

# Characterizing insect communities using multivariate analyses

ENTMLGY 6702 Entomological Techniques and Data Analysis

# Learning objectives

- 1) Distinguish among different ordination techniques
- 2) Understand how to apply these methods to your data
- 3) Interpret the outputs of the ordination analyses

# Traditional taxonomic approach to study insect diversity

Measure unique “types” and compare among samples or communities

Type: taxonomic unit (species, genera, families, orders)

1. **Abundance** measures the number of individuals of each distinct type
2. **Richness** measures the number of distinct types
3. **Evenness** measures the relative abundance of each type
4. **Diversity** measures the number of types and their evenness

# Activity

**What are the advantages and limitations to assessing communities using diversity metrics?**

# Advantages of multivariate ordination methods

- Analysis of multiple environmental factors on many species simultaneously
- Represents sample and species relationships in a low-dimensional space along (ideally) important and interpretable environmental gradients
- Capable of handling noisy and redundant data
- Accommodates sparse data (i.e., large portion of the entries consist of zeros) because most species are infrequent

# Types of ordination techniques



## Indirect gradient analysis (aka unconstrained ordination)

- Utilizes only the species x sample matrix
- Any environmental data are used after the analysis to aid with interpretation

*\*Nonmetric Multidimensional Scaling and Principal Component Analysis*

# Types of ordination techniques



R package  
vegan

## Indirect gradient analysis (aka unconstrained ordination)

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*\*Nonmetric Multidimensional Scaling and Principal Component Analysis*

## Direct gradient analysis (aka constrained ordination)

- Utilizes environmental data in addition to a species x sample matrix
- Assess whether species composition is related to measured environmental data

*\*Canonical Correspondence Analysis and Redundancy Analysis*



1. Hemlock girdled
2. Hemlock logged
3. Hemlock control
4. Hardwood control

$n = 2$

90 x 90 m plots



## Methods in Ecology and Evolution



*Methods in Ecology and Evolution* 2010, 1, 168–179

doi: 10.1111/j.2041-210X.2010.00025.x

### Experimentally testing the role of foundation species in forests: the Harvard Forest Hemlock Removal Experiment

Aaron M. Ellison\*, Audrey A. Barker-Plotkin, David R. Foster and David A. Orwig

Harvard Forest, Harvard University, 324 North Main Street, Petersham, MA 01366, USA





1. Hemlock girdled
2. Hemlock logged
3. Hemlock control
4. Hardwood control

n = 2

90 x 90 m plots



## Harvard Forest Data Archive

HF106

### Environmental data:

Shrub and herbaceous species in the understory

Understory Vegetation in Hemlock Removal Experiment at Harvard Forest since 2003

### Related Publications

### Data

- [hf106-01](#): species codes ([preview](#))
- [hf106-02](#): o-layer and substrate ([preview](#))
- [hf106-03](#): shrub and herb cover ([preview](#))
- [hf106-04](#): seedling count and cover ([preview](#))
- [hf106-05](#): saplings ([preview](#))
- [hf106-06](#): species list ([preview](#))
- [hf106-07](#): sapling heights ([preview](#))





# Nonmetric Multidimensional Scaling (NMDS)

*Used to assess differences in species composition among sites, treatments, etc.*

Represents (as well as possible) the ordering relationships among sites in species space

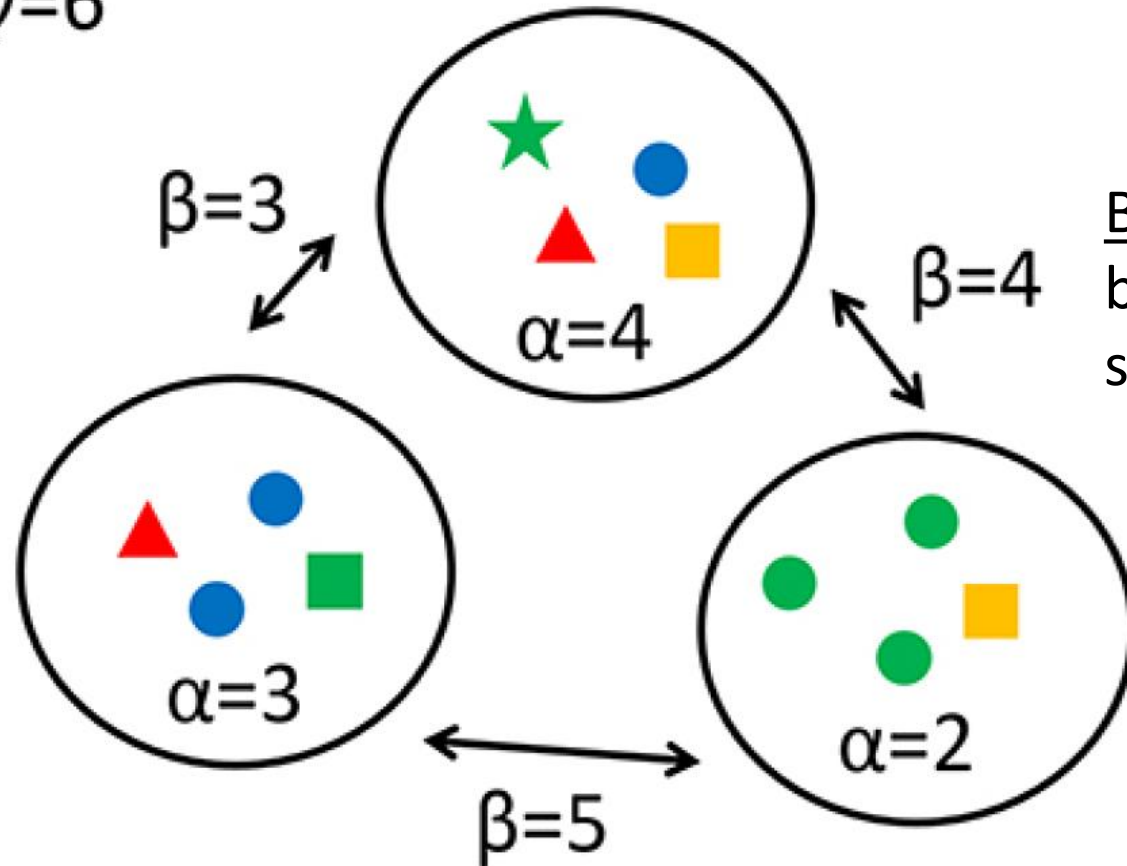
Based on a distance (dissimilarity) matrix as a measure of beta-diversity

Iterative method that maximizes the rank order correlations between the distances in the dissimilarity matrix and the distances in low-dimensional space

Robust technique – no assumptions of normality or linear relationships among variables.

Gamma diversity ( $\gamma$ ) = total number of species across all habitats within a landscape

$\gamma=6$



Beta diversity ( $\beta$ ) = diversity between habitat patches, samples, or sites.

Alpha diversity ( $\alpha$ ) = diversity within a particular habitat patch, sample, or site.

**Figure 5.** Illustration of the concept of alpha, beta, and gamma diversity. Colored symbols represent species, circles represent habitat patches, and the large rectangle represents the landscape.

# Beta diversity metrics

Beta diversity ( $\beta$ ) = diversity between habitat patches, samples, or sites.

Introduced by R.H. Whittaker in 1960

- “The extent of change in community composition, or degree of community differentiation, in relation to a complex-gradient of environment”

$$\beta_W = (\gamma - \alpha) / \alpha$$

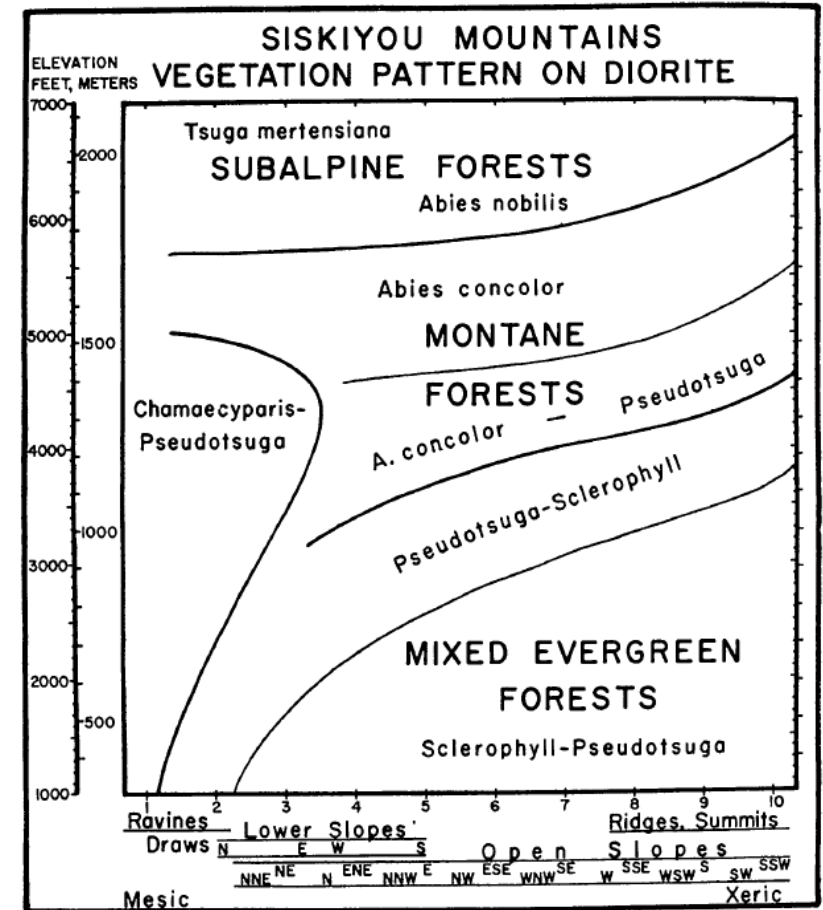


FIG. 11. Mosaic chart of vegetation on quartz diorite, central Siskiyou Mountains, Oregon.

# Measuring the compositional (dis)similarity among communities

Incidence-based or abundance-based dissimilarity matrix

- Sorensen (Bray-Curtis)
- Jaccard
- Euclidean

Create a matrix that compares the number of shared species to the number of unique species among two sites (pairwise)

Whittaker formula:  $\beta_W = (b + c) / (2 * a + b + c)$

a = number of species shared between two samples

b = number of species unique to sample 1

c = number of species unique to sample 2



# Jaccard dissimilarity matrix

vegdist()

```
> dis.matrix.pa <- vegdist(ants4[,1:33], method = "jaccard")
> dis.matrix.pa
```

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
2	0.5789474														
3	0.8823529	0.8000000													
4	0.7058824	0.5000000	0.6000000												
5	0.7368421	0.6923077	0.7142857	0.5000000											
6	0.5652174	0.5555556	0.8750000	0.6875000	0.7222222										
7	0.8235294	0.7000000	0.3333333	0.4000000	0.5714286	0.8125000									
8	0.5882353	0.6923077	0.7142857	0.5000000	0.4444444	0.5625000	0.5714286								
9	0.7222222	0.7692308	0.6666667	0.6250000	0.7000000	0.7777778	0.7142857	0.7000000							
10	0.7619048	0.6428571	0.7777778	0.7272727	0.5454545	0.6842105	0.6666667	0.6666667	0.8461538						
11	0.8888889	0.8181818	0.3333333	0.6666667	0.5714286	0.8823529	0.5000000	0.7500000	0.7142857	0.6666667					
12	0.7368421	0.6923077	0.7142857	0.5000000	0.4444444	0.7222222	0.5714286	0.4444444	0.5555556	0.6666667	0.7500000				
13	0.6315789	0.7333333	0.7777778	0.7272727	0.6666667	0.6111111	0.6666667	0.5454545	0.7500000	0.7142857	0.8000000	0.6666667			
14	0.7777778	0.7619048	0.8750000	0.8333333	0.7222222	0.6086957	0.8125000	0.7222222	0.8421053	0.6111111	0.8125000	0.7222222	0.6111111		
15	0.8823529	0.8000000	0.0000000	0.6000000	0.7142857	0.8750000	0.3333333	0.7142857	0.6666667	0.7777778	0.3333333	0.7142857	0.7777778	0.8750000	
16	0.8000000	0.7857143	0.7142857	0.6666667	0.4444444	0.7894737	0.5714286	0.6000000	0.7000000	0.5454545	0.5714286	0.4444444	0.6666667	0.6470588	0.7142857

```
> |
```



# Run a non-metric multidimensional scaling (NMDS) model

```
> nmds.ants.pa <- metaMDS(dis.matrix.pa, trymax = 500, autotransform = TRUE, k = 2)
```

```
Run 0 stress 0.1183155
Run 1 stress 0.1690299
Run 2 stress 0.1183155
... Procrustes: rmse 8.597158e-06  max resid 1.721618e-05
... Similar to previous best
Run 3 stress 0.169116
Run 4 stress 0.1580036
Run 5 stress 0.1183155
... New best solution
... Procrustes: rmse 5.576468e-06  max resid 1.129933e-05
... Similar to previous best
Run 6 stress 0.1305361
Run 7 stress 0.1894816
Run 8 stress 0.1496685
Run 9 stress 0.1637825
Run 10 stress 0.1493727
Run 11 stress 0.1183155
... Procrustes: rmse 2.566557e-05  max resid 4.673951e-05
... Similar to previous best
Run 12 stress 0.1305361
Run 13 stress 0.1183155
... Procrustes: rmse 5.030353e-05  max resid 9.327251e-05
... Similar to previous best
Run 14 stress 0.1305361
Run 15 stress 0.1183155
... Procrustes: rmse 1.159646e-05  max resid 2.173897e-05
... Similar to previous best
Run 16 stress 0.1305361
Run 17 stress 0.1183155
... New best solution
... Procrustes: rmse 2.715269e-06  max resid 5.792493e-06
... Similar to previous best
Run 18 stress 0.1183155
... Procrustes: rmse 7.432958e-06  max resid 1.413503e-05
... Similar to previous best
Run 19 stress 0.1183155
... Procrustes: rmse 8.136855e-05  max resid 0.000151948
... Similar to previous best
Run 20 stress 0.1787082
*** Best solution repeated 3 times
```

```
> nmds.ants.pa
```

Call:

```
metaMDS(comm = dis.matrix.pa, k = 2, trymax = 500, autotransform = TRUE)
```

global Multidimensional Scaling using monoMDS

Data: dis.matrix.pa

Distance: jaccard

Dimensions: 2

Stress: 0.1183155

Stress type 1, weak ties

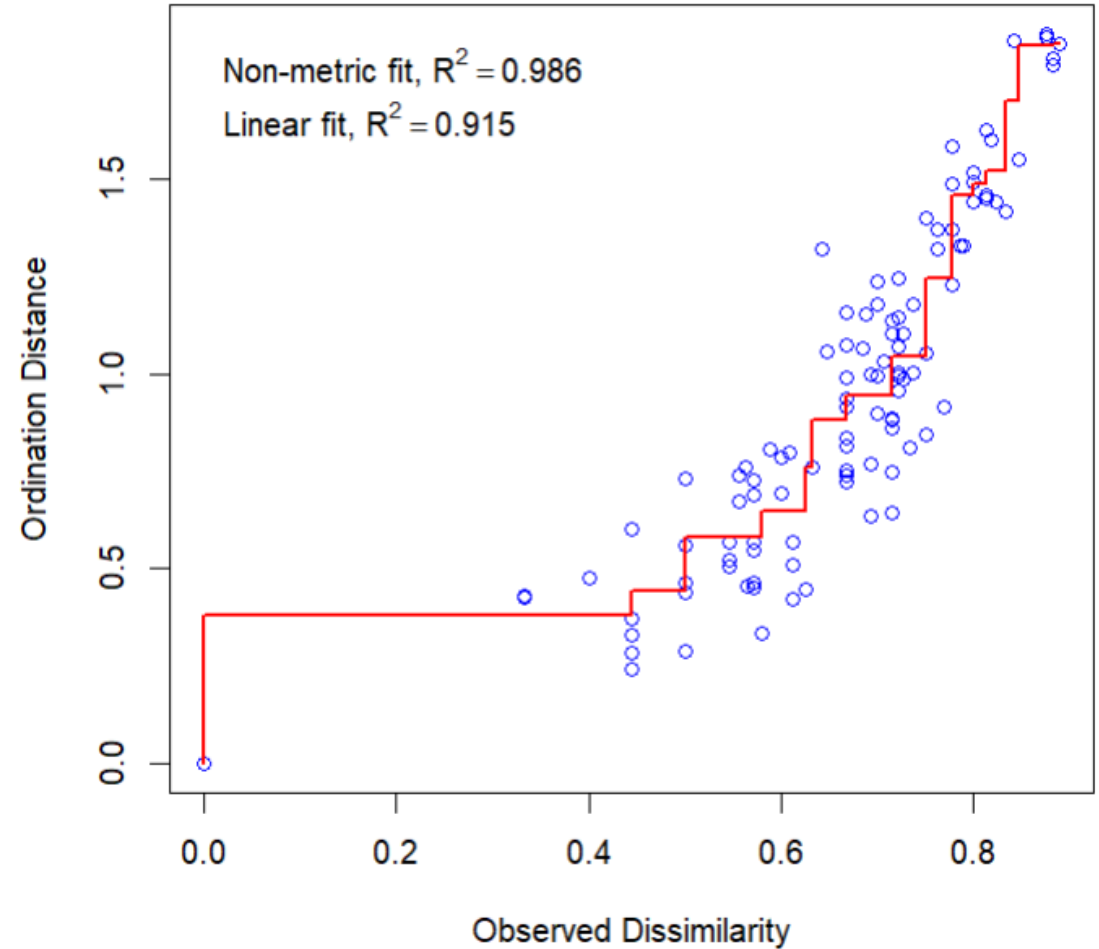
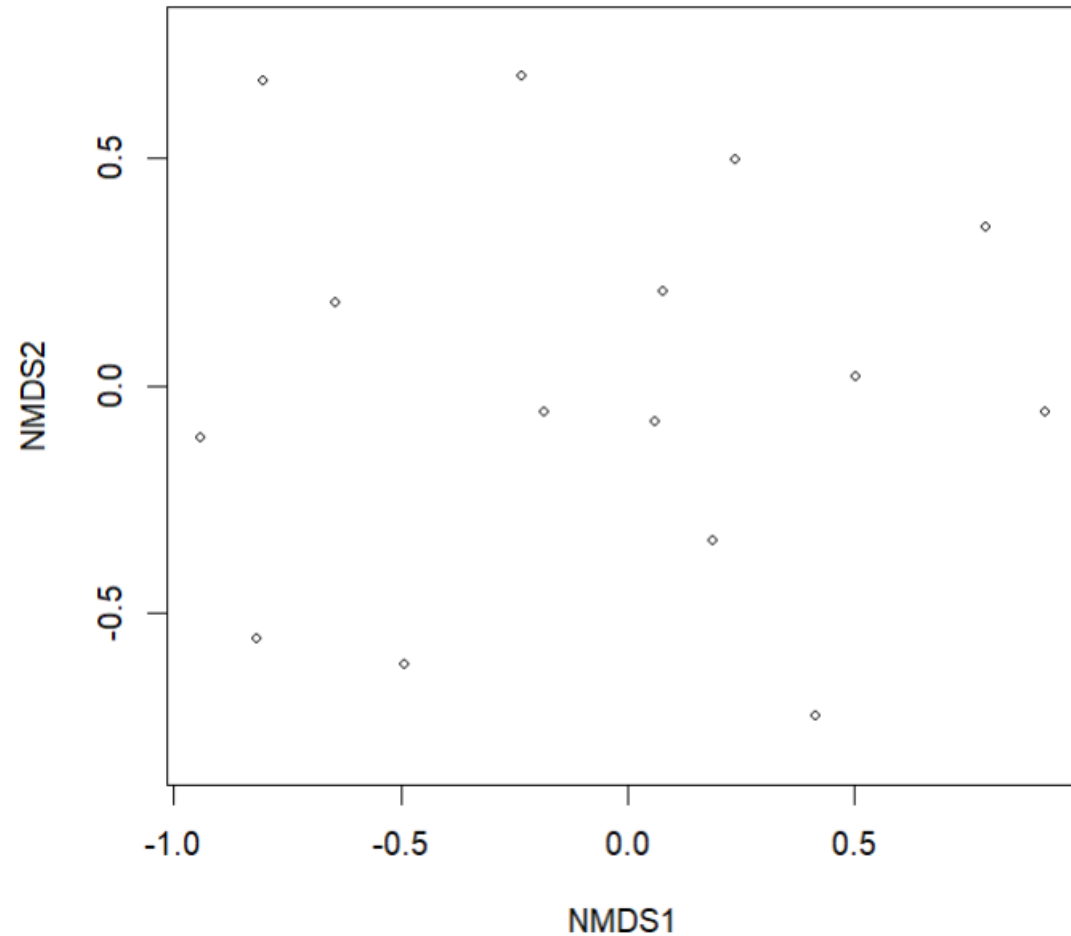
Best solution was repeated 3 times in 20 tries

The best solution was from try 17 (random start)

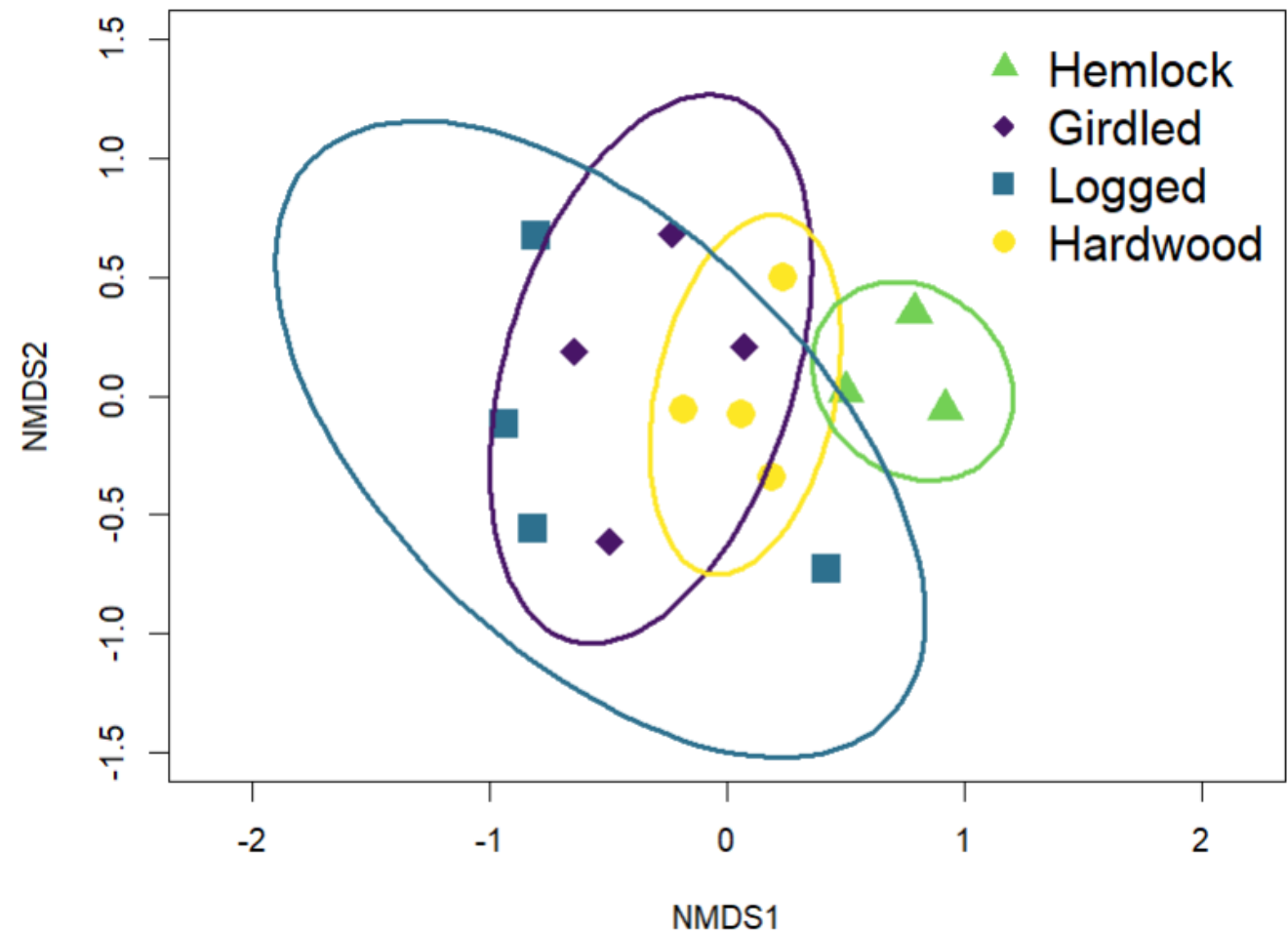
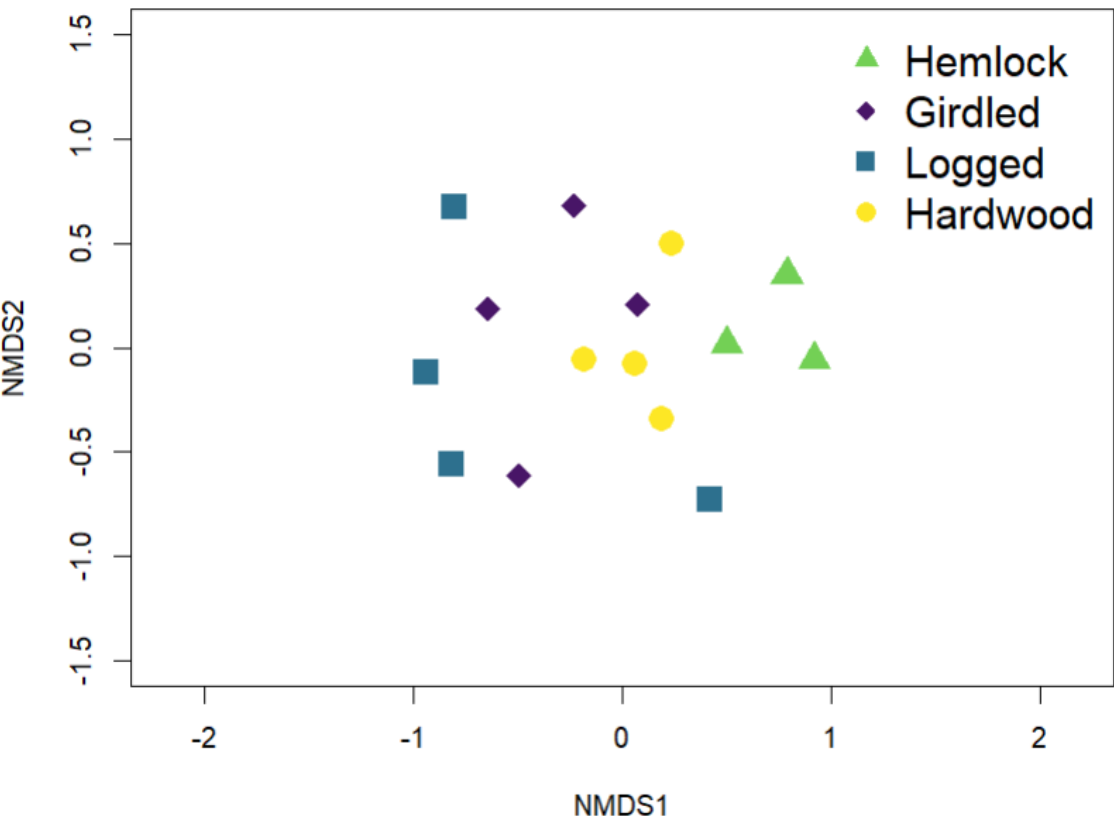
Scaling: centring, PC rotation, halfchange scaling

Species: scores missing

# Run a non-metric multidimensional scaling (NMDS) model



# Visualize with a non-metric multidimensional scaling (NMDS) plot



# **NMDS often paired with PERMANOVA and BETADISPER**

## **Permutational multivariate analysis of variance (PERMANOVA)**

- tests whether the group centroid of communities differs among a categorical grouping factor in multivariate space

## **Homogeneity of multivariate group dispersion (BETADISPER)**

- tests whether the dispersion of a categorical grouping factor from its spatial medial is different between groups.
- Multivariate analogue of Levene's test for homogeneity of variances

# PERMANOVA

```
> adonis2(dis.matrix.pa ~ ants4$treatment, permutations = 999)
```

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Permutation: free

Number of permutations: 999

```
adonis2(formula = dis.matrix.pa ~ ants4$treatment, permutations = 999)
```

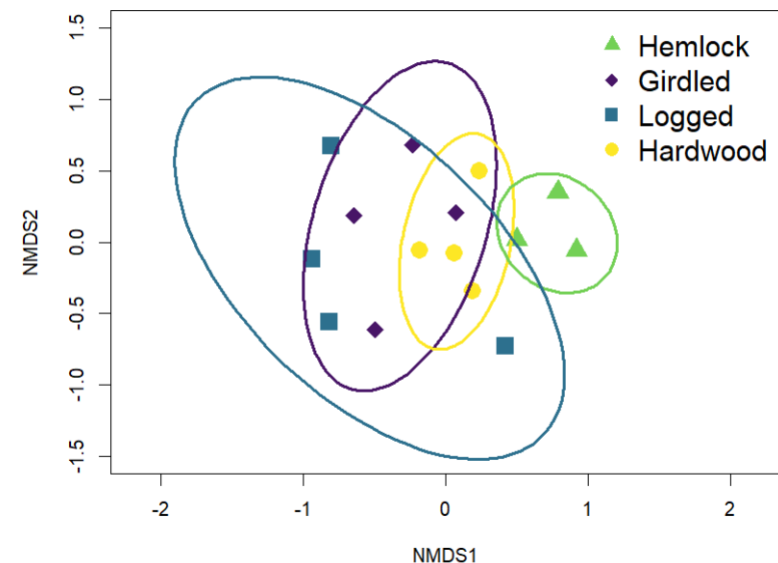
	Df	SumOfSqs	R2	F	Pr(>F)
ants4\$treatment	3	1.4433	0.41295	2.8137	0.001 ***
Residual	12	2.0518	0.58705		
Total	15	3.4950	1.00000		

---

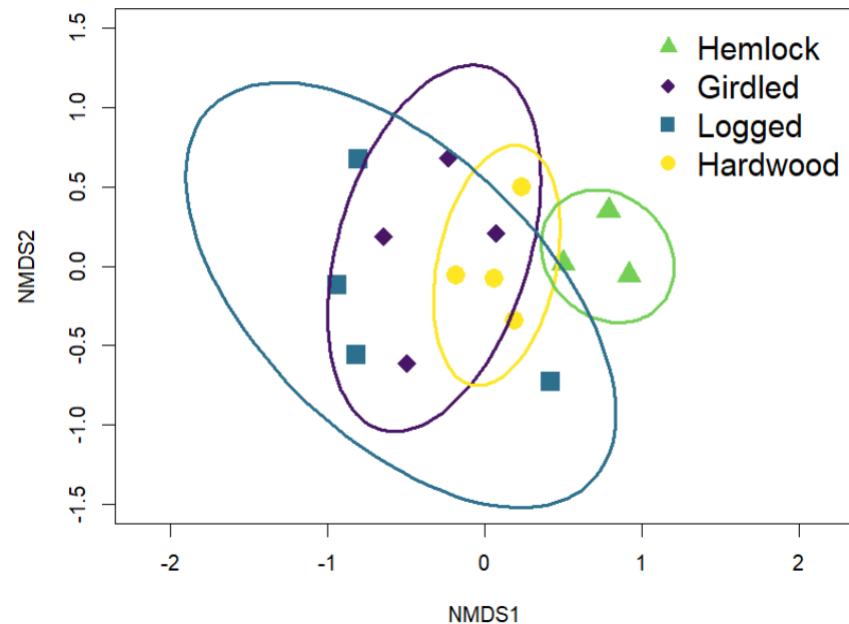
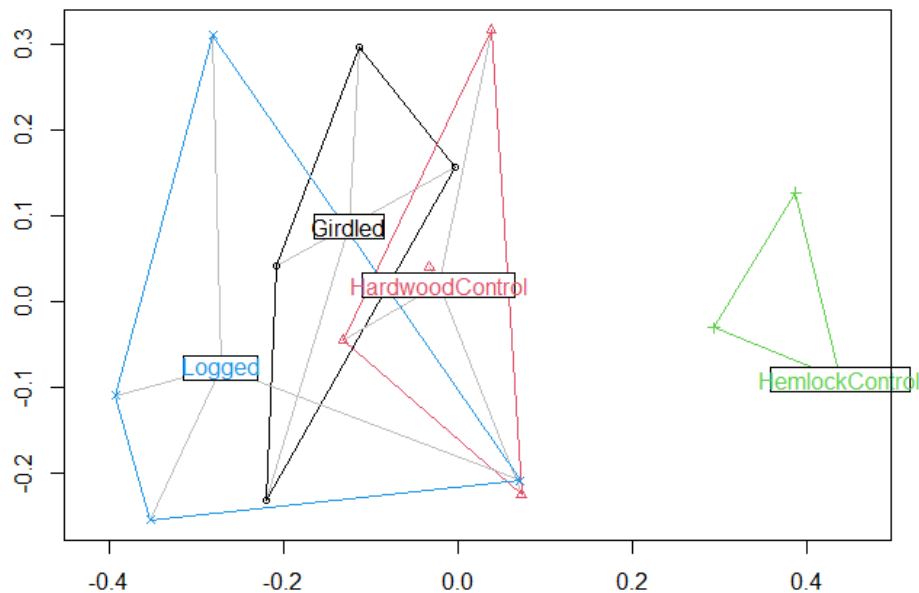
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> pairwise.adonis(dis.matrix.pa, ants4$treatment)
```

	pairs	Df	SumsOfSqs	F.Model	R2	p.value	p.adjusted	sig
1	Logged vs Girdled	1	0.2406823	0.9936814	0.1420827	0.442	1.000	
2	Logged vs HemlockControl	1	0.8663977	5.4361524	0.4753480	0.037	0.222	
3	Logged vs HardwoodControl	1	0.3708324	1.8426037	0.2349480	0.062	0.372	
4	Girdled vs HemlockControl	1	0.6411288	4.5565102	0.4316304	0.029	0.174	
5	Girdled vs HardwoodControl	1	0.2146477	1.1756126	0.1638345	0.395	1.000	
6	HemlockControl vs HardwoodControl	1	0.5528551	5.5425213	0.4801829	0.024	0.144	



# BETADISPER



```
> anova(ants.beta.pa)
Analysis of Variance Table
```

Response: Distances

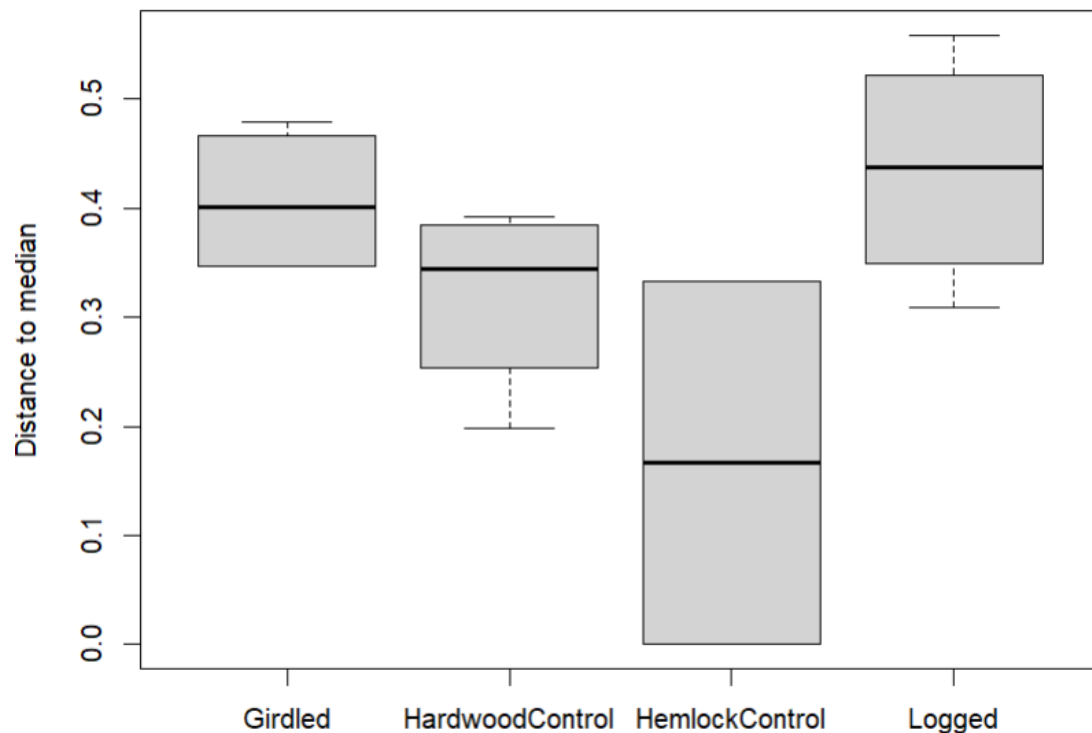
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Groups	3	0.17539	0.058465	3.7923	0.04009 *
Residuals	12	0.18500	0.015417		

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> TukeyHSD(ants.beta.pa, which = "group", conf.level = 0.95)
Tukey multiple comparisons of means
95% family-wise confidence level
```

Fit: aov(formula = distances ~ group, data = df)

\$group	diff	lwr	upr	p adj
HardwoodControl-Girdled	-0.08730021	-0.347960453	0.17336003	0.7554041
HemlockControl-Girdled	-0.23990411	-0.500564356	0.02075613	0.0749247
Logged-Girdled	0.02930838	-0.231351866	0.28996862	0.9865382
HemlockControl-HardwoodControl	-0.15260390	-0.413264145	0.10805634	0.3474641
Logged-HardwoodControl	0.11660859	-0.144051654	0.37726883	0.5637376
Logged-HemlockControl	0.26921249	0.008552249	0.52987273	0.0422404



# Principal Component Analysis (PCA)

*Used to assess relationships among variables along a reduced number of axes*

Eigenvector-based method

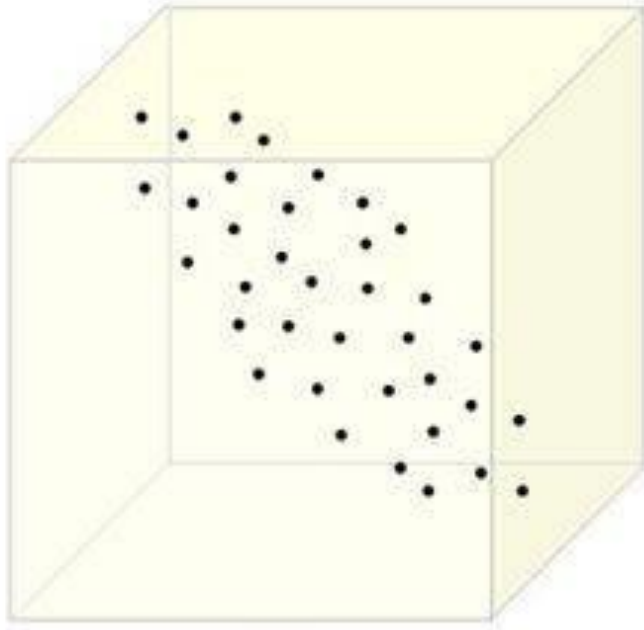
Eigen decomposition of a dispersion matrix (linear covariances or correlations)

Requires raw, quantitative data

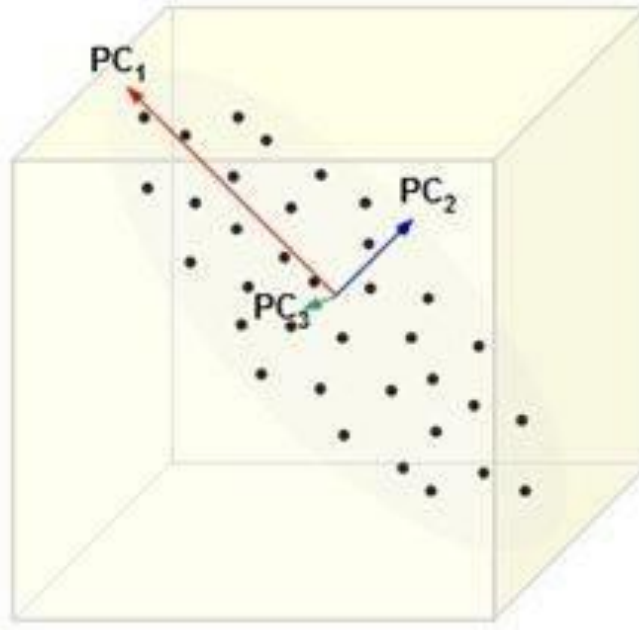
Descriptive / exploratory



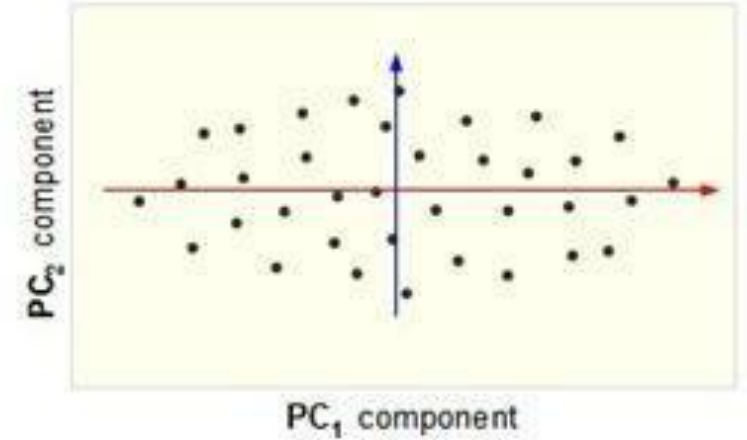
# Principal Component Analysis (PCA)



a



b



c

3D



2D

## Wide format

# 2015 & 2018

[illegible]

# Principal Component Analysis (PCA)

```
> herb.pca <- rda(herb3[,5:23], scale = FALSE)
> summary(herb.pca)
```

Call:  
rda(X = herb3[, 5:23], scale = FALSE)

Partitioning of variance:

	Inertia	Proportion	
Total	14276	1	Total variance
Unconstrained	14276	1	

Eigenvalues, and their contribution to the variance

Importance of components:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigenvalue	1.158e+04	1701.3633	431.56315	272.20286	189.27388	55.837588	24.243215	1.225e+01	6.2733470	2.4520883	1.041e+00	2.706e-01
Proportion Explained	8.111e-01	0.1192	0.03023	0.01907	0.01326	0.003911	0.001698	8.584e-04	0.0004394	0.0001718	7.293e-05	1.896e-05
Cumulative Proportion	8.111e-01	0.9303	0.96049	0.97956	0.99282	0.996728	0.998427	9.993e-01	0.9997245	0.9998963	1.000e+00	1.000e+00

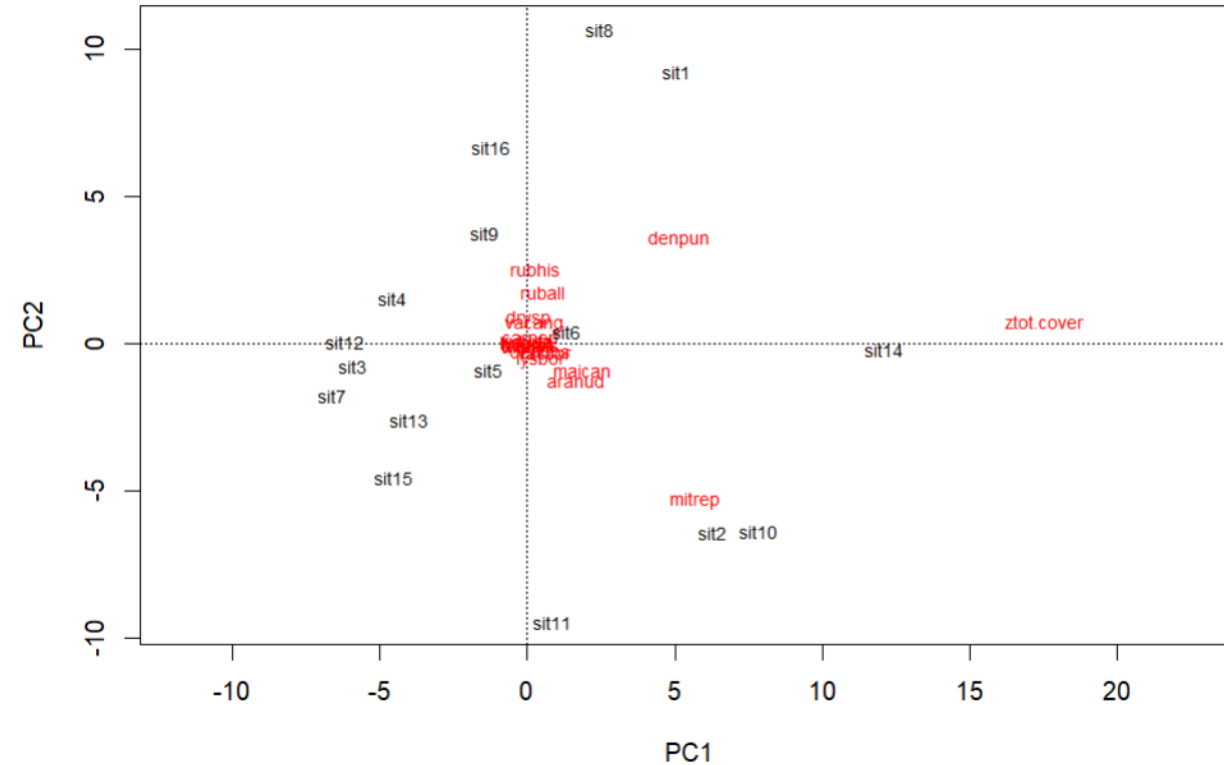
	PC13	PC14	PC15
Eigenvalue	1.156e-01	5.185e-02	1.063e-03
Proportion Explained	8.101e-06	3.632e-06	7.445e-08
Cumulative Proportion	1.000e+00	1.000e+00	1.000e+00

scaling 2 for species and site scores

\* Species are scaled proportional to eigenvalues

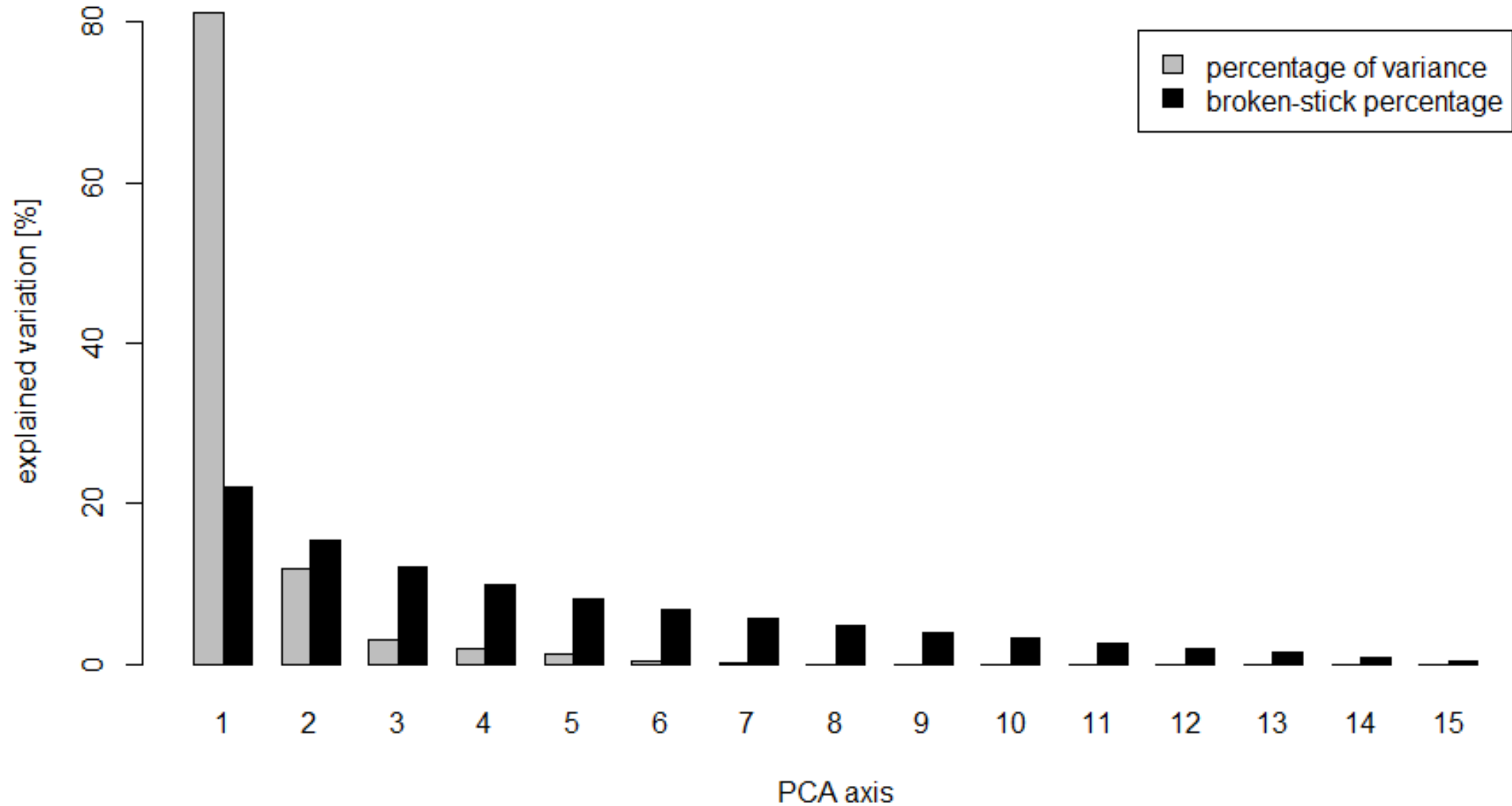
\* Sites are unscaled: weighted dispersion equal on all dimensions

\* General scaling constant of scores: 21.51154



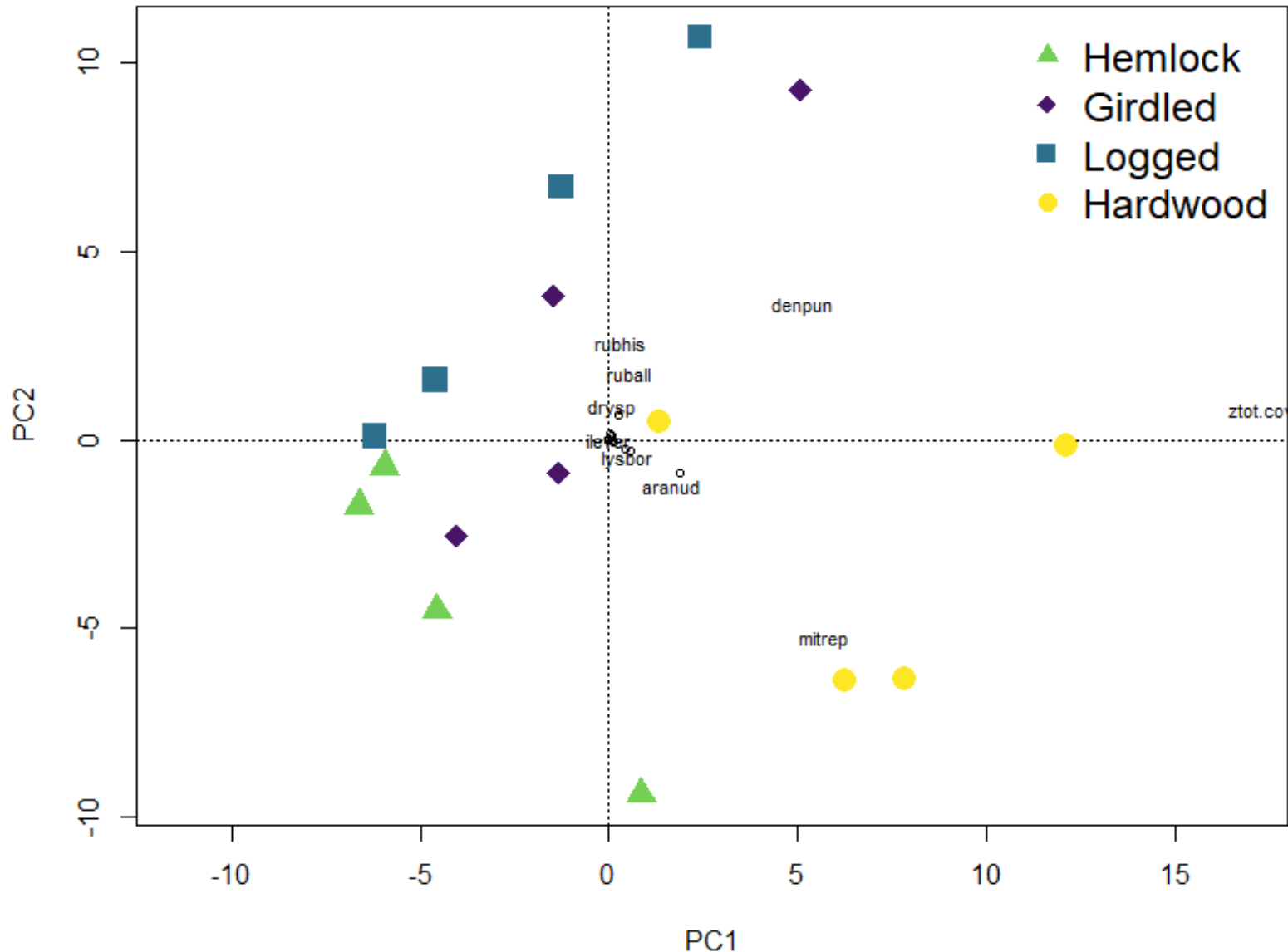
**Axes 1 & 2 represent 93% of the variation**

# Principal Component Analysis (PCA) - Broken Stick Method



# Principal Component Analysis (PCA)

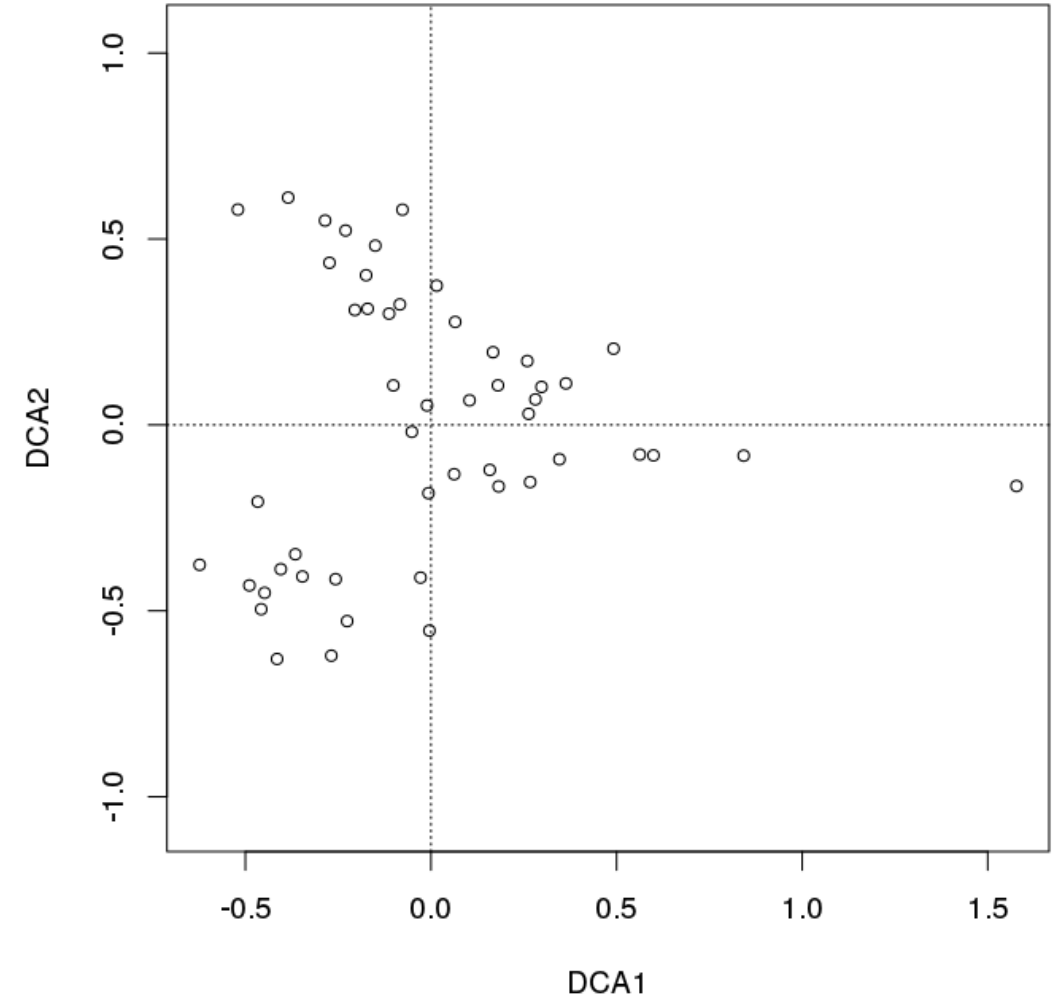
Axis 1: 81.1%  
Axis 2: 11.9%



# Principal Component Analysis (PCA)

Arch or horseshoe effect – distortion in ordination diagram

- 1) Use sample scores on PCA axes as environmental predictor variables
- 2) Identify environmental variables highly correlated with PCA axes



# Types of ordination techniques



R package  
vegan

## Indirect gradient analysis (aka unconstrained ordination)

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*\*Nonmetric Multidimensional Scaling and Principal Component Analysis*

## Direct gradient analysis (aka constrained ordination)

- Utilizes environmental data in addition to a species x sample matrix
- Assess whether species composition is related to measured environmental data

*\*Canonical Correspondence Analysis and Redundancy Analysis*



# Canonical Correspondence Analysis and Redundancy Analysis

*Used to assess whether species composition is related to measured environmental variables*

Explores relationships between two matrices – response and predictor

Combines multiple regression with classical ordination

Can be used to test hypotheses via permutation tests

Linear (RDA) or unimodal (CCA)

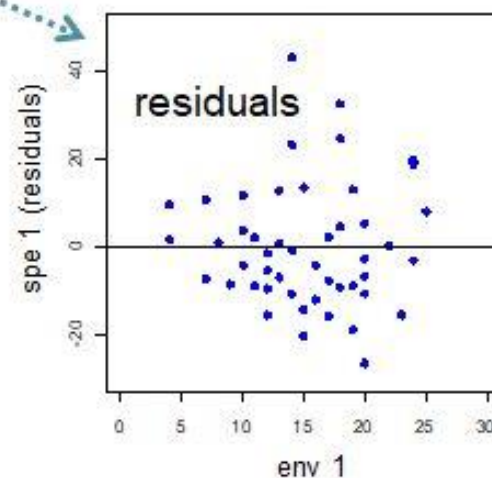
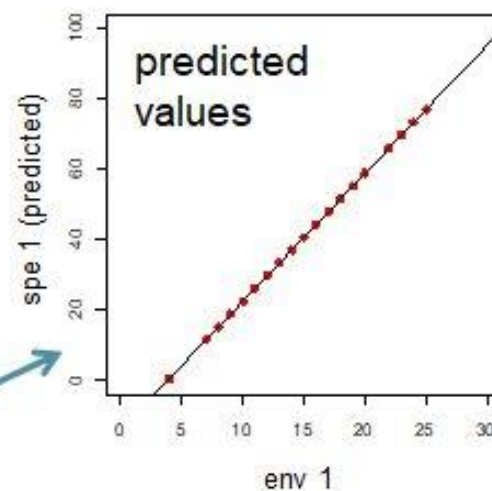
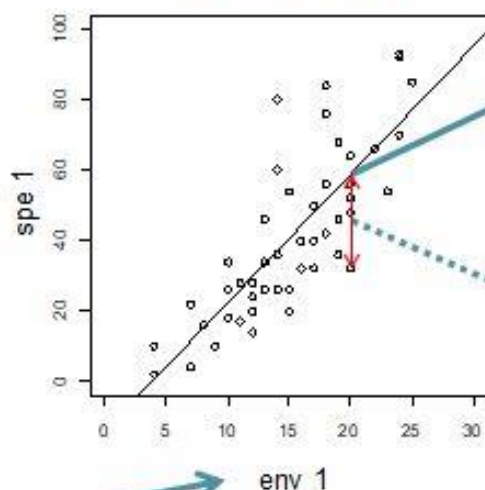
sample × species matrix

	spe 1	spe 2	spe 3
sam 1			
sam 2			
sam 3			
sam 4			
sam 5			
sam 6			
sam 7			

	env 1
sam 1	
sam 2	
sam 3	
sam 4	
sam 5	
sam 6	
sam 7	

matrix of environmental variables  
(single variable in this case)

regression of species  
abundances on  
env. variable



matrix of predicted  
values

	spe 1	spe 2	spe 3
sam 1			
sam 2			
sam 3			
sam 4			
sam 5			
sam 6			
sam 7			

	spe 1	spe 2	spe 3
sam 1			
sam 2			
sam 3			
sam 4			
sam 5			
sam 6			
sam 7			

matrix of residuals

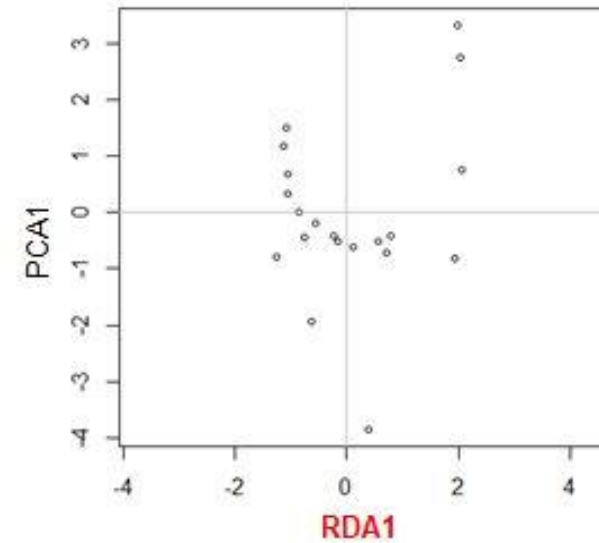
matrix of predicted values

	spe 1	spe 2	spe 3
sam 1			
sam 2			
sam 3			
sam 4			
sam 5			
sam 6			
sam 7			

PCA on  
predicted  
values

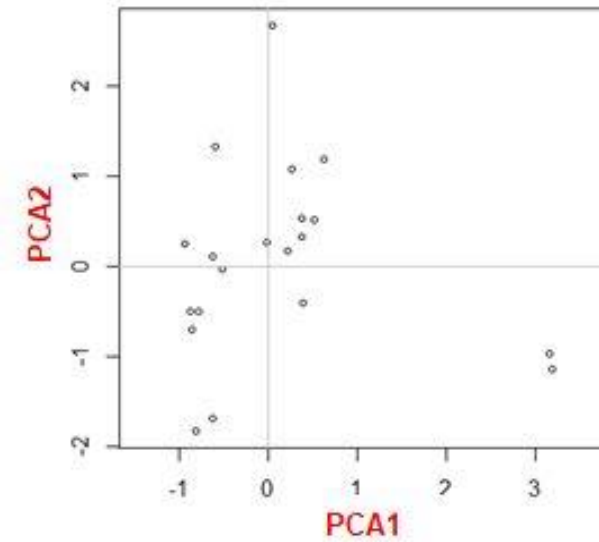


constrained ordination axes



	spe 1	spe 2	spe 3
sam 1			
sam 2			
sam 3			
sam 4			
sam 5			
sam 6			
sam 7			

PCA on  
residuals



matrix of residuals

unconstrained ordination  
axes

# RDA

Axis 1: 42.2%

Axis 2: 32.2%

```
> ants.rda <- rda(ants3[,6:38] ~ ., herb3[,5:23])
> ants.rda
Call: rda(formula = ants3[, 6:38] ~ aranud + carpen +
  lysqua + maican + medvir + mitrep + ruball + rubhis +
  = herb3[, 5:23])
```

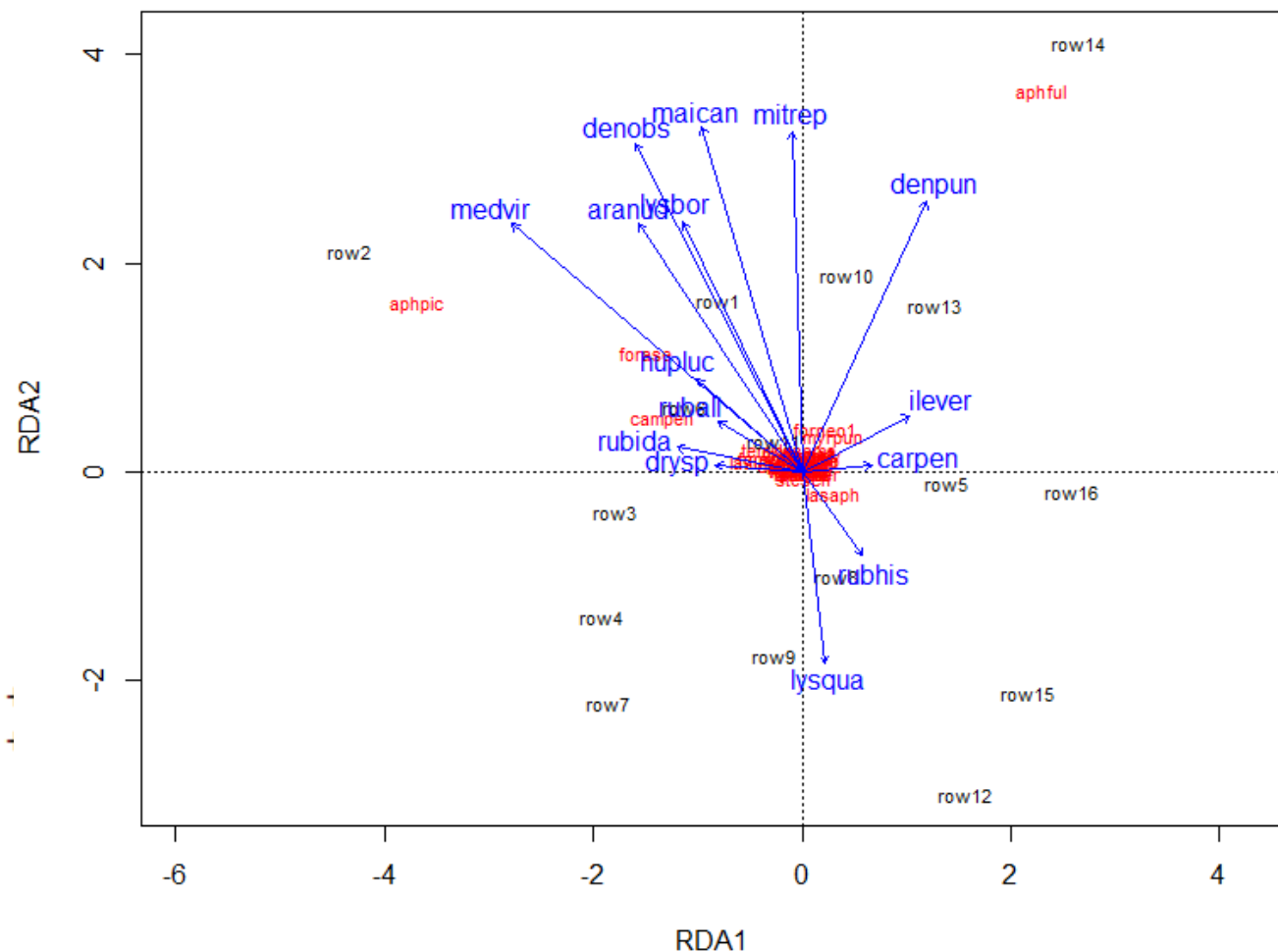
	Inertia	Proportion	Rank
Total	208.5	1.0	
Constrained	208.5	1.0	15
Unconstrained	0.0	0.0	0

Inertia is variance

Some constraints or conditions were aliased because they were redundant

Eigenvalues for constrained axes:

RDA1	RDA2	RDA3	RDA4	RDA5	RDA6	RDA7	RDA8	RDA9	RDA10	RDA11	RDA12	RDA13	RDA14	RDA15
87.96	67.27	21.84	15.90	6.54	3.11	2.15	1.57	0.88	0.56	0.38	0.15	0.09	0.06	0.02



# RDA – Hypothesis testing

ordistep()

```
Step: ants3[, 6:38] ~ medvir + ztot.cover
```

	Df	AIC	F	Pr(>F)
- ztot.cover	1	83.792	5.2702	0.005 **
- medvir	1	84.307	5.8684	0.005 **

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1

	Df	AIC	F	Pr(>F)
+ ilever	1	80.670	1.3260	0.200
+ rubida	1	80.546	1.4292	0.250
+ ruball	1	80.856	1.1715	0.365
+ hupluc	1	81.062	1.0034	0.380
+ drysp	1	81.006	1.0486	0.410
+ lysbor	1	81.174	0.9127	0.455
+ lysqua	1	81.236	0.8625	0.465
+ uvuses	1	81.210	0.8837	0.505
+ carpen	1	81.231	0.8664	0.515
+ denobs	1	81.322	0.7937	0.545
+ rubhis	1	81.298	0.8130	0.565
+ maican	1	81.404	0.7284	0.595
+ vacang	1	81.369	0.7558	0.610
+ mitrep	1	81.574	0.5934	0.730
+ aranud	1	81.807	0.4119	0.855
+ denpun	1	81.870	0.3628	0.880
+ vaccor	1	81.917	0.3266	0.905

summary()

Partitioning of variance:

	Inertia	Proportion
Total	208.46	1.0000
Constrained	97.27	0.4666
Unconstrained	111.19	0.5334

Eigenvalues, and their contribution to the variance

Importance of components:

	RDA1	RDA2	PC1	PC2	PC3
Eigenvalue	52.1979	45.0741	48.4266	27.9073	16.47123
Proportion Explained	0.2504	0.2162	0.2323	0.1339	0.07901
Cumulative Proportion	0.2504	0.4666	0.6989	0.8328	0.91182

	PC11	PC12	PC13
Eigenvalue	0.287031	0.1298173	0.0595555
Proportion Explained	0.001377	0.0006227	0.0002857
Cumulative Proportion	0.999092	0.9997143	1.0000000

Accumulated constrained eigenvalues

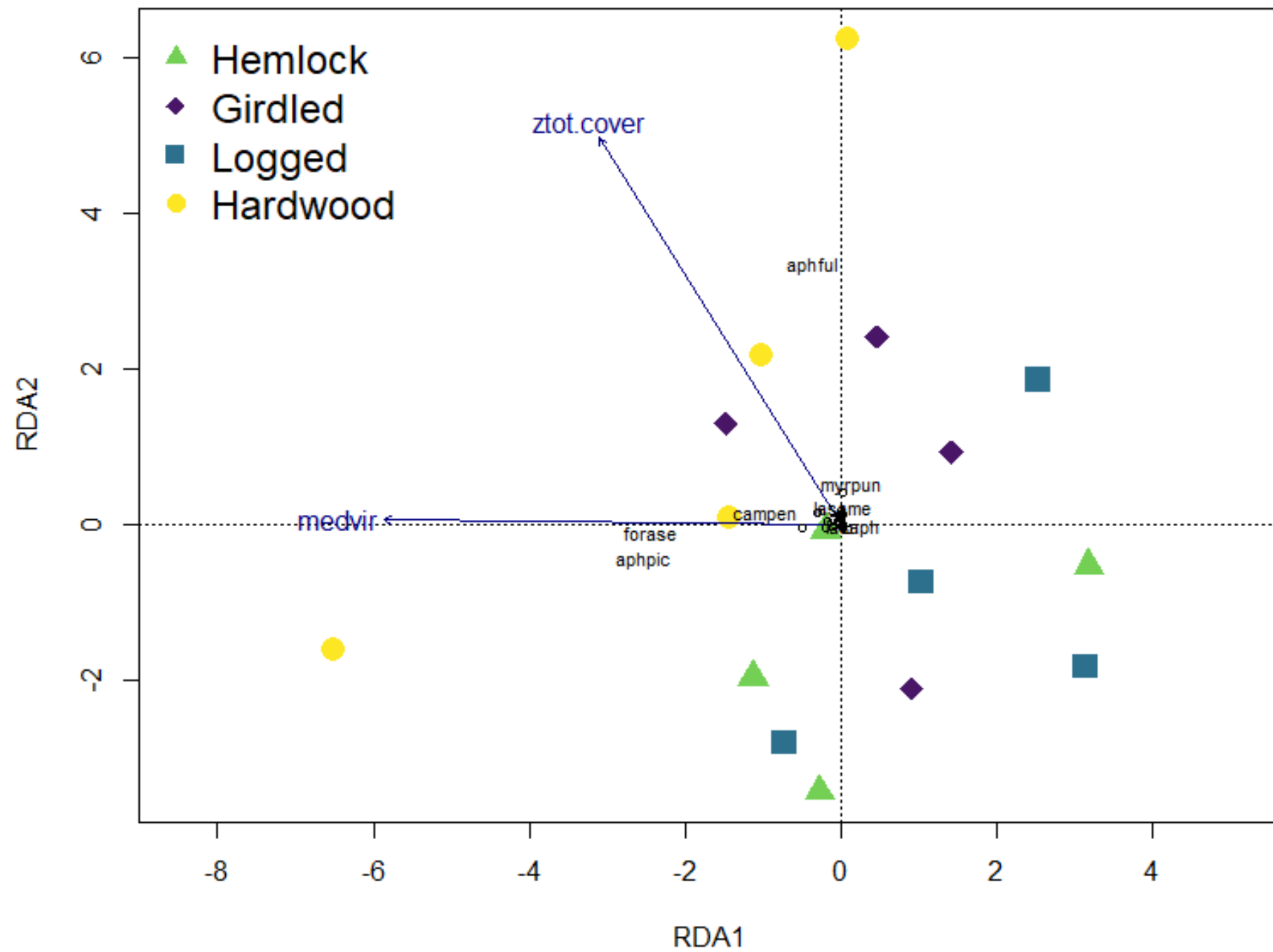
Importance of components:

	RDA1	RDA2
Eigenvalue	52.1979	45.0741
Proportion Explained	0.5366	0.4634
Cumulative Proportion	0.5366	1.0000

Axis 1: 25%

Axis 2: 21.6%

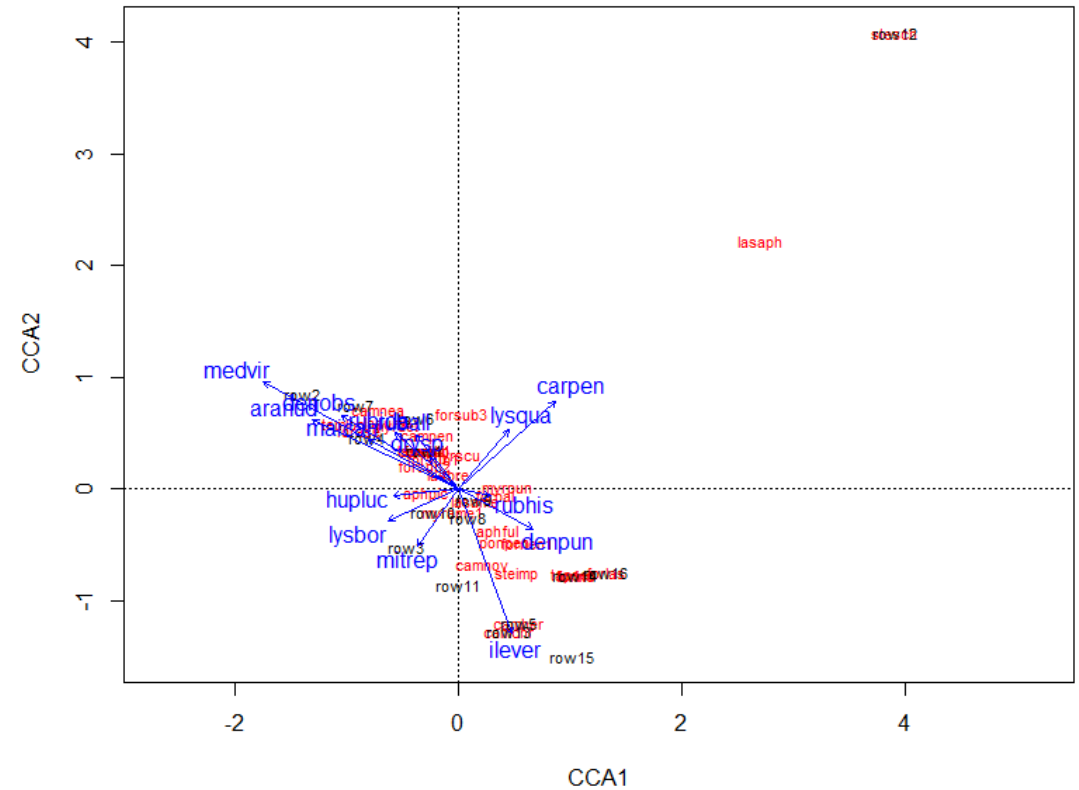
# RDA



# CCA

Axis 1: 20.9%

Axis 2: 17.1%



```
> ants.cca <- cca(ants3[,6:38] ~ ., herb3[,5:23])
> ants.cca
Call: cca(formula = ants3[, 6:38] ~ aranud + carpen + denobs + denpun + drysp + hupluc + ilever + lysbor + lysqua +
maican + medvir + mitrep + ruball + rubhis + rubida + uvuses + vacang + vaccor + ztot.cover, data = herb3[, 5:23])
```

	Inertia	Proportion	Rank
Total	1.365	1.000	
Constrained	1.365	1.000	15
Unconstrained	0.000	0.000	0

Inertia is scaled Chi-square  
Some constraints or conditions were aliased because they were redundant

Eigenvalues for constrained axes:

CCA1	CCA2	CCA3	CCA4	CCA5	CCA6	CCA7	CCA8	CCA9	CCA10	CCA11	CCA12	CCA13	CCA14	CCA15
0.28630	0.23364	0.17296	0.16450	0.10762	0.10227	0.08938	0.07098	0.05823	0.02451	0.01893	0.01702	0.00947	0.00639	0.00249



# CCA – Hypothesis testing

Axis 1: 13.8%

Axis 2: 11.1%

ordistep()

summary()

```
Step: ants3[, 6:38] ~ denobs + medvir
```

	Df	AIC	F	Pr(>F)
- denobs	1	66.879	1.9527	0.025 *
- medvir	1	66.991	2.0583	0.025 *

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.'

	Df	AIC	F	Pr(>F)
+ ruball	1	66.547	1.6765	0.115
+ ilever	1	66.958	1.3295	0.170
+ rubida	1	66.854	1.4170	0.185
+ drysp	1	66.871	1.4023	0.205
+ denpun	1	66.997	1.2970	0.215
+ mitrep	1	66.993	1.3011	0.240
+ ztot.cover	1	67.017	1.2811	0.240
+ uvuses	1	67.098	1.2135	0.305
+ lysbor	1	67.626	0.7851	0.565
+ aranud	1	67.810	0.6388	0.595
+ vaccor	1	67.998	0.4909	0.715
+ hupluc	1	67.685	0.7381	0.740
+ rubhis	1	68.005	0.4858	0.795
+ carpen	1	67.799	0.6477	0.800
+ maican	1	68.085	0.4230	0.830
+ vacang	1	68.146	0.3757	0.845
+ lysqua	1	68.012	0.4799	0.890

Partitioning of scaled Chi-square:

	Inertia	Proportion
Total	1.3647	1.0000
Constrained	0.3415	0.2502
Unconstrained	1.0232	0.7498

Eigenvalues, and their contribution to the scaled Chi-square

Importance of components:

	CCA1	CCA2	CA1	CA2	CA3	CA4
Eigenvalue	0.1891	0.1523	0.2528	0.2107	0.1418	0.10901
Proportion Explained	0.1386	0.1116	0.1852	0.1544	0.1039	0.07988
Cumulative Proportion	0.1386	0.2502	0.4354	0.5898	0.6937	0.77362

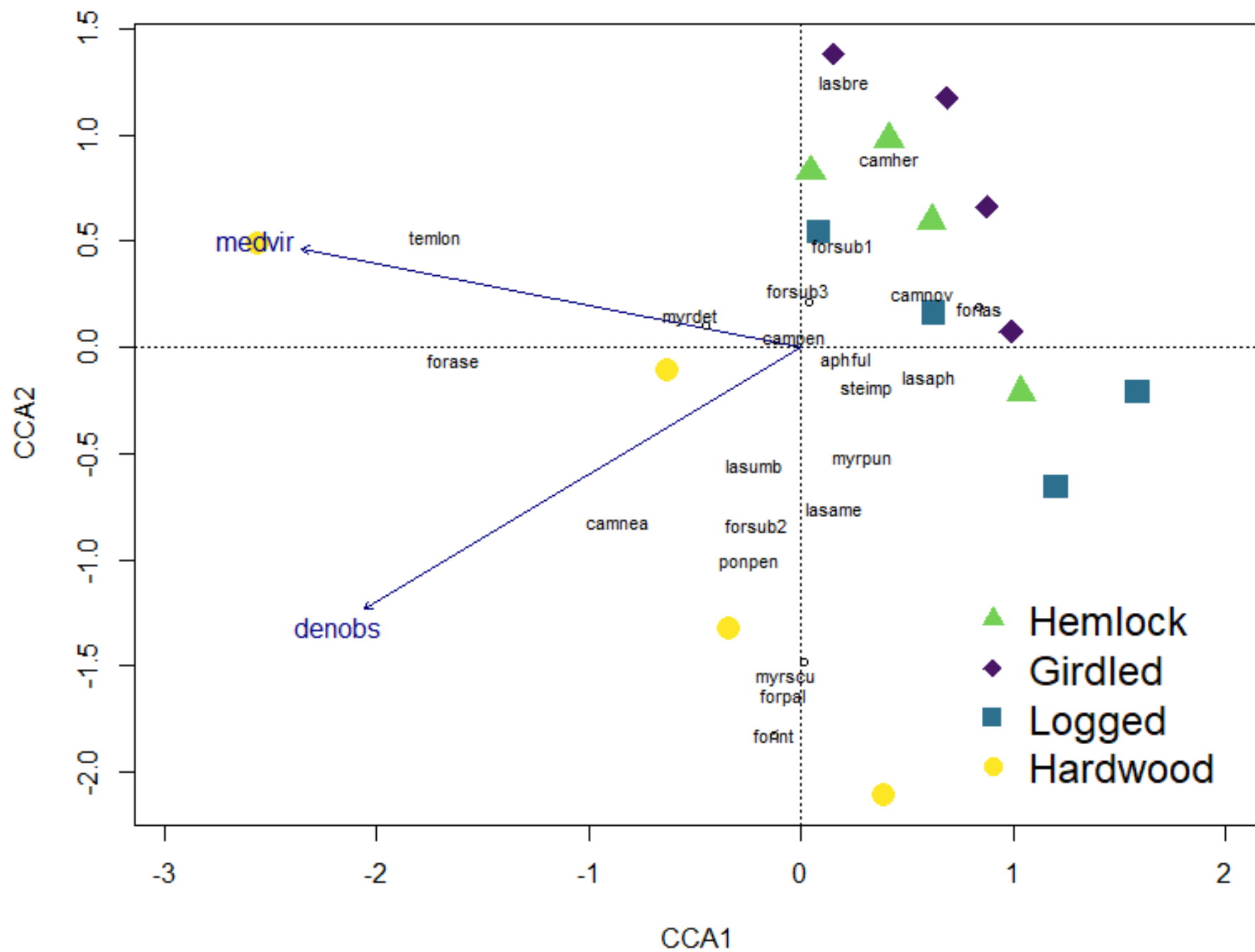
	CA12	CA13
Eigenvalue	0.007006	0.003804
Proportion Explained	0.005134	0.002787
Cumulative Proportion	0.997213	1.000000

Accumulated constrained eigenvalues

Importance of components:

	CCA1	CCA2
Eigenvalue	0.1891	0.1523
Proportion Explained	0.5540	0.4460
Cumulative Proportion	0.5540	1.0000

# CCA



# How do I know which to use: RDA or CCA?

Linear vs unimodal

Detrended correspondence analysis (DCA) to determine the length of the first axis

```
> DCA <- decorana(ants3[,6:38])  
> DCA
```

```
call:  
decorana(veg = ants3[, 6:38])
```

```
Detrended correspondence analysis with 26 segments.  
Rescaling of axes with 4 iterations.  
Total inertia (scaled Chi-square): 1.3647
```

	DCA1	DCA2	DCA3	DCA4
Eigenvalues	0.2666	0.1445	0.13070	0.12551
Additive Eigenvalues	0.2666	0.1444	0.12278	0.12724
Decorana values	0.2863	0.1062	0.06828	0.01932
Axis lengths	1.9859	1.2712	1.10724	1.02441

RDA: Axis length < 4

CCA: Axis length > 4