Community Analysis Hymenoptera

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Data

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:
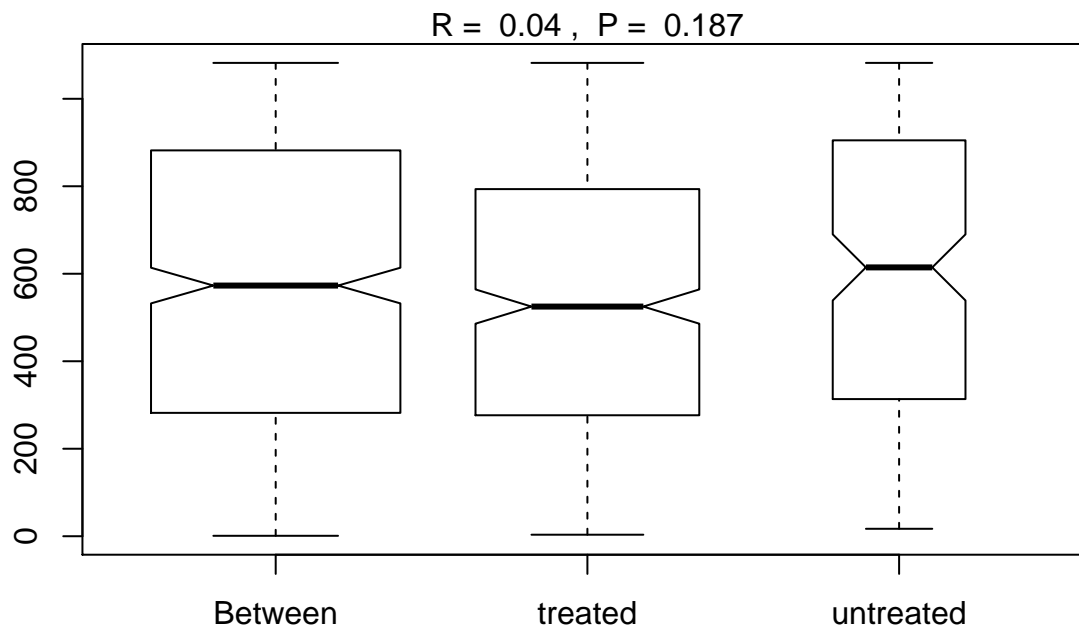

Figure 1: Anosim analisis between Treated and Untreated Fields

NMDS Treated Untreated

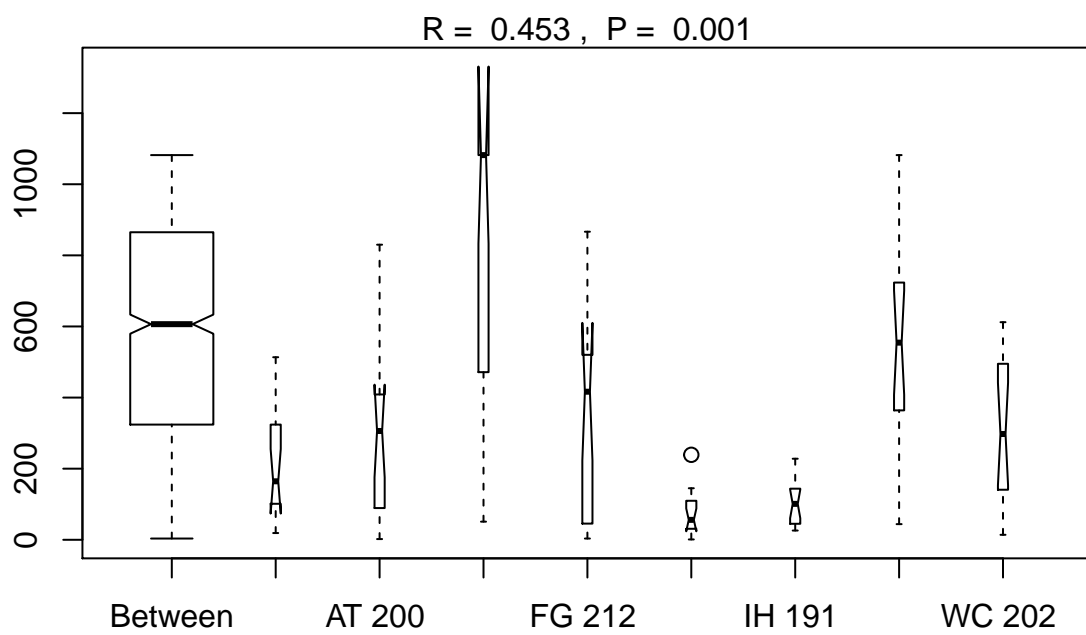## NMDS Management Areas

Alpha diversity

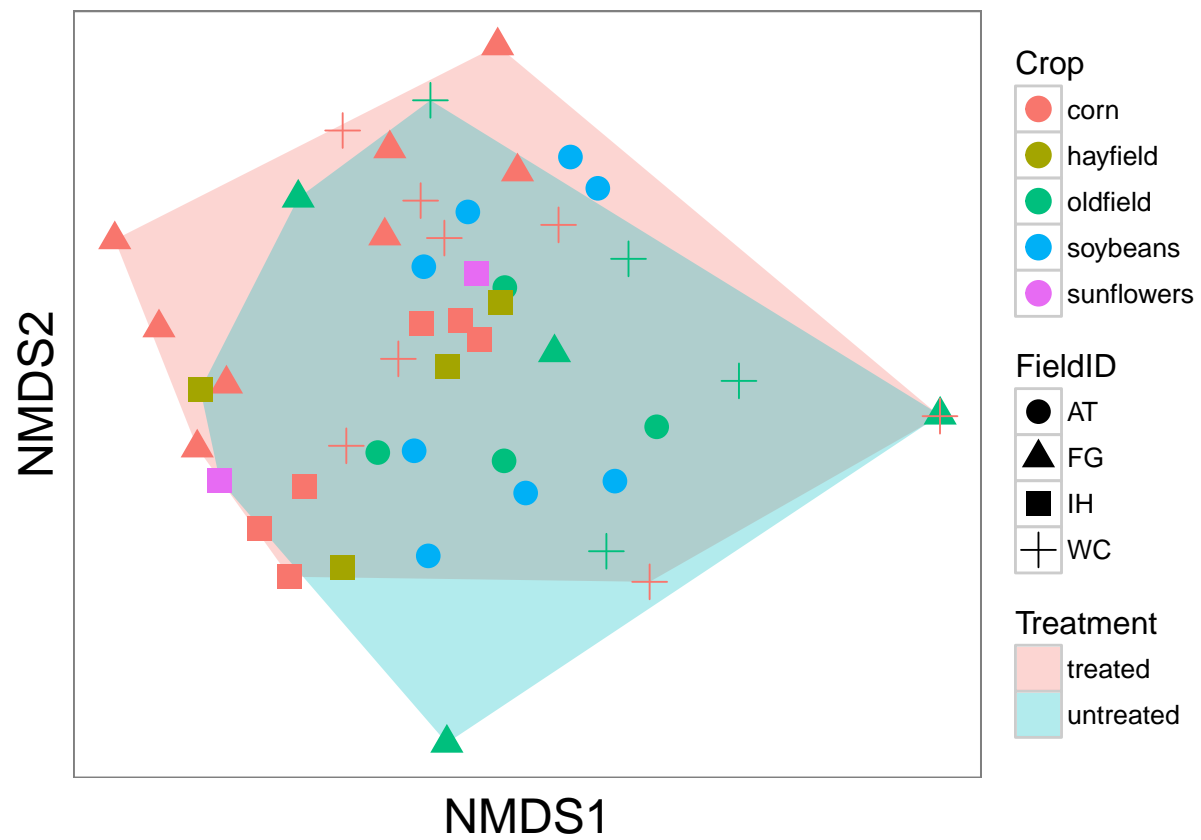Figure 2: Anosim analisis between different management areas

Figure 3: Multidimensional Scaling Showing the Overlap of communities between treated and untreated areas
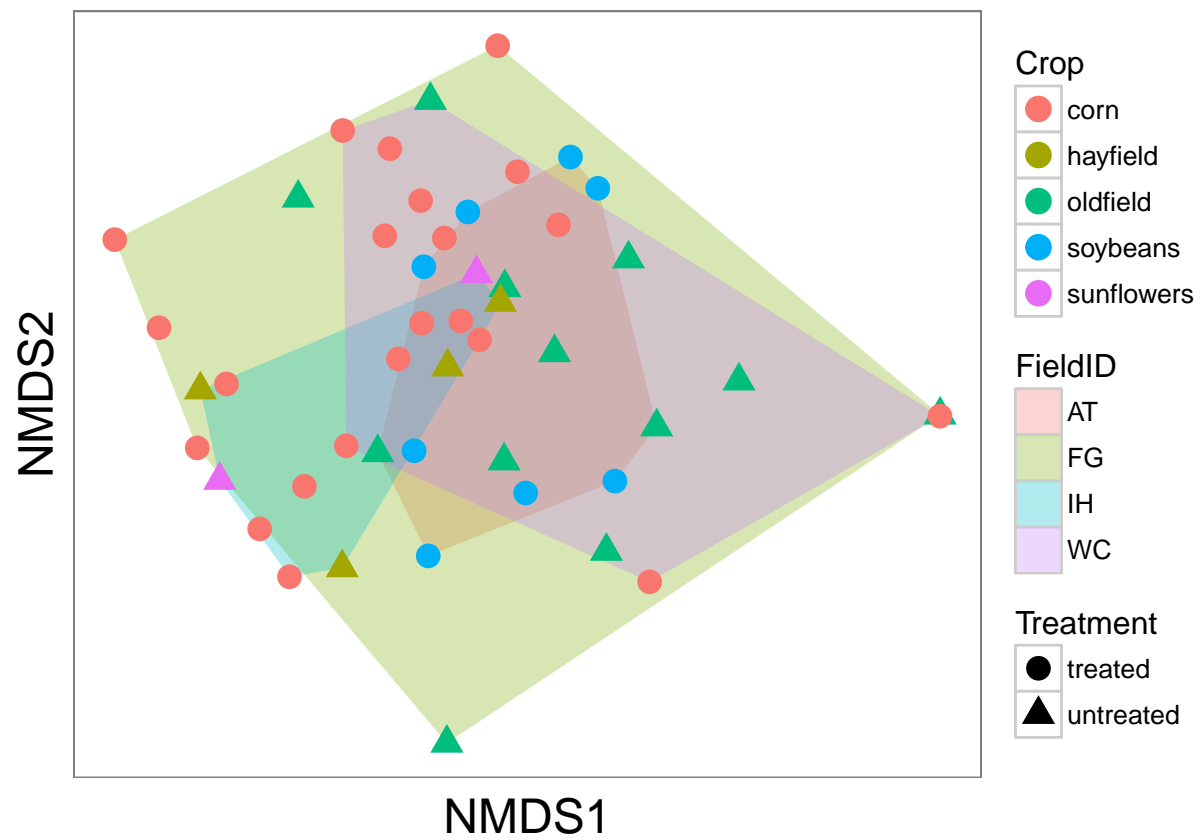
Figure 4: Multidimensional Scaling Showing the Overlap of communities between Management Areas
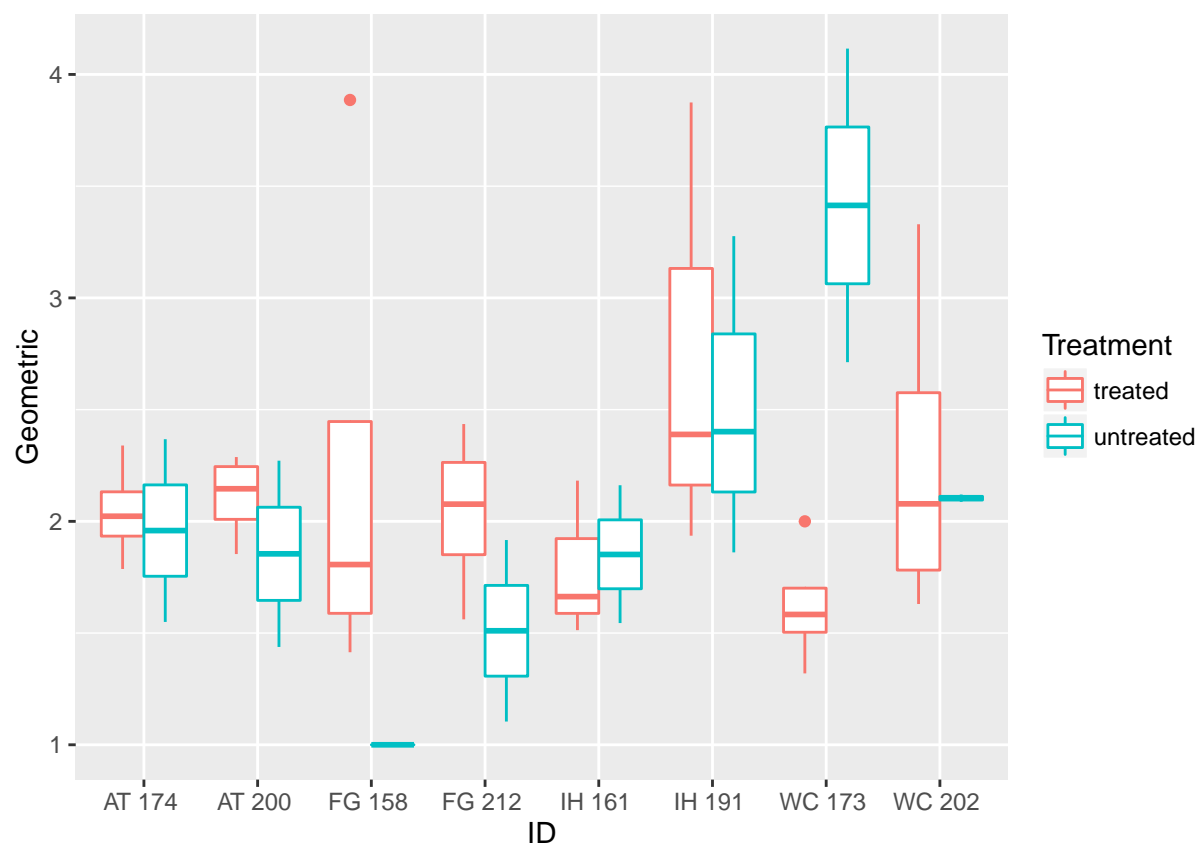
Figure 5: Alpha diversity grouped by site and Treatment

| ID	Treatment	Median	Mean	SD
AT 174	treated	2.022910	2.043021	0.2291168
AT 174	untreated	1.958683	1.958683	0.5782509
AT 200	treated	2.145766	2.108201	0.1951894
AT 200	untreated	1.854673	1.854673	0.5894461
FG 158	treated	1.806673	2.228347	1.1279804
FG 158	untreated	1.000000	1.000000	0.0000000
FG 212	treated	2.076917	2.037688	0.3749527
FG 212	untreated	1.510217	1.510217	0.5743512
IH 161	treated	1.663227	1.786187	0.3511177
IH 161	untreated	1.851749	1.852721	0.3083508
IH 191	treated	2.388991	2.733118	1.0141702
IH 191	untreated	2.401496	2.513003	0.7141058
WC 173	treated	1.583207	1.621480	0.2816919
WC 173	untreated	3.414006	3.414006	0.9922870
WC 202	treated	2.078432	2.279134	0.7585371
WC 202	untreated	2.103638	2.103638	0.0231601
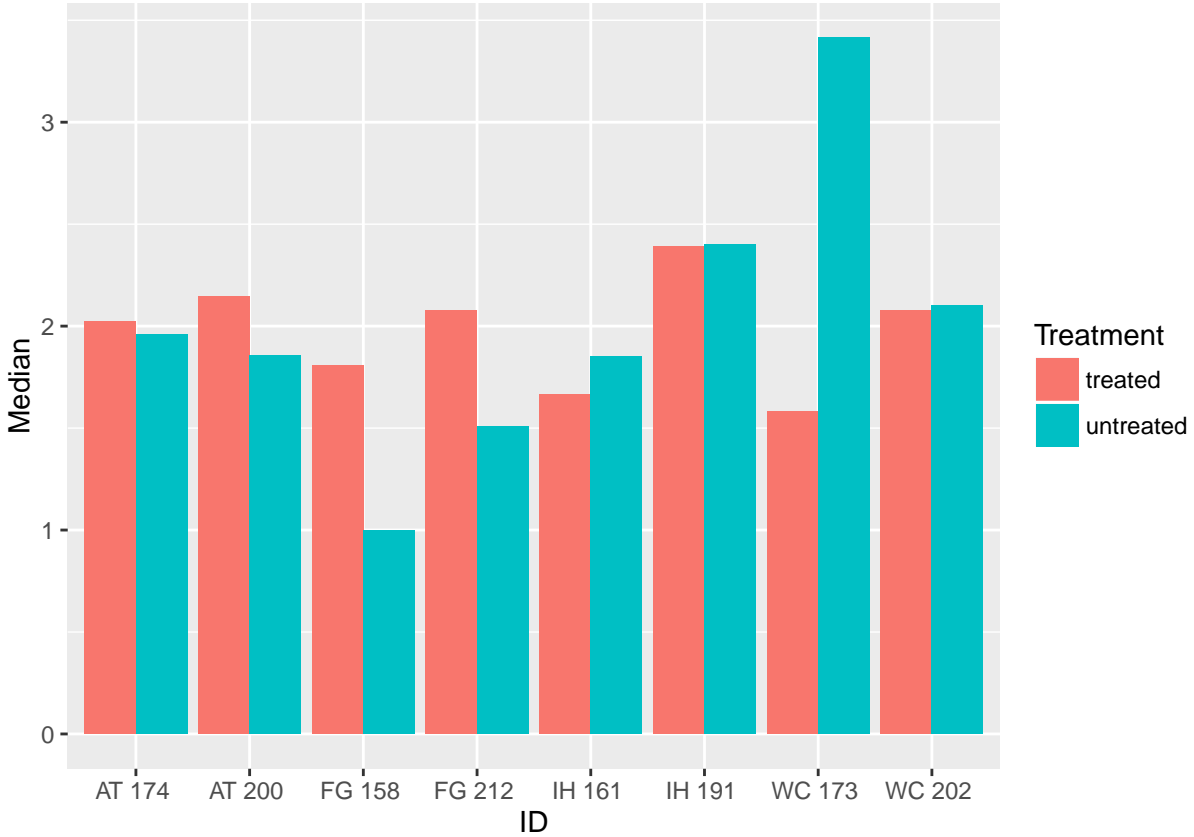
Figure 6: Alpha diversity grouped by site and Treatment

```
## Warning: package 'lubridate' was built under R version 3.2.5

##
## Attaching package: 'lubridate'
```

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	Model 9	M
(Intercept)	2.03***	2.14***	2.03***	2.19***	2.09***	2.01***	1.93***	2.44***	2.01***	1
	(0.18)	(0.17)	(0.24)	(0.23)	(0.10)	(0.12)	(0.15)	(0.39)	(0.19)	(
AvgMgWidth	−0.03*	−0.03*	−0.02*	−0.01				−0.03*	−0.02*	−
	(0.01)	(0.01)	(0.01)	(0.01)				(0.01)	(0.01)	(
CtoMEdge	0.17		0.29*	0.25*		0.15		0.19		(
	(0.10)		(0.11)	(0.11)		(0.11)		(0.10)		
MargArea	1.02*	0.95						1.01*	0.87	
	(0.50)	(0.51)						(0.50)	(0.51)	
DistNearTr			0.00							
			(0.00)							
FieldIDFG			−0.67*	−0.47						−
			(0.30)	(0.28)						(
FieldIDIH			0.44	0.37						
			(0.28)	(0.28)						
FieldIDWC			−0.06	0.15						
			(0.29)	(0.26)						
DaysSinceP							0.01		0.00	
							(0.00)		(0.00)	(
CollectTime								−0.00		
								(0.00)		
Humidity										
PercMgMow										
Treatmentuntreated										
NumSpBloom										
Log Likelihood	-43.94	-45.41	-40.05	-41.62	-47.97	-46.88	-46.89	-43.16	-44.50	-
AICc	99.39	99.80	99.99	100.20	100.21	100.33	100.34	100.48	100.51	1
Delta	0.00	0.41	0.61	0.81	0.83	0.94	0.96	1.09	1.12	
Weight	0.08	0.06	0.06	0.05	0.05	0.05	0.05	0.05	0.04	
Num. obs.	46	46	46	46	46	46	46	46	46	

$^{***}p < 0.001$, $^{**}p < 0.01$, $^{*}p < 0.05$

Table 2: Statistical models

```
## The following object is masked from 'package:base':
##
##     date
```

```
## Fixed term is "(Intercept)"
```

```
## The table was written to the file 'lme.doc'.
```

```
ggplot(Alpharesults, aes(x = Jdate, y = Geometric)) + geom_point(aes(color=Treatment, shape = FieldID))
```