

# Statistics for the Sciences

## Correspondence Analysis

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# Outline

- Idea of CA
- Example
- Lab

# Idea of CA

- Correspondence analysis (CA) is a statistical visualization method for picturing the associations between the levels of a two-way contingency table.
  - ▶ CA is for the relationship between **two categorical variables**.
  - ▶ The term *correspondance* denotes a system of associations between the levels of the two sets.
- CA is used to check in a two-way contingency table whether certain levels of one categorical variable are associated with some levels of another.
- CA is a geometric technique for displaying the rows and columns of a two-way contingency table as points in a low-dimensional space, such that the positions of the row and column points are consistent with their associations in the table.

# Idea of CA

- The form of a contingency table for two categorical variables

Two-Way Contingency Table

Row	Column				Marginals
	1	2	...	c	
1	$O_{11}$	$O_{12}$	...	$O_{1c}$	$R_{1\cdot}$
2	$O_{21}$	$O_{22}$	...	$O_{2c}$	$R_{2\cdot}$
.	.	.		.	.
.	.	.		.	.
.	.	.		.	.
r	$O_{r1}$	$O_{r2}$	...	$O_{rc}$	$R_{r\cdot}$
Marginals	$C_{\cdot 1}$	$C_{\cdot 2}$	...	$C_{\cdot c}$	n

# Idea of CA

- Divide each cell count by the total number of observations  $n$ , we get the matrix of joint cell probabilities.
  - ▶ In the following table,  $p_{ij} = O_{ij}/n, i = 1, \dots, r, j = 1, \dots, n$ .
  - ▶ They are actually estimates the cell probabilities.

Two-Way Table of Proportions

row	Column				Marginals
	1	2	...	c	
1	$p_{11}$	$p_{12}$	...	$p_{1c}$	$p_{1\cdot}$
2	$p_{21}$	$p_{22}$	...	$p_{2c}$	$p_{2\cdot}$
.	.	.		.	.
.	.	.		.	.
.	.	.		.	.
r	$p_{r1}$	$p_{r2}$	...	$p_{rc}$	$p_{r\cdot}$
Marginals	$p_{\cdot 1}$	$p_{\cdot 2}$	...	$p_{\cdot c}$	1

# Idea of CA

- Consider a  $3 \times 3$  contingency table

```
##           Col1 Col2 Col3
## Row1      3    2    4
## Row2      3    6    6
## Row3     10    5    9
```

- The matrix **P** of joint cell probabilities

```
## [1] "matrix of joint cell probabilities P="
```

```
##           Col1      Col2      Col3
## Row1 0.0625000 0.04166667 0.08333333
## Row2 0.0625000 0.12500000 0.12500000
## Row3 0.2083333 0.10416667 0.18750000
```

# Idea of CA

- Calculate the row margin  $\mathbf{r}$ 
  - ▶ called row masses

```
##           [,1]  
## Row1 0.1875  
## Row2 0.3125  
## Row3 0.5000
```

- Calculate the column margin  $\mathbf{c}$ 
  - ▶ called column masses

```
##           [,1]  
## Col1 0.3333333  
## Col2 0.2708333  
## Col3 0.3958333
```

# Idea of CA

##		Col1	Col2	Col3	Rtotal
##	Row1	0.0625000	0.04166667	0.08333333	0.1875
##	Row2	0.0625000	0.12500000	0.12500000	0.3125
##	Row3	0.2083333	0.10416667	0.18750000	0.5000
##	Ctotal	0.3333333	0.27083333	0.39583333	1.0000



# Idea of CA

- Put the row masses in a diagonal matrix  $\mathbf{D}_r$ ,  $p_{i\cdot}$ ,  $i = 1, 2, 3$

```
##           [,1]    [,2] [,3]
## [1,] 0.1875 0.0000  0.0
## [2,] 0.0000 0.3125  0.0
## [3,] 0.0000 0.0000  0.5
```

- Put the column masses in a diagonal matrix  $\mathbf{D}_c$ ,  $p_{\cdot j}$ ,  $j = 1, 2, 3$

```
##           [,1]    [,2]    [,3]
## [1,] 0.3333333 0.0000000 0.0000000
## [2,] 0.0000000 0.2708333 0.0000000
## [3,] 0.0000000 0.0000000 0.3958333
```

# Idea of CA

- The matrix of row conditional probabilities
  - ▶ Each row of  $\mathbf{P}$  divided by row masses

```
##           Col1      Col2      Col3
## [1,] 0.3333333 0.2222222 0.4444444
## [2,] 0.2000000 0.4000000 0.4000000
## [3,] 0.4166667 0.2083333 0.3750000
```

- The matrix of column conditional probabilities
  - ▶ Each column of  $\mathbf{P}$  divided by column masses

```
##           [,1]      [,2]      [,3]
## Row1 0.1875 0.1538462 0.2105263
## Row2 0.1875 0.4615385 0.3157895
## Row3 0.6250 0.3846154 0.4736842
```

# Idea of CA

- The expected proportions  $\mathbf{E} = \mathbf{rc}^T$ 
  - ▶ the proportions we expect in the case there is no relationship between the two categorical variables
  - ▶ that is,  $p_{ij} = p_{i\cdot} \times p_{\cdot j}$

##		Col1	Col2	Col3
##	Row1	0.0625000	0.05078125	0.07421875
##	Row2	0.1041667	0.08463542	0.12369792
##	Row3	0.1666667	0.13541667	0.19791667

# Idea of CA

- The residuals  $\mathbf{R} = \mathbf{P} - \mathbf{E}$  quantify the difference between the observed data and the data we would expect under the assumption that there is no relationship between the row and column categories of the table

##		Col1	Col2	Col3
##	Row1	0.00000000	-0.009114583	0.009114583
##	Row2	-0.04166667	0.040364583	0.001302083
##	Row3	0.04166667	-0.031250000	-0.010416667

# Idea of CA

- Dividing the residuals by the expected values, we obtain the matrix  $\mathbf{I}_r$  of indexed residuals
  - ▶ the further the value from the table, the larger the observed proportion relative to the expected proportion

##		Col1	Col2	Col3
##	Row1	0.00	-0.1794872	0.12280702
##	Row2	-0.40	0.4769231	0.01052632
##	Row3	0.25	-0.2307692	-0.05263158

# Idea of CA

- Finally, calculate the matrix of standardized residuals  $\mathbf{Z}$ , obtained by multiplying each element of  $\mathbf{I}_r$  by each element of  $\sqrt{\mathbf{E}}$

```
##           [,1]      [,2]      [,3]
## [1,]  0.0000000 -0.04044689  0.03345646
## [2,] -0.1290994  0.13874726  0.00370218
## [3,]  0.1020621 -0.08492078 -0.02341465
```

# Idea of CA

- The standardized residuals matrix  $\mathbf{Z}$  is used in correspondence analysis to visualize and interpret the relationships between row and column categories in a contingency table.
- Then a mathematical tool Singular Value Decomposition (SVD) will be used to Decompose  $\mathbf{Z}$ 
  - ▶ The squared singular values correspond to the eigenvalues of  $\mathbf{Z}$
  - ▶ In the reduced dimensional space, the left singular vectors represent the row coordinates, and
  - ▶ the right singular vectors represent the column coordinates.
  - ▶ then calculate the row and column scores
- The eigenvalues represent the amount of variance explained by each dimension in the reduced space.
  - ▶ Larger eigenvalues indicate dimensions that explain more variance.
- The row and column scores provide the coordinates for plotting the rows and columns in a biplot. These scores show the relationship between row and column categories.

# One Application of CA

- The application of CA in ecology is radically different.
- For example, Abundance data
  - ▶ Abundance data are gathered from various physical samples (e.g., areas or volumes) where different species are identified and counted.
  - ▶ This results in a matrix is not a statistical contingency table, as the counts are not derived from random sampling.
- Since ecological samples (e.g., fixed-size quadrats in botany or fixed volumes in marine research) are often uniform in size, an important question arises:
  - ▶ Should abundances be profiled relative to the total abundance within each sample?
- CA can help us visualize relationships between species and environmental factors.



# Example

- (lemminvert2.csv): Lemmens et al. (2015) did a detailed study of various biotic communities in artificial ponds in Belgium. They sampled 28 ponds that represented different types of management, a combination of fish farming strategies (no fish, farming young fish, low intensity management, no management), and drainage frequencies ( $> 10$  years ago, occasional, annual). They also quantified taxon abundances for fish, zooplankton, and macro-invertebrates (different families and species within some groups) and covers of submerged, floating, and emergent vegetation.
  - ▶ The macroinvertebrate dataset only included 23 ponds and we will use these data to illustrate CA by examining the ordination of the macroinvertebrate community (abundances of families).

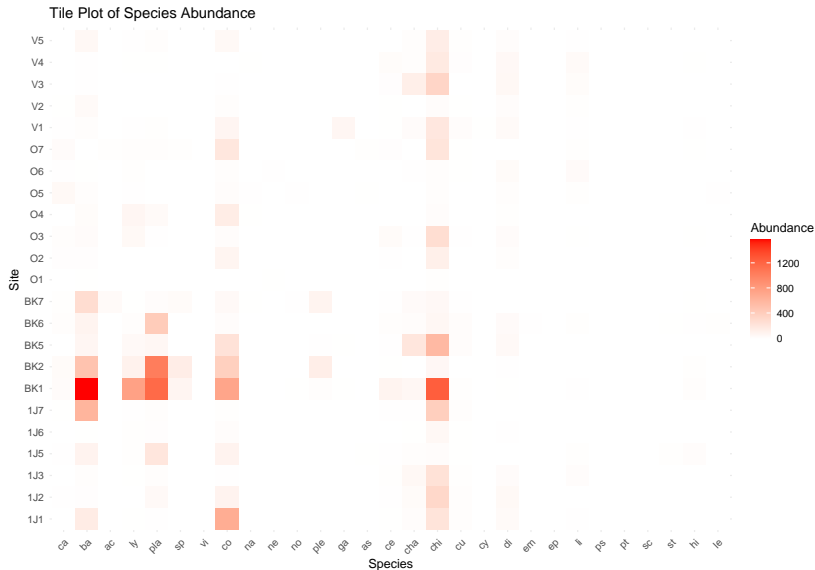
# Example

- Remove the first 2nd and 3rd columns, and check some statistics

```
##      site ca  ba ac  ly  pla  sp vi  co na ne no ple ga as ce cha  chi cu cy di
## 1    1J1  0  158  0   3    5   0  0 671  0  0  0   0  0  0  4  23  222 19  0 40
## 2    1J2  6   13  0   0   50   0  0  95  0  0  0   0  0  0  7  37  322 17  0 52
## 3    1J3  0   20  0   3   16   0  0   8  0  0  0   0  1  0  9  60  240 12  0 30
## 4    1J5  5   98  0  10  206   2  0  98  0  0  0   0  2  4  5  20   26  4  0  2
## 5    1J6  0    3  0   9   14   0  0  23  0  0  0   0  1  0  0   3   60  3  0  5
## 6    1J7  3  605  0   7   19   0  0   9  0  0  0   0  0  0  7   5  394 19  0  0
## 7    BK1 31 1571  0 763 1164  80  0 730  0  0  3  20  4  0 88  68 1236 12  0  4
## 8    BK2 36  494  0 109 1035 147  0 389  2  0  1 141  0  0  3   0   62  0  0  6
## 9    BK5  0   73  1  46   64   0  0 239  2  0  0   5  4  0  6 204  569 24  0 47
## 10   BK6 16   90  0  15  421   0  0  25  0  0  0   0  1  1 20  22   69 21  0 38
## 11   BK7 12  282 42   4   25  36  0  46  3  0  7  91  1  1  6  38   54  8  0  0
## 12   01  0    4  0  0   0   0  0  2  0  3  0   0  0  0  2  0   12  0  0  0
## 13   02 13   13  0  0   1   0  0 83  0  0  0   1  0  0  0  8   2  124  0  0 19
## 14   03 15   31  0 51   6   1  0 24  0  0  0   0  0  0 34   8  274  5  0 29
## 15   04  0   28  2 72   39  2  0 150  3  0  0   1  0  0  0   1   21  1  0  9
## 16   05 53   18  0  6    2   0  0 22  5  0  6   0  0  4  1   0   16  0  0 19
## 17   06  6    3  0 10   0   0  0 18  0  6  0   0  0  0  0   5   19  4  0 35
## 18   07 30    0 10 20   18  9  1 197  0  2  0   0  0  9 14   0  215  3  0  2
## 19   V1  6   16  0  5    9   0  0 81  0  0  0   0 74  1  3  29  196 26  3 39
## 20   V2  3   39  0  0   0   0  0 15  0  0  0   0  0  1  3   2   22  4  0 26
## 21   V3  0    6  0  2    0   1  0  6  0  0  0   0  1  0 14  131  342  0  0 57
## 22   V4  0    6  0  4    3   0  0  2  4  0  0   0  0  0 27   16  176 14  0 56
## 23   V5  0   58  0  7   18  2  0 51  1  0  0   0  0  0  0   18  147  9  0 21
##      em ep li ps pt sc st hi le
## 1    0  0  8  0  0  0  1  0  1
## 2    0  0  1  0  2  0  0  0  0
## 3    0  0 25  0  0  0  0  1  0
```

# Example

- Get a tile plot to check relative abundance of each species within each site



# Example

- Regard variables site as row names/labels

```
##      ca  ba ac  ly  pla  sp vi  co na ne no ple ga as ce cha  chi cu cy di em ep
## 1    0 158 0   3    5    0 0 671 0 0 0   0 0 0 4 23 222 19 0 40 0 0
## 2    6   13 0   0   50    0 0 95 0 0 0   0 0 0 7 37 322 17 0 52 0 0
## 3    0   20 0   3   16    0 0 8 0 0 0   0 1 0 9 60 240 12 0 30 0 0
## 4    5   98 0  10  206    2 0 98 0 0 0   0 2 4 5 20  26 4 0 2 0 0
## 5    0    3 0   9   14    0 0 23 0 0 0   0 1 0 0 3  60 3 0 5 1 1
## 6    3  605 0   7   19    0 0 9 0 0 0   0 0 0 7 5 394 19 0 0 0 0
## 7   31 1571 0 763 1164  80 0 730 0 0 3  20 4 0 88 68 1236 12 0 4 0 0
## 8   36  494 0 109 1035 147 0 389 2 0 1 141 0 0 3  0  62 0 0 6 0 0
## 9    0   73 1  46   64    0 0 239 2 0 0  5 4 0 6 204 569 24 0 47 0 0
## 10  16   90 0  15  421    0 0 25 0 0 0   0 1 1 20 22  69 21 0 38 5 0
## 11  12  282 42  4   25  36 0 46 3 0 7  91 1 1 6 38  54 8 0 0 0 0
## 12  0    4 0  0  0    0 0 0 2 0 3 0 0 0 2 0 0  12 0 0 0 0 0
## 13 13   13 0  0  1    0 0 83 0 0 1  0 0 0 8  2 124 0 0 19 0 0
## 14 15   31 0 51   6    1 0 24 0 0 0  0 0 0 34 8 274 5 0 29 0 0
## 15  0   28 2 72   39    2 0 150 3 0 0  1 0 0 0 1  21 1 0 9 0 0
## 16 53   18 0 6    2    0 0 22 5 0 6  0 0 4 1  0 16 0 0 19 0 0
## 17 6    3 0 10  0    0 0 18 0 6 0  0 0 0 0 5  19 4 0 35 0 0
## 18 30    0 10 20   18  9 1 197 0 2 0  0 0 9 14  0 215 3 0 2 0 0
## 19 6   16 0 5    9    0 0 81 0 0 0  0 74 1 3 29 196 26 3 39 0 0
## 20 3   39 0 0  0    0 0 15 0 0 0  0 0 1 3  2  22 4 0 26 0 0
## 21 0    6 0 2  0    1 0 6 0 0 0  0 1 0 14 131 342 0 0 57 0 0
## 22 0    6 0 4  3    0 0 2 4 0 0  0 0 0 27 16 176 14 0 56 0 0
## 23 0   58 0 7   18    2 0 51 1 0 0  0 0 0 0 18 147 9 0 21 0 0
##      li ps pt sc st hi le
## 1    8 0 0 0 1 0 1
## 2    1 0 2 0 0 0 0
## 3   25 0 0 0 0 1 0
```

# Example

```
##
## Principal inertias (eigenvalues):
##      1      2      3      4      5      6      7
## Value 0.364603 0.156342 0.147145 0.135003 0.124771 0.098519 0.080732
## Percentage 27.91% 11.97% 11.26% 10.33% 9.55% 7.54% 6.18%
##      8      9     10     11     12     13     14
## Value 0.046041 0.040712 0.031388 0.026204 0.018642 0.01379 0.006885
## Percentage 3.52% 3.12% 2.4% 2.01% 1.43% 1.06% 0.53%
##      15     16     17     18     19     20     21
## Value 0.005144 0.004454 0.003261 0.001128 0.000886 0.000536 0.000155
## Percentage 0.39% 0.34% 0.25% 0.09% 0.07% 0.04% 0.01%
##      22
## Value 9.8e-05
## Percentage 0.01%
##
## Rows:
##      1J1      1J2      1J3      1J5      1J6      1J7      BK1
## Mass 0.061626 0.032120 0.022676 0.028172 0.006723 0.056984 0.309519
## ChiDist 1.201693 0.933132 1.171392 1.148363 1.722272 1.105904 0.468482
## Inertia 0.088992 0.027968 0.031116 0.037152 0.019942 0.069693 0.067932
## Dim. 1 0.396955 1.179828 1.641302 -0.779788 0.789258 -0.044049 -0.485453
## Dim. 2 0.106377 -0.129481 -0.215181 1.095410 -0.109035 -1.811533 -0.508792
##      BK2      BK5      BK6      BK7      01      02      03
## Mass 0.129975 0.068563 0.041351 0.035268 0.001334 0.014193 0.025878
## ChiDist 1.001979 0.895062 1.218067 1.798732 5.509043 0.966582 1.024400
## Inertia 0.130490 0.054928 0.061352 0.114109 0.040483 0.013260 0.027156
## Dim. 1 -1.426088 1.082130 -0.791462 -0.897415 1.532024 0.998728 1.050517
## Dim. 2 0.743469 -0.592846 1.540257 -0.609251 3.187125 0.369797 -0.398976
##      04      05      06      07      V1      V2      V3
## Mass 0.017661 0.009124 0.007683 0.028972 0.026891 0.006776 0.031480
## ChiDist 1.149777 3.381547 3.207381 1.112261 2.268350 1.423040 1.483498
## Inertia 0.023347 0.104330 0.079040 0.035842 0.138368 0.013722 0.069280
## Dim. 1 -0.329851 0.691269 2.177059 0.638978 1.709381 1.016049 1.978599
## Dim. 2 0.299910 5.343375 4.392634 0.739371 0.633688 1.111008 -0.339015
##      V4      V5
## Mass 0.018781 0.018248
## ChiDist 1.645441 0.623136
## Inertia 0.050850 0.007086
## Dim. 1 1.927954 0.817559
```

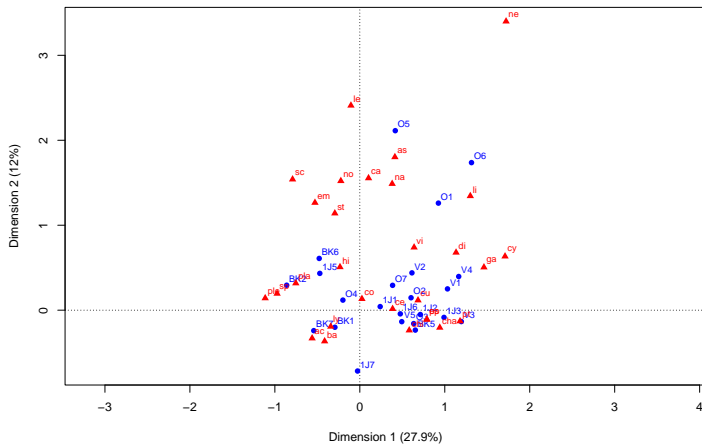
# Example

- Proportion of variation explained

```
##
## Principal inertias (eigenvalues):
##
## dim      value      %   cum%   scree plot
## 1         0.364603  27.9  27.9   *****
## 2         0.156342  12.0  39.9    ***
## 3         0.147145  11.3  51.1    ***
## 4         0.135003  10.3  61.5    ***
## 5         0.124771   9.6  71.0    **
## 6         0.098519   7.5  78.6    **
## 7         0.080732   6.2  84.7    **
## 8         0.046041   3.5  88.3     *
## 9         0.040712   3.1  91.4     *
## 10        0.031388   2.4  93.8     *
## 11        0.026204   2.0  95.8     *
## 12        0.018642   1.4  97.2
## 13        0.013790   1.1  98.3
## 14        0.006885   0.5  98.8
## 15        0.005144   0.4  99.2
## 16        0.004454   0.3  99.5
## 17        0.003261   0.2  99.8
## 18        0.001128   0.1  99.9
## 19        0.000886   0.1  99.9
## 20        0.000536   0.0 100.0
## 21        0.000155   0.0 100.0
## 22        9.8e-050   0.0 100.0
##
## -----
## Total: 1 306439 100.0
```

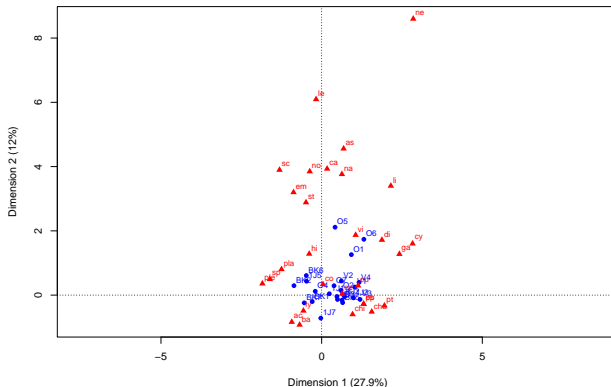
# Example

- Visualization of relationships among categories
- row/col points near each other are positively associated
- The red points are for columns



## Example

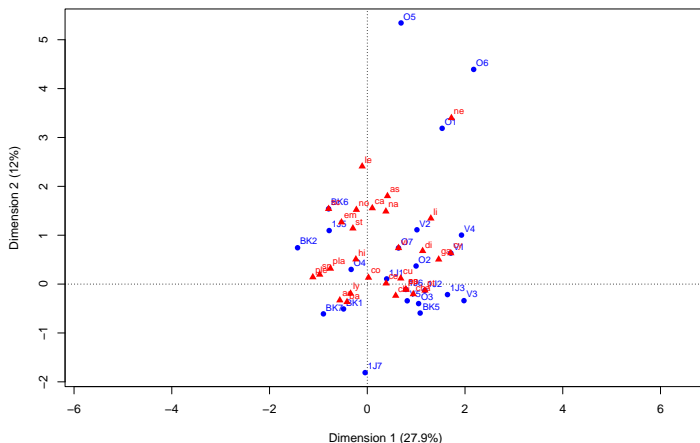
- In standard CA, the distances between row and column coordinates are exaggerated, and there isn't a straightforward interpretation of relationships between row and column categories.
- To interpret the relationships between row coordinates, we use **row principal normalization**
  - ▶ Points that are closer together in the plot indicate rows (sites) that have similar species compositions.





# Example

- To interpret the relationships between column coordinates, we use **column principal normalization**
  - ▶ Points that are closer together in the plot indicate columns (species) that have similar distributions across the rows (sites).



- CA is for a contingency table. In SPSS so we need to reshape the data from

	var <sub>1</sub>	var <sub>2</sub>	...	var <sub>29</sub>
row1	x <sub>11</sub>	x <sub>12</sub>	...	x <sub>1,29</sub>
row2	x <sub>21</sub>	x <sub>22</sub>	...	x <sub>2,29</sub>
⋮	⋮	...	⋮	⋮
row23	x <sub>23,1</sub>	x <sub>23,2</sub>	...	x <sub>23,29</sub>

# Lab

- to

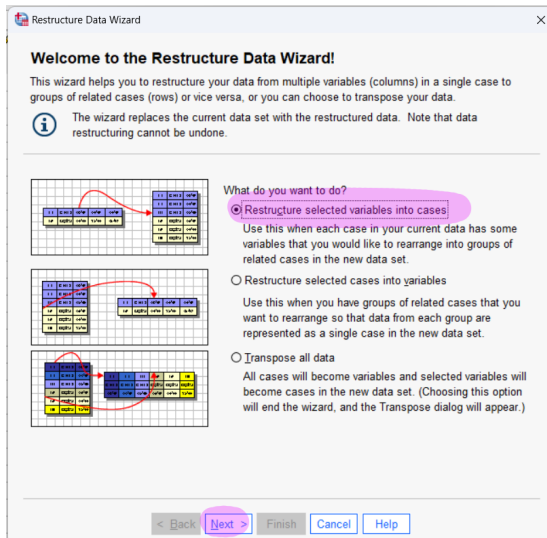
Row	Column	Count
row1	var <sub>1</sub>	$x_{11}$
⋮	⋮	⋮
row1	var <sub>29</sub>	$x_{1,29}$
row2	var <sub>1</sub>	$x_{21}$
⋮	⋮	⋮
row2	var <sub>29</sub>	$x_{2,29}$
⋮	⋮	⋮
row23	var <sub>1</sub>	$x_{23,1}$
⋮	⋮	⋮
row23	var <sub>29</sub>	$x_{23,29}$

- We import the data with measures of all numerical variables as Scale

File Edit View Data Transform Analyze Graphs Utilities Extensions Window Help											
<input type="text" value="Search application"/>											
	Name	Type	Width	Decimals	Label	Values	Missing	Columns	Align	Measure	Role
1	site	String	3	0		None	None	7	Left	Nominal	Input
2	manag	String	2	0		None	None	4	Left	Nominal	Input
3	managsymb	Numeric	1	0		None	None	8	Right	Nominal	Input
4	caen	Numeric	2	0		None	None	8	Right	Scale	Input
5	baet	Numeric	4	0		None	None	8	Right	Scale	Input
6	acrol	Numeric	2	0		None	None	8	Right	Scale	Input
7	lymn	Numeric	3	0		None	None	8	Right	Scale	Input
8	plan	Numeric	4	0		None	None	8	Right	Scale	Input
9	sphaer	Numeric	3	0		None	None	8	Right	Scale	Input
10	vivip	Numeric	1	0		None	None	8	Right	Scale	Input
11	cortx	Numeric	3	0		None	None	8	Right	Scale	Input
12	nauc	Numeric	1	0		None	None	8	Right	Scale	Input
13	nepid	Numeric	1	0		None	None	8	Right	Scale	Input
14	noto	Numeric	1	0		None	None	8	Right	Scale	Input
15	pleid	Numeric	3	0		None	None	8	Right	Scale	Input
16	gamm	Numeric	2	0		None	None	8	Right	Scale	Input
17	asell	Numeric	1	0		None	None	8	Right	Scale	Input
18	cerat	Numeric	2	0		None	None	8	Right	Scale	Input
19	chaob	Numeric	3	0		None	None	8	Right	Scale	Input
20	chiro	Numeric	4	0		None	None	8	Right	Scale	Input
21	culic	Numeric	2	0		None	None	8	Right	Scale	Input
22	cylind	Numeric	1	0		None	None	8	Right	Scale	Input
23	dixid	Numeric	2	0		None	None	8	Right	Scale	Input
24	empid	Numeric	1	0		None	None	8	Right	Scale	Input
25	ephyd	Numeric	1	0		None	None	8	Right	Scale	Input
26	limon	Numeric	2	0		None	None	8	Right	Scale	Input
27	psych	Numeric	1	0		None	None	8	Right	Scale	Input
28	ptych	Numeric	1	0		None	None	8	Right	Scale	Input
29	sciom	Numeric	1	0		None	None	8	Right	Scale	Input
30	strat	Numeric	2	0		None	None	8	Right	Scale	Input

# Lab

- Click on Data → Restructure...



Restructure Data Wizard - Step 2 of 7

## Variables to Cases: Number of Variable Groups

You have chosen to restructure selected variables into groups of related cases in the new file.

A group of related variables, called a variable group, represents measurements on one variable.

For example, the variable may be width. If it is recorded in three separate measurements, each one representing a different point in time--w1, w2, and w3, then the data are arranged in a group of variables.

If there is more than one variable in the file often it is also recorded in a variable group, for example height, recorded in h1, h2, and h3.

How many variable groups do you want to restructure?

☒ One (for example, w1, w2, and w3)

☐ More than one (for example, w1, w2, w3 and h1, h2, h3, etc.)

How Many?

<

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Finish

Cancel

Help

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Statistics for the Sciences

January 18, 2025

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Restructure Data Wizard - Step 3 of 7

### Variables to Cases: Select Variables

For each variable group you have in the current data the restructured file will have one target variable.

In this step, choose how to identify case groups in the restructured data, and choose which variables belong with each target variable.

Optionally, you can also choose variables to copy to the new file as Fixed Variables.

Variables in the Current File:

- site
- manag
- managsymb
- caen
- baet
- acrol
- lymn
- plan
- sphaer
- vivip
- corix
- nauc
- nepid
- noto
- pleid
- gamm
- asell

Case Group Identification

Use selected variable

Variable: site

Variables to be Transposed

Target Variable: trans1

Fixed Variable(s):

< Back Next > Finish Cancel Help

# Lab

- Add all numerical variables to the Variables to be Transposed box, and name the Target Variable as Count

Restructure Data Wizard - Step 3 of 7

### Variables to Cases: Select Variables

For each variable group you have in the current data the restructured file will have one target variable.

In this step, choose how to identify case groups in the restructured data, and choose which variables belong with each target variable.

Optionally, you can also choose variables to copy to the new file as Fixed Variables.

---

Variables in the Current File:

- gamm
- asell
- cerat
- chaob
- chiro
- culic
- cylind
- dioxid
- empid
- ephyd
- limon
- psych
- ptych
- sciom
- strat
- hirud
- lepid

Case Group Identification

Use selected variable

Variable: site

Variables to be Transposed

Target Variable: Count

- caen
- baet
- acrol
- lymn

Fixed Variable(s):

< Back Next > Finish Cancel Help



Restructure Data Wizard - Step 4 of 7

### Variables to Cases: Create Index Variables

In the current data, values for a variable group appear in a single case in multiple variables. For example, a single case contains the values for w1, w2, and w3.

In the new data, values for a variable group will appear in multiple cases in a single variable. For example, there will be three cases, one each for w1, w2, and w3.

An index is a new variable that identifies the group of new cases that was created from the original case. For example, an index named "w" would have the values 1, 2, and 3.

---

1	1	1	0.07
1	1	2	0.11
1	1	3	0.05
2	1	1	0.08
2	1	2	0.04
2	1	3	0.06

1	1	1	0.07	
1	1	1	2	0.11
1	1	1	3	0.05
1	1	2	1	0.08
1	1	2	2	0.04
1	1	2	3	0.06

1	1	0.08	2	0.07
2	1	0.11	2	0.11
3	1	0.07	2	0.05
4	1	0.06	2	0.08
5	1	0.09	2	0.04
6	1	0.02	2	0.06

How many index variables do you want to create?

☒ One

Use this when a variable group records the effects of a single factor, treatment or condition.

☐ More than one    How many?

Use this when a variable group records the effects of more than one factor, treatment or condition.

☐ None

Use this if index information is stored in one of the sets of variables to be transposed.

---

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Next >
Finish
Cancel
Help

# Lab

- Use variable names as index

Restructure Data Wizard - Step 5 of 7

### Variables to Cases: Create One Index Variable

You have chosen to create one index variable. The variable's values can be sequential numbers or the names of variables in a group.

In the table you can specify the name and label for the index variable.

What kind of index values?

☐ Sequential numbers  
Index Values: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, ...

☒ Variable names  
Index Values: caen, baet, acrol, lymn, plan, sphaer, vivip, corix, nauc, nepid, noto, ... ▾

Edit the Index Variable Name and Label:

	Name	Label	Levels	Index Values
1	Index1		29	caen, baet, acrol, l...

# Lab

- Drop the other two variables.

Restructure Data Wizard - Step 6 of 7

## Variables to Cases: Options

In this step you can set options that will be applied to the restructured data file.

---

Handling of Variables not Selected

☒ Drop variable(s) from the new data file

☐ Keep and treat as fixed variable(s)

System Missing or Blank Values in all Transposed Variables

☒ Create a case in the new file

☐ Discard the data

Case Count Variable

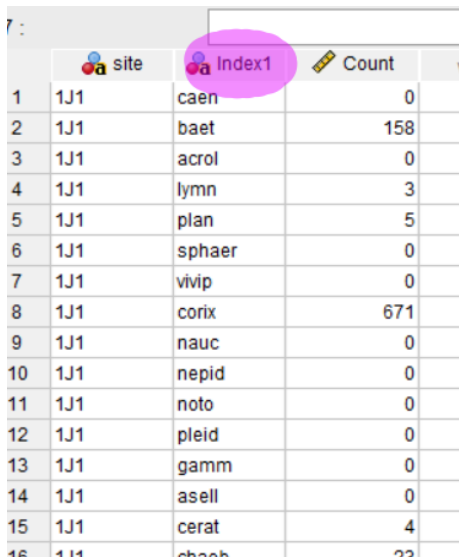
☐ Count the number of new cases created by the case in the current data

Name:

Label:

# Lab

- The long data will be like this
  - ▶ Let's change the name of Index1 to Species

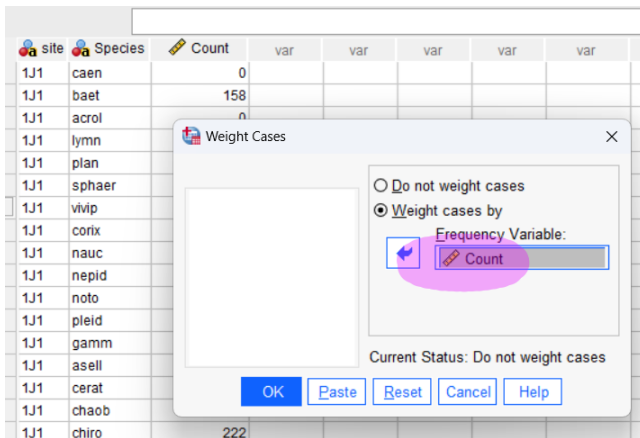


A screenshot of a data table interface. The table has four columns: 'site', 'Index1', 'Count', and a partially visible 'v' column. The 'Index1' header is circled in pink. The table contains 16 rows of data, each with a row number, a 'site' value (all '1J1'), an 'Index1' value (various species codes), and a 'Count' value.

	site	Index1	Count	v
1	1J1	caen	0	
2	1J1	baet	158	
3	1J1	acrol	0	
4	1J1	lymn	3	
5	1J1	plan	5	
6	1J1	sphaer	0	
7	1J1	vivip	0	
8	1J1	corix	671	
9	1J1	nauc	0	
10	1J1	nepid	0	
11	1J1	noto	0	
12	1J1	pleid	0	
13	1J1	gamm	0	
14	1J1	asell	0	
15	1J1	cerat	4	
16	1J1	chaob	23	

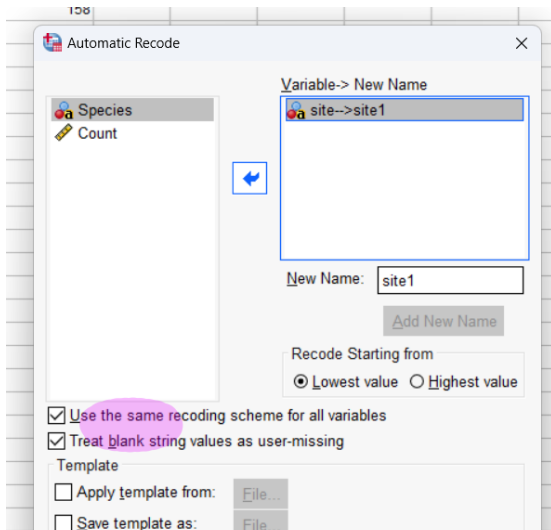
# Lab

- We regard the values of Count as frequencies, so
  - ▶ Click on Data → Weight Cases...



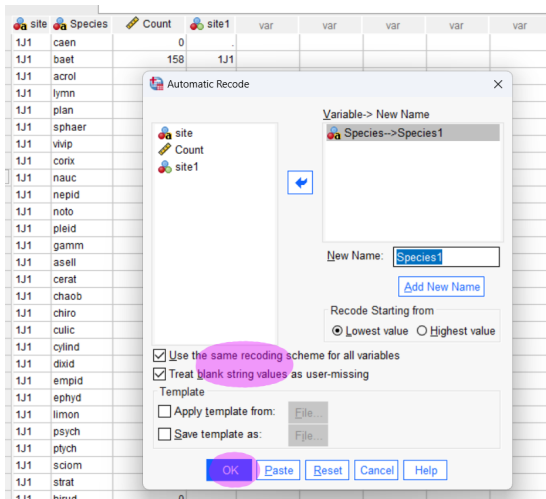
# Lab

- To conduct CA in SPSS, we need the two categorical variables Site and Species numerical
  - ▶ Click on Transform → Automatic Recode ...








# Lab

- Do the same thing to Species



# Lab

- The data now is like this

	 site	 Species	 Count	 site1	 Species1	var
1	1J1	caen	0	.	.	
2	1J1	baet	158	1J1	baet	
3	1J1	acrol	0	.	.	
4	1J1	lymn	3	1J1	lymn	
5	1J1	plan	5	1J1	plan	
6	1J1	sphaer	0	.	.	
7	1J1	vivip	0	.	.	
8	1J1	corix	671	1J1	corix	
9	1J1	nauc	0	.	.	
10	1J1	nepid	0	.	.	
11	1J1	noto	0	.	.	
12	1J1	pleid	0	.	.	
13	1J1	gamm	0	.	.	
14	1J1	asell	0	.	.	
15	1J1	cerat	4	1J1	cerat	
16	1J1	chaob	23	1J1	chaob	
17	1J1	chiro	222	1J1	chiro	
18	1J1	culic	19	1J1	culic	
19	1J1	cyli	0	.	.	
20	1J1	dixid	40	1J1	dixid	
21	1J1	empid	0	.	.	
22	1J1	ephyd	0	.	.	



- The data now is like this

	Name	Type	Width	Decimals	Label	Values	Missing	Columns	Align	Measure	Role
1	site	String	3	0		None	None	5	Left	Nominal	Input
2	Species	String	6	0		None	None	9	Left	Nominal	Input
3	Count	Numeric	2	0		None	None	11	Right	Scale	Input
4	site1	Numeric	2	0		{1, 1J1}...	None	7	Right	Nominal	Input
5	Species1	Numeric	2	0		{1, acrol}...	None	10	Right	Nominal	Input
6											
7											
8											
9											
10											
11											
12											
13											
14											
15											
16											
17											
18											
19											
20											
21											
22											
23											
24											

Value Labels

Spelling...

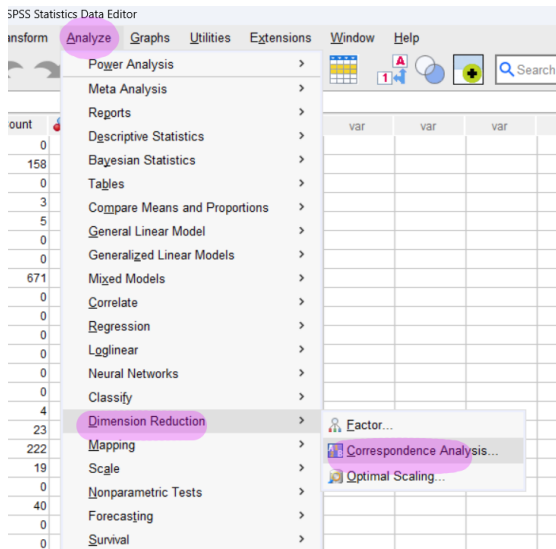
Value Labels:

Value	Label
1	acrol
2	asell
3	baet
4	caen
5	cerat
6	chaob
7	chiro
8	corix
9	culic

OK Reset Cancel Help

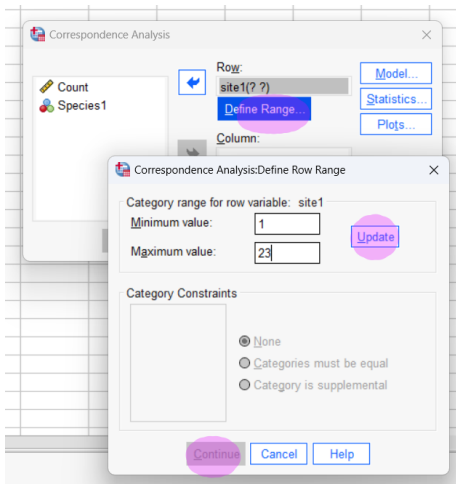
# Lab

- Finally,



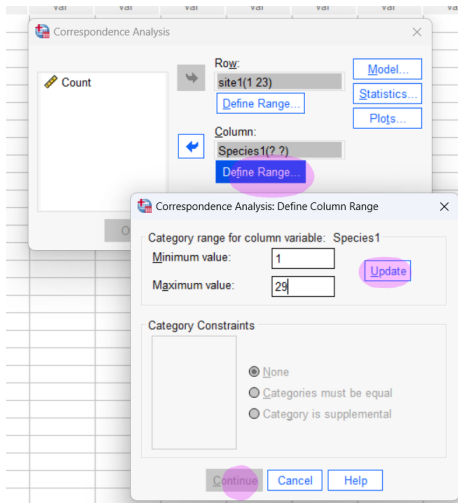
# Lab

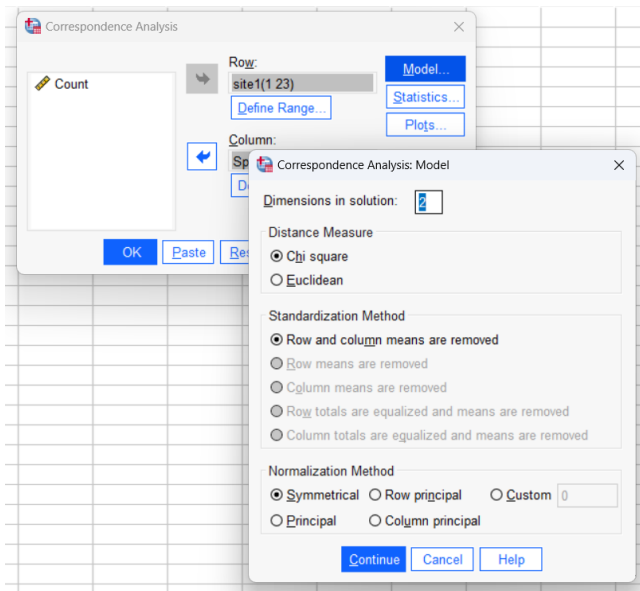
- Row variable

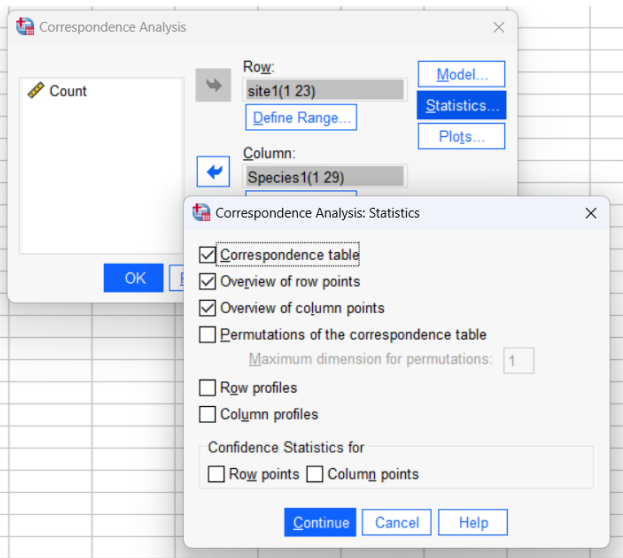


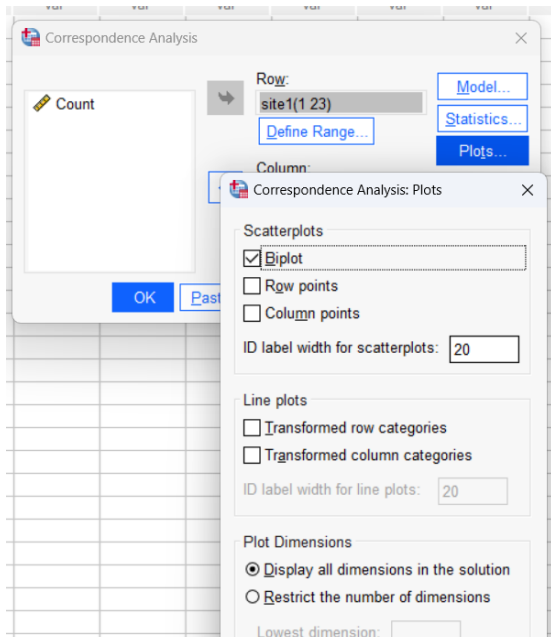
# Lab

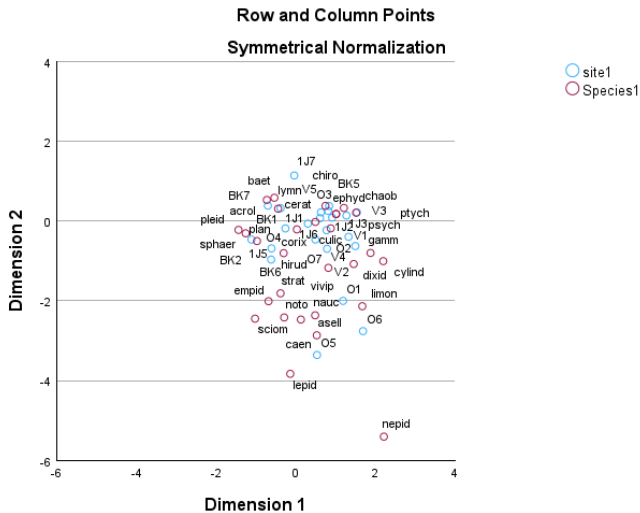
- Column variable













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