LineageNA1 WFBin   
## -2.197 1.887 -17.371 1.792   
## VegBin:LineageNA1   
## 16.294   
##   
## Degrees of Freedom: 97 Total (i.e. Null); 93 Residual  
## Null Deviance: 101.8   
## Residual Deviance: 80.18 AIC: 90.18

#SoilBin ~ VegBin + Lineage + WFBin + VegBin:Lineage  
  
#Is positive soil predicted by positive veg, lineage, wildfire? (model from stepwise fit)  
LRSoil\_Gen <- glm(SoilBin ~ VegBin + Lineage + WFBin + VegBin:Lineage, family=binomial, data=AllSites)  
summary(LRSoil\_Gen)

##   
## Call:  
## glm(formula = SoilBin ~ VegBin + Lineage + WFBin + VegBin:Lineage,   
## family = binomial, data = AllSites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.35373 -0.66805 -0.45904 -0.00008 2.14597   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.1972 0.7454 -2.948 0.0032 \*\*  
## VegBin 1.8871 0.8445 2.235 0.0254 \*   
## LineageNA1 -17.3706 1314.9792 -0.013 0.9895   
## WFBin 1.7918 1.0408 1.721 0.0852 .   
## VegBin:LineageNA1 16.2945 1314.9792 0.012 0.9901   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 101.838 on 97 degrees of freedom  
## Residual deviance: 80.179 on 93 degrees of freedom  
## AIC: 90.179  
##   
## Number of Fisher Scoring iterations: 17

summ(LRSoil\_Gen, exp = TRUE)

## MODEL INFO:  
## Observations: 98  
## Dependent Variable: SoilBin  
## Type: Generalized linear model  
## Family: binomial   
## Link function: logit   
##   
## MODEL FIT:  
## <U+03C7>²(4) = 21.66, p = 0.00  
## Pseudo-R² (Cragg-Uhler) = 0.31  
## Pseudo-R² (McFadden) = 0.21  
## AIC = 90.18, BIC = 103.10   
##   
## Standard errors: MLE  
## --------------------------------------------------------------------  
## exp(Est.) 2.5% 97.5% z val. p  
## ----------------------- ------------- ------ ------- -------- ------  
## (Intercept) 0.11 0.03 0.48 -2.95 0.00  
## VegBin 6.60 1.26 34.54 2.23 0.03  
## LineageNA1 0.00 0.00 Inf -0.01 0.99  
## WFBin 6.00 0.78 46.14 1.72 0.09  
## VegBin:LineageNA1 11928966.46 0.00 Inf 0.01 0.99  
## --------------------------------------------------------------------

1-pchisq(101.838-80.179, 97-93)

## [1] 0.0002343011

export\_summs(LRSoil\_Gen, soil\_null, scale = TRUE)

|  |  |  |
| --- | --- | --- |
|  | Model 1 | Model 2 |
| (Intercept) | -2.20 \*\* | -1.30 \*\*\* |
|  | (0.75) | (0.25) |
| VegBin | 1.89 \* |  |
|  | (0.84) |  |
| LineageNA1 | -17.37 |  |
|  | (1314.98) |  |
| WFBin | 1.79 |  |
|  | (1.04) |  |
| VegBin:LineageNA1 | 16.29 |  |
|  | (1314.98) |  |
| N | 98 | 98 |
| AIC | 90.18 | 103.84 |
| BIC | 103.10 | 106.42 |
| Pseudo R2 | 0.31 | 0.00 |
| All continuous predictors are mean-centered and scaled by 1 standard deviation. \*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05. | | |

## Interpretation

For a given site, the presence of positive vegetation changes the log odds of there being positive soil by 1.89.

Intercept = 1 (as in, yes there’s pos soil on plot), it looks like there’s a significant predictive quality for whether a site has positive veg as to whether there is positive soil. In other words, a site with positive veg is more likely to have positive soil than a site without positive veg.

It is plausible that the data emanate from a logistic model that includes these variables. We can reject the null hypothesis that the deviance of the model with these variables is the same as the deviance of the model with only the constant.

chi square 0.0002343011

## NA1

NAS\_null = glm(SoilBin~1, family = binomial, data=NA1Sites)  
NAS\_full = glm(SoilBin~WFBin \* TrtBin \* VegBin, family=binomial, data=NA1Sites)  
step(NAS\_null, scope = list(upper=NAS\_full), direction="both", test="Chisq", data=NA1Sites)

## Start: AIC=46.65  
## SoilBin ~ 1  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + VegBin 1 34.795 38.795 9.8547 0.001694 \*\*  
## <none> 44.650 46.650   
## + WFBin 1 44.141 48.141 0.5087 0.475707   
## + TrtBin 1 44.474 48.474 0.1756 0.675156   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=38.79  
## SoilBin ~ VegBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + WFBin 1 31.750 37.750 3.0447 0.081002 .   
## + TrtBin 1 32.521 38.521 2.2741 0.131554   
## <none> 34.795 38.795   
## - VegBin 1 44.650 46.650 9.8547 0.001694 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=37.75  
## SoilBin ~ VegBin + WFBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## <none> 31.750 37.750   
## - WFBin 1 34.795 38.795 3.0447 0.0810025 .   
## + TrtBin 1 31.326 39.326 0.4241 0.5148768   
## + WFBin:VegBin 1 31.750 39.750 0.0000 0.9998973   
## - VegBin 1 44.141 48.141 12.3907 0.0004315 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = SoilBin ~ VegBin + WFBin, family = binomial, data = NA1Sites)  
##   
## Coefficients:  
## (Intercept) VegBin WFBin   
## -20.568 19.182 1.792   
##   
## Degrees of Freedom: 51 Total (i.e. Null); 49 Residual  
## Null Deviance: 44.65   
## Residual Deviance: 31.75 AIC: 37.75

#SoilBin ~ VegBin + WFBin  
  
#Is NA1 Positive soil predicted by positive veg and wildfire? (model from stepwise fit)  
LRSoil\_NA1 <- glm(SoilBin ~ VegBin + WFBin, family=binomial, data=NA1Sites)  
summary(LRSoil\_NA1)

##   
## Call:  
## glm(formula = SoilBin ~ VegBin + WFBin, family = binomial, data = NA1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.35373 -0.66805 -0.00012 -0.00005 1.79412   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -20.568 2168.034 -0.009 0.9924   
## VegBin 19.182 2168.034 0.009 0.9929   
## WFBin 1.792 1.041 1.721 0.0852 .  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 44.65 on 51 degrees of freedom  
## Residual deviance: 31.75 on 49 degrees of freedom  
## AIC: 37.75  
##   
## Number of Fisher Scoring iterations: 18

summ(LRSoil\_NA1, exp = TRUE)

## MODEL INFO:  
## Observations: 52  
## Dependent Variable: SoilBin  
## Type: Generalized linear model  
## Family: binomial   
## Link function: logit   
##   
## MODEL FIT:  
## <U+03C7>²(2) = 12.90, p = 0.00  
## Pseudo-R² (Cragg-Uhler) = 0.38  
## Pseudo-R² (McFadden) = 0.29  
## AIC = 37.75, BIC = 43.60   
##   
## Standard errors: MLE  
## ---------------------------------------------------------------  
## exp(Est.) 2.5% 97.5% z val. p  
## ----------------- -------------- ------ ------- -------- ------  
## (Intercept) 0.00 0.00 Inf -0.01 0.99  
## VegBin 214013538.89 0.00 Inf 0.01 0.99  
## WFBin 6.00 0.78 46.14 1.72 0.09  
## ---------------------------------------------------------------

1-pchisq(44.650-31.75, 51-49)

## [1] 0.001580522

export\_summs(LRSoil\_NA1, NAS\_null, scale = TRUE)

|  |  |  |
| --- | --- | --- |
|  | Model 1 | Model 2 |
| (Intercept) | -20.57 | -1.70 \*\*\* |
|  | (2168.03) | (0.38) |
| VegBin | 19.18 |  |
|  | (2168.03) |  |
| WFBin | 1.79 |  |
|  | (1.04) |  |
| N | 52 | 52 |
| AIC | 37.75 | 46.65 |
| BIC | 43.60 | 48.60 |
| Pseudo R2 | 0.38 | 0.00 |
| All continuous predictors are mean-centered and scaled by 1 standard deviation. \*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05. | | |

## Interpretation

For a given NA1 site, there are no factors with a predictive quality, but at the same time, the model selected is the most appropriate one.

It is plausible that the data emanate from a logistic model that includes these variables. We can reject the null hypothesis that the deviance of the model with these variables is the same as the deviance of the model with only the constant.

chi square 0.001580522

## EU1

EUS\_null = glm(SoilBin~1, family = binomial, data=EU1Sites)  
EUS\_full = glm(SoilBin~WFBin \* TrtBin \* VegBin, family=binomial, data=EU1Sites)  
step(EUS\_null, scope = list(upper=EUS\_full), direction="both", test="Chisq", data=EU1Sites)

## Start: AIC=56.78  
## SoilBin ~ 1  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## + VegBin 1 48.429 52.429 6.3477 0.01175 \*  
## <none> 54.777 56.777   
## + TrtBin 1 53.405 57.405 1.3721 0.24145   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=52.43  
## SoilBin ~ VegBin  
##   
## Df Deviance AIC LRT Pr(>Chi)   
## <none> 48.429 52.429   
## + TrtBin 1 48.429 54.429 0.0001 0.99041   
## - VegBin 1 54.777 56.777 6.3477 0.01175 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = SoilBin ~ VegBin, family = binomial, data = EU1Sites)  
##   
## Coefficients:  
## (Intercept) VegBin   
## -2.197 1.887   
##   
## Degrees of Freedom: 45 Total (i.e. Null); 44 Residual  
## Null Deviance: 54.78   
## Residual Deviance: 48.43 AIC: 52.43

#SoilBin ~ VegBin  
  
#Is EU1 Positive soil predicted by positive veg? (model from stepwise fit)  
LRSoil\_EU1 <- glm(SoilBin ~ VegBin, family=binomial, data=EU1Sites)  
summary(LRSoil\_EU1)

##   
## Call:  
## glm(formula = SoilBin ~ VegBin, family = binomial, data = EU1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.049 -1.049 -0.459 1.312 2.146   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.1972 0.7453 -2.948 0.0032 \*\*  
## VegBin 1.8871 0.8444 2.235 0.0254 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 54.777 on 45 degrees of freedom  
## Residual deviance: 48.429 on 44 degrees of freedom  
## AIC: 52.429  
##   
## Number of Fisher Scoring iterations: 4

summ(LRSoil\_EU1, exp = TRUE)

## MODEL INFO:  
## Observations: 46  
## Dependent Variable: SoilBin  
## Type: Generalized linear model  
## Family: binomial   
## Link function: logit   
##   
## MODEL FIT:  
## <U+03C7>²(1) = 6.35, p = 0.01  
## Pseudo-R² (Cragg-Uhler) = 0.19  
## Pseudo-R² (McFadden) = 0.12  
## AIC = 52.43, BIC = 56.09   
##   
## Standard errors: MLE  
## ------------------------------------------------------------  
## exp(Est.) 2.5% 97.5% z val. p  
## ----------------- ----------- ------ ------- -------- ------  
## (Intercept) 0.11 0.03 0.48 -2.95 0.00  
## VegBin 6.60 1.26 34.54 2.23 0.03  
## ------------------------------------------------------------

1-pchisq(54.777-48.429, 45-44)

## [1] 0.01175137

export\_summs(LRSoil\_EU1, EUS\_null, scale = TRUE)

|  |  |  |
| --- | --- | --- |
|  | Model 1 | Model 2 |
| (Intercept) | -2.20 \*\* | -0.93 \*\* |
|  | (0.75) | (0.33) |
| VegBin | 1.89 \* |  |
|  | (0.84) |  |
| N | 46 | 46 |
| AIC | 52.43 | 56.78 |
| BIC | 56.09 | 58.61 |
| Pseudo R2 | 0.19 | 0.00 |
| All continuous predictors are mean-centered and scaled by 1 standard deviation. \*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05. | | |

## Interpretation

For a given EU1 site, the presence of positive vegetation changes the log odds of there being positive soil by 1.89.

Intercept = 1 (as in, yes there’s pos soil on plot), it looks like there’s a significant predictive quality for whether a site has positive veg as to whether there is positive soil. In other words, a site with positive veg is more likely to have positive soil than a site without positive veg.

It is plausible that the data emanate from a logistic model that includes these variables. We can reject the null hypothesis that the deviance of the model with these variables is the same as the deviance of the model with only the constant.

chi square 0.01175137

#Take Away Message Treatment is predicted to affect (reduce) residual vegegation infected by both NA1 and EU1. In turn, whether or not there is positive veg is predicted to affect whether soil is also found to be positive, though this is speaking generally and not for NA1 specifically. Treatment is predicted to reduce veg, which reduces the likelihood of positive soil.

## Logistic Regression for predicting veg by time since treatment

#Is positive veg predicted by time since treatment?  
LRVeg\_t = glm(VegBin~YrSinceTrt, data=AllSites)  
summary(LRVeg\_t)

##   
## Call:  
## glm(formula = VegBin ~ YrSinceTrt, data = AllSites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.6221 -0.5722 0.3779 0.3779 0.6772   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.62207 0.05954 10.447 <2e-16 \*\*\*  
## YrSinceTrt -0.02494 0.01601 -1.557 0.123   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.2438396)  
##   
## Null deviance: 24.000 on 97 degrees of freedom  
## Residual deviance: 23.409 on 96 degrees of freedom  
## AIC: 143.79  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(24.000-23.409, 97-96)

## [1] 0.4420327

#NA1  
LRVeg\_tNA1 = glm(VegBin~YrSinceTrt, data=NA1Sites)  
summary(LRVeg\_tNA1)

##   
## Call:  
## glm(formula = VegBin ~ YrSinceTrt, data = NA1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.6269 -0.5473 0.3731 0.3731 0.5742   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.62688 0.08695 7.209 2.82e-09 \*\*\*  
## YrSinceTrt -0.01676 0.01764 -0.950 0.347   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.2493472)  
##   
## Null deviance: 12.692 on 51 degrees of freedom  
## Residual deviance: 12.467 on 50 degrees of freedom  
## AIC: 79.307  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(12.692-12.467, 51-50)

## [1] 0.6352563

#EU1  
LRVeg\_tEU1 = glm(VegBin~YrSinceTrt, data=EU1Sites)  
summary(LRVeg\_tEU1)

##   
## Call:  
## glm(formula = VegBin ~ YrSinceTrt, data = EU1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.7735 -0.3380 0.2265 0.2265 0.8798   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.77352 0.09022 8.574 6.14e-11 \*\*\*  
## YrSinceTrt -0.21777 0.06379 -3.414 0.00139 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.2031201)  
##   
## Null deviance: 11.3043 on 45 degrees of freedom  
## Residual deviance: 8.9373 on 44 degrees of freedom  
## AIC: 61.175  
##   
## Number of Fisher Scoring iterations: 2

summ(LRVeg\_tEU1, exp = TRUE)

## MODEL INFO:  
## Observations: 46  
## Dependent Variable: VegBin  
## Type: Linear regression   
##   
## MODEL FIT:  
## <U+03C7>²(1) = 2.37, p = 0.00  
## Pseudo-R² (Cragg-Uhler) = 0.27  
## Pseudo-R² (McFadden) = 0.16  
## AIC = 61.18, BIC = 66.66   
##   
## Standard errors: MLE  
## ------------------------------------------------------------  
## exp(Est.) 2.5% 97.5% t val. p  
## ----------------- ----------- ------ ------- -------- ------  
## (Intercept) 2.17 1.82 2.59 8.57 0.00  
## YrSinceTrt 0.80 0.71 0.91 -3.41 0.00  
## ------------------------------------------------------------  
##   
## Estimated dispersion parameter = 0.2

1-pchisq(11.3043-8.9373, 45-44)

## [1] 0.123925

## Logistic Regression for predicting soil by time since treatment

#Is positive veg predicted by time since treatment?  
LRSoil\_t = glm(SoilBin~YrSinceTrt, data=AllSites)  
summary(LRSoil\_t)

##   
## Call:  
## glm(formula = SoilBin ~ YrSinceTrt, data = AllSites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2306 -0.2306 -0.2145 -0.1502 0.8658   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.230607 0.049898 4.622 1.19e-05 \*\*\*  
## YrSinceTrt -0.008037 0.013419 -0.599 0.551   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.1712351)  
##   
## Null deviance: 16.500 on 97 degrees of freedom  
## Residual deviance: 16.439 on 96 degrees of freedom  
## AIC: 109.15  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(16.500-16.439, 97-96)

## [1] 0.8049223

#NA1  
LRSoil\_tNA1 = glm(SoilBin~YrSinceTrt, data=NA1Sites)  
summary(LRSoil\_tNA1)

##   
## Call:  
## glm(formula = SoilBin ~ YrSinceTrt, data = NA1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.1894 -0.1588 -0.1421 -0.1421 0.8579   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.142109 0.064014 2.220 0.031 \*  
## YrSinceTrt 0.003937 0.012989 0.303 0.763   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.1351363)  
##   
## Null deviance: 6.7692 on 51 degrees of freedom  
## Residual deviance: 6.7568 on 50 degrees of freedom  
## AIC: 47.454  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(6.7692-6.7568, 51-50)

## [1] 0.9113346

#EU1  
LRSoil\_tEU1 = glm(SoilBin~YrSinceTrt, data=EU1Sites)  
summary(LRSoil\_tEU1)

##   
## Call:  
## glm(formula = SoilBin ~ YrSinceTrt, data = EU1Sites)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.3676 -0.3676 -0.1899 0.6324 0.8990   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.36760 0.09019 4.076 0.000189 \*\*\*  
## YrSinceTrt -0.08885 0.06377 -1.393 0.170556   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.2030013)  
##   
## Null deviance: 9.3261 on 45 degrees of freedom  
## Residual deviance: 8.9321 on 44 degrees of freedom  
## AIC: 61.149  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(9.3261-8.9321, 45-44)

## [1] 0.5302043

# Tanoak “density” and Vegetation

## Generally

TO\_null = glm(VegBin~1, data=AllTO)  
TO\_full = glm(VegBin~TotalTO \* Num\_Seedlings \* TotalStump, data=AllTO)  
step(TO\_null, scope = list(upper=TO\_full), direction="both", test="Chisq", data=AllTO)

## Start: AIC=147.71  
## VegBin ~ 1  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + TotalStump 1 19.725 127.46 22.2484 2.396e-06 \*\*\*  
## + TotalTO 1 22.722 141.60 8.1024 0.004421 \*\*   
## <none> 24.640 147.71   
## + Num\_Seedlings 1 24.348 148.52 1.1921 0.274910   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=127.46  
## VegBin ~ TotalStump  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + Num\_Seedlings 1 19.322 127.40 2.0629 0.1509   
## <none> 19.725 127.46   
## + TotalTO 1 19.408 127.84 1.6188 0.2033   
## - TotalStump 1 24.640 147.71 22.2484 2.396e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=127.4  
## VegBin ~ TotalStump + Num\_Seedlings  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## <none> 19.322 127.40   
## - Num\_Seedlings 1 19.725 127.46 2.0629 0.1509   
## + TotalTO 1 19.082 128.15 1.2517 0.2632   
## + Num\_Seedlings:TotalStump 1 19.307 129.32 0.0807 0.7764   
## - TotalStump 1 24.348 148.52 23.1192 1.523e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = VegBin ~ TotalStump + Num\_Seedlings, data = AllTO)  
##   
## Coefficients:  
## (Intercept) TotalStump Num\_Seedlings   
## 0.75992 -0.02028 -0.02990   
##   
## Degrees of Freedom: 99 Total (i.e. Null); 97 Residual  
## Null Deviance: 24.64   
## Residual Deviance: 19.32 AIC: 127.4

#VegBin ~ TotalStump + Num\_Seedlings  
  
#Is positive veg predicted by stumps and seedlings? (model from stepwise fit)  
LRVeg\_TO <- glm(VegBin ~ TotalStump + Num\_Seedlings, data=AllTO)  
summary(LRVeg\_TO)

##   
## Call:  
## glm(formula = VegBin ~ TotalStump + Num\_Seedlings, data = AllTO)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.7599 -0.4484 0.2401 0.3298 0.7557   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.759917 0.068978 11.017 < 2e-16 \*\*\*  
## TotalStump -0.020284 0.004038 -5.023 2.32e-06 \*\*\*  
## Num\_Seedlings -0.029898 0.021027 -1.422 0.158   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.1991987)  
##   
## Null deviance: 24.640 on 99 degrees of freedom  
## Residual deviance: 19.322 on 97 degrees of freedom  
## AIC: 127.4  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(24.640-19.322, 99-97)

## [1] 0.0700182

## NA1

NA1TO <- subset(AllTO, AllTO$Lineage == "NA1")  
  
NATO\_null = glm(VegBin~1, data=NA1TO)  
NATO\_full = glm(VegBin~TotalTO \* Num\_Seedlings \* TotalStump, data=NA1TO)  
step(NATO\_null, scope = list(upper=NATO\_full), direction="both", test="Chisq", data=NA1TO)

## Start: AIC=78.24  
## VegBin ~ 1  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + TotalStump 1 9.8652 67.134 13.1029 0.0002948 \*\*\*  
## + TotalTO 1 11.8201 76.534 3.7022 0.0543394 .   
## <none> 12.6923 78.237   
## + Num\_Seedlings 1 12.6765 80.172 0.0649 0.7989848   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=67.13  
## VegBin ~ TotalStump  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## <none> 9.8652 67.134   
## + Num\_Seedlings 1 9.7201 68.363 0.7705 0.3800521   
## + TotalTO 1 9.7466 68.504 0.6293 0.4276055   
## - TotalStump 1 12.6923 78.237 13.1029 0.0002948 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = VegBin ~ TotalStump, data = NA1TO)  
##   
## Coefficients:  
## (Intercept) TotalStump   
## 0.71606 -0.02173   
##   
## Degrees of Freedom: 51 Total (i.e. Null); 50 Residual  
## Null Deviance: 12.69   
## Residual Deviance: 9.865 AIC: 67.13

#VegBin ~ TotalStump  
  
#Is positive NA1 veg predicted by stumps? (model from stepwise fit)  
LRVeg\_TONA1 <- glm(VegBin ~ TotalStump, data=NA1TO)  
summary(LRVeg\_TONA1)

##   
## Call:  
## glm(formula = VegBin ~ TotalStump, data = NA1TO)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.7161 -0.4064 0.2839 0.2839 0.7402   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.71606 0.07173 9.982 1.71e-13 \*\*\*  
## TotalStump -0.02173 0.00574 -3.785 0.000412 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.1973046)  
##   
## Null deviance: 12.6923 on 51 degrees of freedom  
## Residual deviance: 9.8652 on 50 degrees of freedom  
## AIC: 67.134  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(12.6923-9.8652, 51-50)

## [1] 0.09268559

## EU1

EU1TO <- subset(AllTO, AllTO$Lineage == "EU1")  
  
EUTO\_null = glm(VegBin~1, data=EU1TO)  
EUTO\_full = glm(VegBin~TotalTO \* Num\_Seedlings \* TotalStump, data=EU1TO)  
step(EUTO\_null, scope = list(upper=EUTO\_full), direction="both", test="Chisq", data=EU1TO)

## Start: AIC=69.98  
## VegBin ~ 1  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + TotalStump 1 8.8511 60.730 11.2536 0.0007947 \*\*\*  
## + TotalTO 1 10.1094 66.844 5.1392 0.0233913 \*   
## <none> 11.3043 69.983   
## + Num\_Seedlings 1 11.0161 70.795 1.1883 0.2756668   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=60.73  
## VegBin ~ TotalStump  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## <none> 8.8511 60.730   
## + TotalTO 1 8.6677 61.767 0.9631 0.3264168   
## + Num\_Seedlings 1 8.6836 61.851 0.8792 0.3484156   
## - TotalStump 1 11.3043 69.983 11.2536 0.0007947 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = VegBin ~ TotalStump, data = EU1TO)  
##   
## Coefficients:  
## (Intercept) TotalStump   
## 0.71577 -0.02002   
##   
## Degrees of Freedom: 45 Total (i.e. Null); 44 Residual  
## Null Deviance: 11.3   
## Residual Deviance: 8.851 AIC: 60.73

#VegBin ~ TotalStump  
  
#Is positive NA1 veg predicted by stumps? (model from stepwise fit)  
LRVeg\_TOEU1 <- glm(VegBin ~ TotalStump, data=EU1TO)  
summary(LRVeg\_TOEU1)

##   
## Call:  
## glm(formula = VegBin ~ TotalStump, data = EU1TO)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.7158 -0.4656 0.2842 0.2842 0.7446   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.715770 0.078941 9.067 1.25e-11 \*\*\*  
## TotalStump -0.020016 0.005732 -3.492 0.0011 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.201162)  
##   
## Null deviance: 11.3043 on 45 degrees of freedom  
## Residual deviance: 8.8511 on 44 degrees of freedom  
## AIC: 60.73  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(11.3043-8.8511, 45-44)

## [1] 0.1172855

## Interpretation

Stumps = treatment, so this reinforces previous conclusions.

# Tanoak “density” and Soil

## Generally

TOS\_null = glm(SoilBin~1, data=AllTO)  
TOS\_full = glm(SoilBin~TotalTO \* Num\_Seedlings \* TotalStump, data=AllTO)  
step(TOS\_null, scope = list(upper=TOS\_full), direction="both", test="Chisq", data=AllTO)

## Start: AIC=108.15  
## SoilBin ~ 1  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + TotalStump 1 15.591 103.94 6.2137 0.01268 \*  
## + TotalTO 1 16.131 107.34 2.8059 0.09392 .  
## <none> 16.590 108.15   
## + Num\_Seedlings 1 16.382 108.89 1.2593 0.26179   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=103.94  
## SoilBin ~ TotalStump  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## <none> 15.591 103.94   
## + Num\_Seedlings 1 15.342 104.33 1.6056 0.20510   
## + TotalTO 1 15.493 105.31 0.6240 0.42956   
## - TotalStump 1 16.590 108.15 6.2137 0.01268 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = SoilBin ~ TotalStump, data = AllTO)  
##   
## Coefficients:  
## (Intercept) TotalStump   
## 0.271366 -0.009038   
##   
## Degrees of Freedom: 99 Total (i.e. Null); 98 Residual  
## Null Deviance: 16.59   
## Residual Deviance: 15.59 AIC: 103.9

#SoilBin ~ TotalStump  
  
#Is positive soil predicted by stumps? (model from stepwise fit)  
LRS\_TO <- glm(SoilBin ~ TotalStump, data=AllTO)  
summary(LRS\_TO)

##   
## Call:  
## glm(formula = SoilBin ~ TotalStump, data = AllTO)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.27137 -0.27137 -0.21714 0.03591 0.81901   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.271366 0.046800 5.798 8.18e-08 \*\*\*  
## TotalStump -0.009038 0.003606 -2.507 0.0138 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.159087)  
##   
## Null deviance: 16.590 on 99 degrees of freedom  
## Residual deviance: 15.591 on 98 degrees of freedom  
## AIC: 103.94  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(16.950-15.591, 99-98)

## [1] 0.2437109

## NA1

NATOS\_null = glm(SoilBin~1, data=NA1TO)  
NATOS\_full = glm(SoilBin~TotalTO \* Num\_Seedlings \* TotalStump, data=NA1TO)  
step(NATOS\_null, scope = list(upper=NATOS\_full), direction="both", test="Chisq", data=NA1TO)

## Start: AIC=45.55  
## SoilBin ~ 1  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + TotalStump 1 6.3967 44.606 2.94325 0.08624 .  
## <none> 6.7692 45.549   
## + TotalTO 1 6.5773 46.054 1.49545 0.22137   
## + Num\_Seedlings 1 6.7666 47.529 0.02025 0.88684   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=44.61  
## SoilBin ~ TotalStump  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## <none> 6.3967 44.606   
## - TotalStump 1 6.7692 45.549 2.94325 0.08624 .  
## + TotalTO 1 6.3432 46.169 0.43722 0.50847   
## + Num\_Seedlings 1 6.3760 46.437 0.16888 0.68111   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = SoilBin ~ TotalStump, data = NA1TO)  
##   
## Coefficients:  
## (Intercept) TotalStump   
## 0.204353 -0.007887   
##   
## Degrees of Freedom: 51 Total (i.e. Null); 50 Residual  
## Null Deviance: 6.769   
## Residual Deviance: 6.397 AIC: 44.61

#SoilBin ~ TotalStump  
  
#Is positive NA1 soil predicted by stumps? (model from stepwise fit)  
LRS\_TONA1 <- glm(SoilBin ~ TotalStump, data=NA1TO)  
summary(LRS\_TONA1)

##   
## Call:  
## glm(formula = SoilBin ~ TotalStump, data = NA1TO)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.20435 -0.20435 -0.17281 -0.04464 0.81142   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.204353 0.057761 3.538 0.000881 \*\*\*  
## TotalStump -0.007887 0.004622 -1.706 0.094145 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.1279345)  
##   
## Null deviance: 6.7692 on 51 degrees of freedom  
## Residual deviance: 6.3967 on 50 degrees of freedom  
## AIC: 44.606  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(6.7692-6.3967, 51-50)

## [1] 0.5416447

## EU1

EUTOS\_null = glm(SoilBin~1, data=EU1TO)  
EUTOS\_full = glm(SoilBin~TotalTO \* Num\_Seedlings \* TotalStump, data=EU1TO)  
step(EUTOS\_null, scope = list(upper=EUTOS\_full), direction="both", test="Chisq", data=EU1TO)

## Start: AIC=61.13  
## SoilBin ~ 1  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## + TotalStump 1 8.5309 59.035 4.0998 0.04289 \*  
## + TotalTO 1 8.8759 60.858 2.2760 0.13139   
## <none> 9.3261 61.134   
## + Num\_Seedlings 1 9.0378 61.690 1.4444 0.22943   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Step: AIC=59.03  
## SoilBin ~ TotalStump  
##   
## Df Deviance AIC scaled dev. Pr(>Chi)   
## <none> 8.5309 59.035   
## + Num\_Seedlings 1 8.3146 59.853 1.1814 0.27708   
## + TotalTO 1 8.4418 60.552 0.4825 0.48727   
## - TotalStump 1 9.3261 61.134 4.0998 0.04289 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

##   
## Call: glm(formula = SoilBin ~ TotalStump, data = EU1TO)  
##   
## Coefficients:  
## (Intercept) TotalStump   
## 0.3683 -0.0114   
##   
## Degrees of Freedom: 45 Total (i.e. Null); 44 Residual  
## Null Deviance: 9.326   
## Residual Deviance: 8.531 AIC: 59.03

#SoilBin ~ TotalStump  
  
#Is positive NA1 veg predicted by stumps? (model from stepwise fit)  
LRS\_TOEU1 <- glm(SoilBin ~ TotalStump, data=EU1TO)  
summary(LRS\_TOEU1)

##   
## Call:  
## glm(formula = SoilBin ~ TotalStump, data = EU1TO)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.3683 -0.3683 -0.2202 0.6317 0.7456   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.368326 0.077500 4.753 2.17e-05 \*\*\*  
## TotalStump -0.011396 0.005627 -2.025 0.0489 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.193883)  
##   
## Null deviance: 9.3261 on 45 degrees of freedom  
## Residual deviance: 8.5309 on 44 degrees of freedom  
## AIC: 59.035  
##   
## Number of Fisher Scoring iterations: 2

1-pchisq(9.3261-8.5309, 45-44)

## [1] 0.3725324

## Interpretation

Stumps = treatment, so this reinforces previous conclusions.

# Are current treatments effectively reducing P. ramorum infections in soil and vegetation?

#Setting up data  
Veg <- AllSites %>% select(9, 19)  
  
VegTable <- table(Veg$TrtBin, Veg$VegBin)  
  
chisq.test(VegTable)$expected

##   
## 0 1  
## 0 19.28571 25.71429  
## 1 22.71429 30.28571

Veg.f <- fisher.test(VegTable)  
Veg.f

##   
## Fisher's Exact Test for Count Data  
##   
## data: VegTable  
## p-value = 3.332e-05  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.05364789 0.41086459  
## sample estimates:  
## odds ratio   
## 0.154806

Soil <- AllSites %>% select(9, 23)  
  
SoilTable <- table(Soil$TrtBin, Soil$SoilBin)  
  
chisq.test(SoilTable)$expected

##   
## 0 1  
## 0 35.35714 9.642857  
## 1 41.64286 11.357143

Soil.f <- fisher.test(SoilTable)  
Soil.f

##   
## Fisher's Exact Test for Count Data  
##   
## data: SoilTable  
## p-value = 0.6226  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.2424979 2.1196489  
## sample estimates:  
## odds ratio   
## 0.7212714

#For Veg only: We reject the null hypothesis that there is no significant relationship between the two variables (treatment and positive vegetation) using Fisher's exact test.  
  
  
#For Soil only: We accept the null hypothesis that there is no significant relationship between the two variables (treatment and positive soil) using Fisher's exact test.

# Is wildfire better than current treatments at removing P. ramorum from sites?

#Veg  
Firev\_full = glm(VegBin~WFBin \* TrtBin, family=binomial, data=AllFire)  
summary(Firev\_full)

##   
## Call:  
## glm(formula = VegBin ~ WFBin \* TrtBin, family = binomial, data = AllFire)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.7941 -0.9854 0.7302 0.7302 2.0963   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.1856 0.3445 3.441 0.000579 \*\*\*  
## WFBin 0.2007 1.1699 0.172 0.863810   
## TrtBin -1.6556 0.4765 -3.475 0.000511 \*\*\*  
## WFBin:TrtBin -1.8101 1.6131 -1.122 0.261795   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 137.19 on 99 degrees of freedom  
## Residual deviance: 114.40 on 96 degrees of freedom  
## AIC: 122.4  
##   
## Number of Fisher Scoring iterations: 4

1-pchisq(137.19-114.40, 99-96)

## [1] 4.466451e-05

#Soil  
Fires\_full = glm(SoilBin~WFBin \* TrtBin, family=binomial, data=AllFire)  
summary(Fires\_full)

##   
## Call:  
## glm(formula = SoilBin ~ WFBin \* TrtBin, family = binomial, data = AllFire)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.35373 -0.73024 -0.62901 -0.00022 1.85346   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.1856 0.3445 -3.441 0.000579 \*\*\*  
## WFBin 1.5911 0.9757 1.631 0.102956   
## TrtBin -0.3342 0.5411 -0.618 0.536820   
## WFBin:TrtBin -17.6373 1318.7272 -0.013 0.989329   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 102.791 on 99 degrees of freedom  
## Residual deviance: 94.585 on 96 degrees of freedom  
## AIC: 102.58  
##   
## Number of Fisher Scoring iterations: 16

1-pchisq(102.791-94.585, 99-96)

## [1] 0.04194074

# Ordination of seedling data

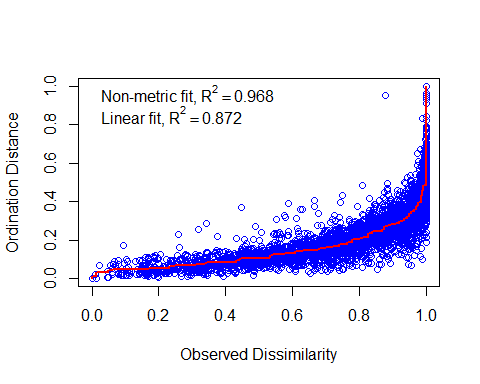
## NMDS

PCASeeds <- AllSeeds[5:35]  
DistSeed <- vegdist(PCASeeds, method = "bray")  
  
NMDS.scree <- function(x) { #where x is the name of the data frame variable  
 plot(rep(1, 10), replicate(10, metaMDS(x, autotransform = F, k = 1)$stress), xlim = c(1, 10),ylim = c(0, 0.30), xlab = "# of Dimensions", ylab = "Stress", main = "NMDS stress plot")  
 for (i in 1:10) {  
 points(rep(i + 1,10),replicate(10, metaMDS(x, autotransform = F, k = i + 1)$stress))  
 }  
}  
  
#NMDS.scrree(DistSeed) chunk excluded to save space

NMDS1 <- metaMDS(DistSeed, k = 2, trymax = 100, trace = F)  
NMDS1

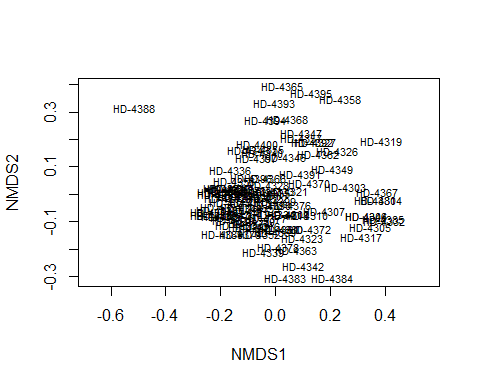
##   
## Call:  
## metaMDS(comm = DistSeed, k = 2, trymax = 100, trace = F)   
##   
## global Multidimensional Scaling using monoMDS  
##   
## Data: DistSeed   
## Distance: bray   
##   
## Dimensions: 2   
## Stress: 0.1791693   
## Stress type 1, weak ties  
## Two convergent solutions found after 24 tries  
## Scaling: centring, PC rotation   
## Species: scores missing

Stress <- stressplot(NMDS1)



Stressplot <- plot(NMDS1, type = "t")

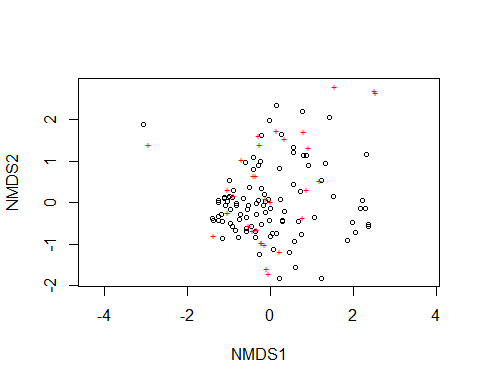
## species scores not available



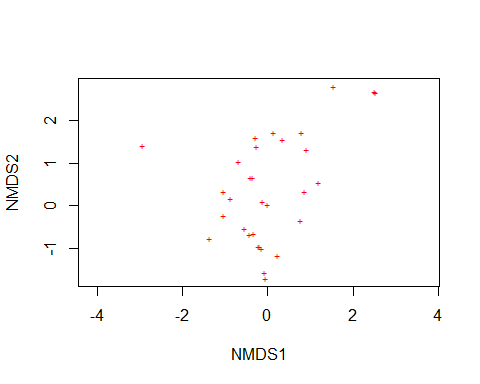
NMDS2 <- metaMDS(PCASeeds, k = 2, trymax = 100, trace = F)  
NMDS2

##   
## Call:  
## metaMDS(comm = PCASeeds, k = 2, trymax = 100, trace = F)   
##   
## global Multidimensional Scaling using monoMDS  
##   
## Data: wisconsin(sqrt(PCASeeds))   
## Distance: bray   
##   
## Dimensions: 2   
## Stress: 0.2403277   
## Stress type 1, weak ties  
## No convergent solutions - best solution after 100 tries  
## Scaling: centring, PC rotation, halfchange scaling   
## Species: expanded scores based on 'wisconsin(sqrt(PCASeeds))'

NMDS3 <- metaMDS(PCASeeds, k = 2, trymax = 100, trace = F, autotransform = FALSE, distance="bray")  
NMDS3plot <- plot(NMDS3)



NMDS3plotsp <- plot(NMDS3, display = "species")

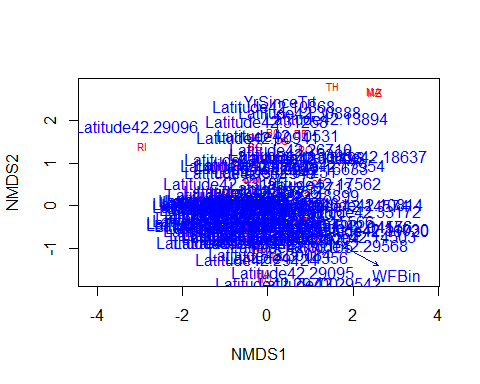


## Interpretation (including effects variables)

#Interpretation  
EFSites <- select(SODSite.ord, 3, 8:11, 19, 23, 26)  
  
ef <- envfit(NMDS3, EFSites, permutations = 999, na.rm = TRUE)  
ef

##   
## \*\*\*VECTORS  
##   
## NMDS1 NMDS2 r2 Pr(>r)   
## WFBin 0.87856 -0.47763 0.1145 0.005 \*\*  
## TrtBin 0.96714 -0.25426 0.0189 0.404   
## VegBin -0.97955 -0.20120 0.0514 0.085 .   
## SoilBin 0.08801 -0.99612 0.0191 0.371   
## YrSinceTrt 0.12224 0.99250 0.0666 0.045 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## Permutation: free  
## Number of permutations: 999  
##   
## \*\*\*FACTORS:  
##   
## Centroids:  
## NMDS1 NMDS2  
## LineageEU1 -0.1165 -0.1744  
## LineageNA1 0.1035 0.1503  
## LineageU 0.0395 0.1788  
## Latitude42.04176 1.9675 -0.4714  
## Latitude42.04178 -0.5874 0.9568  
## Latitude42.04251 0.2101 0.8194  
## Latitude42.04669 -0.9703 -0.1582  
## Latitude42.05423 -1.0199 0.1129  
## Latitude42.05744 -0.8439 -0.6635  
## Latitude42.10531 0.2613 1.6453  
## Latitude42.10585 -0.0039 -0.8259  
## Latitude42.10656 -0.2212 0.3505  
## Latitude42.10814 2.2173 0.0486  
## Latitude42.10868 0.1472 2.3417  
## Latitude42.11756 -1.0901 -0.0735  
## Latitude42.12200 -0.8983 0.2805  
## Latitude42.12313 -0.2501 0.9772  
## Latitude42.12455 -0.9122 0.1308  
## Latitude42.12464 -0.2922 0.8988  
## Latitude42.12821 -0.2806 0.0466  
## Latitude42.13082 -1.2454 0.0566  
## Latitude42.13193 0.6879 -0.4568  
## Latitude42.13223 -0.3451 -0.2964  
## Latitude42.13775 -1.0929 0.0912  
## Latitude42.13796 -1.0289 0.0312  
## Latitude42.13819 -1.1010 0.1342  
## Latitude42.13894 1.4119 2.0595  
## Latitude42.14111 -0.7466 -0.4170  
## Latitude42.14356 0.4651 -1.2009  
## Latitude42.14503 2.0535 -0.7141  
## Latitude42.14556 1.9675 -0.4714  
## Latitude42.14574 1.9012 0.0102  
## Latitude42.15398 0.5631 1.2158  
## Latitude42.15498 0.8613 1.1439  
## Latitude42.15566 1.0708 -0.3653  
## Latitude42.16633 0.9237 0.8835  
## Latitude42.16720 2.3563 -0.5723  
## Latitude42.16843 -0.0265 -0.4206  
## Latitude42.16854 -0.0472 0.0660  
## Latitude42.16951 0.0605 -0.7465  
## Latitude42.17562 1.2407 0.5419  
## Latitude42.17954 1.3374 0.9510  
## Latitude42.18637 2.3088 1.1681  
## Latitude42.19457 0.2839 -0.4347  
## Latitude42.26547 -0.7315 -0.2894  
## Latitude42.26710 0.5600 1.3262  
## Latitude42.26913 -0.9767 0.1443  
## Latitude42.27436 -1.3987 -0.3779  
## Latitude42.27922 -0.3572 -0.6877  
## Latitude42.28273 -1.1805 -0.2759  
## Latitude42.28407 -0.5525 -0.1628  
## Latitude42.29095 0.5972 -1.5623  
## Latitude42.29096 -3.0638 1.8727  
## Latitude42.29124 -0.2516 -1.2465  
## Latitude42.29204 0.7532 -0.7590  
## Latitude42.29327 -0.4625 -0.5725  
## Latitude42.29333 0.3347 -0.2200  
## Latitude42.29334 -0.1741 -0.0791  
## Latitude42.29337 -0.2031 -0.5214  
## Latitude42.29474 -0.8085 -0.0617  
## Latitude42.29542 1.2344 -1.8242  
## Latitude42.29568 1.8615 -0.9153  
## Latitude42.29694 0.2811 -0.4440  
## Latitude42.29700 0.2245 -1.8215  
## Latitude42.30084 0.0713 -1.1370  
## Latitude42.30105 0.5838 -0.9477  
## Latitude42.30636 0.7997 1.1352  
## Latitude42.30655 -0.3510 -0.8511  
## Latitude42.30704 -1.2556 -0.3454  
## Latitude42.30888 0.7791 2.2021  
## Latitude42.30941 -0.2127 1.6164  
## Latitude42.31030 2.3526 -0.5383  
## Latitude42.31258 -0.0149 1.9865  
## Latitude42.32048 -0.5745 -0.3698  
## Latitude42.32142 -0.7647 -0.8514  
## Latitude42.32148 0.2503 0.0699  
## Latitude42.32526 -0.5655 -0.6307  
## Latitude42.32640 -1.3784 -0.4387  
## Latitude42.32713 0.5459 0.4415  
## Latitude42.33172 2.1758 -0.1313  
## Latitude42.331949 -0.4104 0.7844  
## Latitude42.33195 -0.9810 0.5302  
## Latitude42.33229 -0.1125 -0.2363  
## Latitude42.332505 -0.3374 -0.0198  
## Latitude42.33258 -0.5293 -0.0647  
## Latitude42.33277 -0.5103 0.3520  
## Latitude42.33300 -0.1221 0.0225  
## Latitude42.333081 -0.8098 -0.0210  
## Latitude42.33312 -0.1449 0.2024  
## Latitude42.334215 -0.0067 -0.1379  
## Latitude42.33597 -1.2377 0.0031  
## Latitude42.33622 -1.1953 -0.4513  
## Latitude42.33895 0.1584 -0.7531  
## Latitude42.34534 -1.1524 -0.8592  
## Latitude42.345979 -0.9013 -0.5639  
## Latitude42.35349 -0.9506 -0.4936  
## Latitude42.35360 -0.5643 -0.7046  
## Latitude42.418810 -0.3980 1.0883  
## Latitude42.48899 0.7314 0.2552  
## Latitude42.49711 -0.6523 0.1025  
## Longitude-124.09534 -0.9703 -0.1582  
## Longitude-124.10088 0.2101 0.8194  
## Longitude-124.10239 -0.5874 0.9568  
## Longitude-124.10240 1.9675 -0.4714  
## Longitude-124.13448 0.0605 -0.7465  
## Longitude-124.13562 -0.0472 0.0660  
## Longitude-124.13837 -0.0265 -0.4206  
## Longitude-124.14009 2.3563 -0.5723  
## Longitude-124.14064 0.9237 0.8835  
## Longitude-124.14400 1.0708 -0.3653  
## Longitude-124.14850 1.9012 0.0102  
## Longitude-124.15112 2.0535 -0.7141  
## Longitude-124.15621 1.9675 -0.4714  
## Longitude-124.15952 0.4651 -1.2009  
## Longitude-124.16058 -0.7466 -0.4170  
## Longitude-124.16406 -1.1010 0.1342  
## Longitude-124.16514 -1.0289 0.0312  
## Longitude-124.16682 -1.0929 0.0912  
## Longitude-124.19550 -1.0901 -0.0735  
## Longitude-124.19627 -0.2806 0.0466  
## Longitude-124.19671 0.6879 -0.4568  
## Longitude-124.19982 -0.8439 -0.6635  
## Longitude-124.23937 0.7314 0.2552  
## Longitude-124.25471 1.4119 2.0595  
## Longitude-124.25945 -0.8983 0.2805  
## Longitude-124.26122 -0.3451 -0.2964  
## Longitude-124.26237 -0.2501 0.9772  
## Longitude-124.26263 -1.2454 0.0566  
## Longitude-124.26584 0.5631 1.2158  
## Longitude-124.27132 -0.9122 0.1308  
## Longitude-124.27197 -0.2922 0.8988  
## Longitude-124.27666 -1.0199 0.1129  
## Longitude-124.28152 -0.9767 0.1443  
## Longitude-124.28308 2.2173 0.0486  
## Longitude-124.28326 0.1472 2.3417  
## Longitude-124.28467 -0.2212 0.3505  
## Longitude-124.28574 0.2613 1.6453  
## Longitude-124.28612 -0.0039 -0.8259  
## Longitude-124.29369 -0.6523 0.1025  
## Longitude-124.29518 0.8613 1.1439  
## Longitude-124.29751 -1.3987 -0.3779  
## Longitude-124.30651 -1.1805 -0.2759  
## Longitude-124.3080 0.5600 1.3262  
## Longitude-124.30960 -0.7315 -0.2894  
## Longitude-124.32102 -0.3572 -0.6877  
## Longitude-124.32211 -0.5525 -0.1628  
## Longitude-124.32393 -0.8085 -0.0617  
## Longitude-124.32932 0.7532 -0.7590  
## Longitude-124.34254 1.3374 0.9510  
## Longitude-124.34256 2.3088 1.1681  
## Longitude-124.34475 1.2407 0.5419  
## Longitude-124.349987 -0.3980 1.0883  
## Longitude-124.3507 0.2839 -0.4347  
## Longitude-124.35761 -1.1420 -0.4636  
## Longitude-124.35783 -1.2487 -0.4391  
## Longitude-124.36069 -1.2377 0.0031  
## Longitude-124.37257 -0.5745 -0.3698  
## Longitude-124.38130 0.2811 -0.4440  
## Longitude-124.38137 0.2245 -1.8215  
## Longitude-124.38197 -0.4625 -0.5725  
## Longitude-124.38251 -0.5655 -0.6307  
## Longitude-124.38308 1.2344 -1.8242  
## Longitude-124.38348 1.8615 -0.9153  
## Longitude-124.38366 -0.5103 0.3520  
## Longitude-124.38381 -0.5293 -0.0647  
## Longitude-124.38386 -0.1125 -0.2363  
## Longitude-124.38458 -3.0638 1.8727  
## Longitude-124.38474 0.5972 -1.5623  
## Longitude-124.38645 0.0713 -1.1370  
## Longitude-124.38664 0.5838 -0.9477  
## Longitude-124.39236 -0.2031 -0.5214  
## Longitude-124.39334 0.7791 2.2021  
## Longitude-124.39407 0.3347 -0.2200  
## Longitude-124.39408 -0.1741 -0.0791  
## Longitude-124.39460 2.1758 -0.1313  
## Longitude-124.39725 -1.2556 -0.3454  
## Longitude-124.39801 -0.3510 -0.8511  
## Longitude-124.39847 2.3526 -0.5383  
## Longitude-124.39883 -0.2516 -1.2465  
## Longitude-124.399209 -0.3374 -0.0198  
## Longitude-124.40005 -0.2127 1.6164  
## Longitude-124.40015 0.7997 1.1352  
## Longitude-124.400150 -0.0067 -0.1379  
## Longitude-124.400605 -0.8098 -0.0210  
## Longitude-124.40082 -0.1449 0.2024  
## Longitude-124.40105 -0.1221 0.0225  
## Longitude-124.402473 -0.4104 0.7844  
## Longitude-124.40257 -0.9810 0.5302  
## Longitude-124.40437 0.2503 0.0699  
## Longitude-124.40442 -0.7647 -0.8514  
## Longitude-124.40617 -0.0149 1.9865  
## Longitude-124.40664 -0.9506 -0.4936  
## Longitude-124.40678 -0.5643 -0.7046  
## Longitude-124.40679 0.5459 0.4415  
## Longitude-124.40685 -1.3784 -0.4387  
## Longitude-124.40870 0.1584 -0.7531  
## Longitude-124.41295 -0.9013 -0.5639  
## Longitude-124.41411 -1.1524 -0.8592  
##   
## Goodness of fit:  
## r2 Pr(>r)   
## Lineage 0.0215 0.365   
## Latitude 0.9980 0.041 \*  
## Longitude 0.9980 0.245   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## Permutation: free  
## Number of permutations: 999

efplot <- plot(NMDS3, type = "t", display = "species")  
efplot2 <- plot(ef, p.max = 0.05)

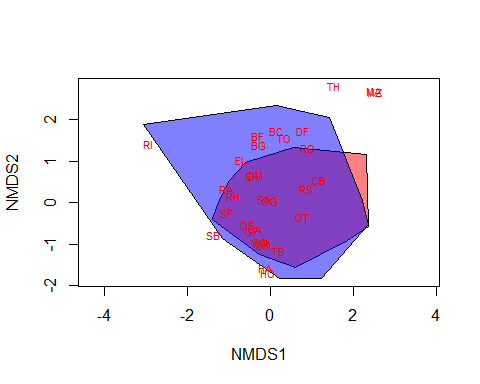


efplot2

## NULL

## Interpretation by treatment

group = c(rep("Untreated", 56), rep("Treated", 43))  
colors = c(rep("red", 56), rep("blue", 43))  
  
ordiplot(NMDS3, type = "n")  
for(i in unique(group)) {  
 ordihull(NMDS3$point[grep(i, group),], draw="polygon",  
 groups = group[group == i],col = colors[grep(i,group)],label=F) }  
  
orditorp(NMDS3, display = "species", col = "red", air = 0.01)



#orditorp(NMDS3, display = "sites", col = c(rep("red",12),  
# rep("blue", 12)), air = 0.01, cex = 1.25)