Community ecology with multiple data tables: the interface between data management and analysis

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Département de Sciences Biologiques

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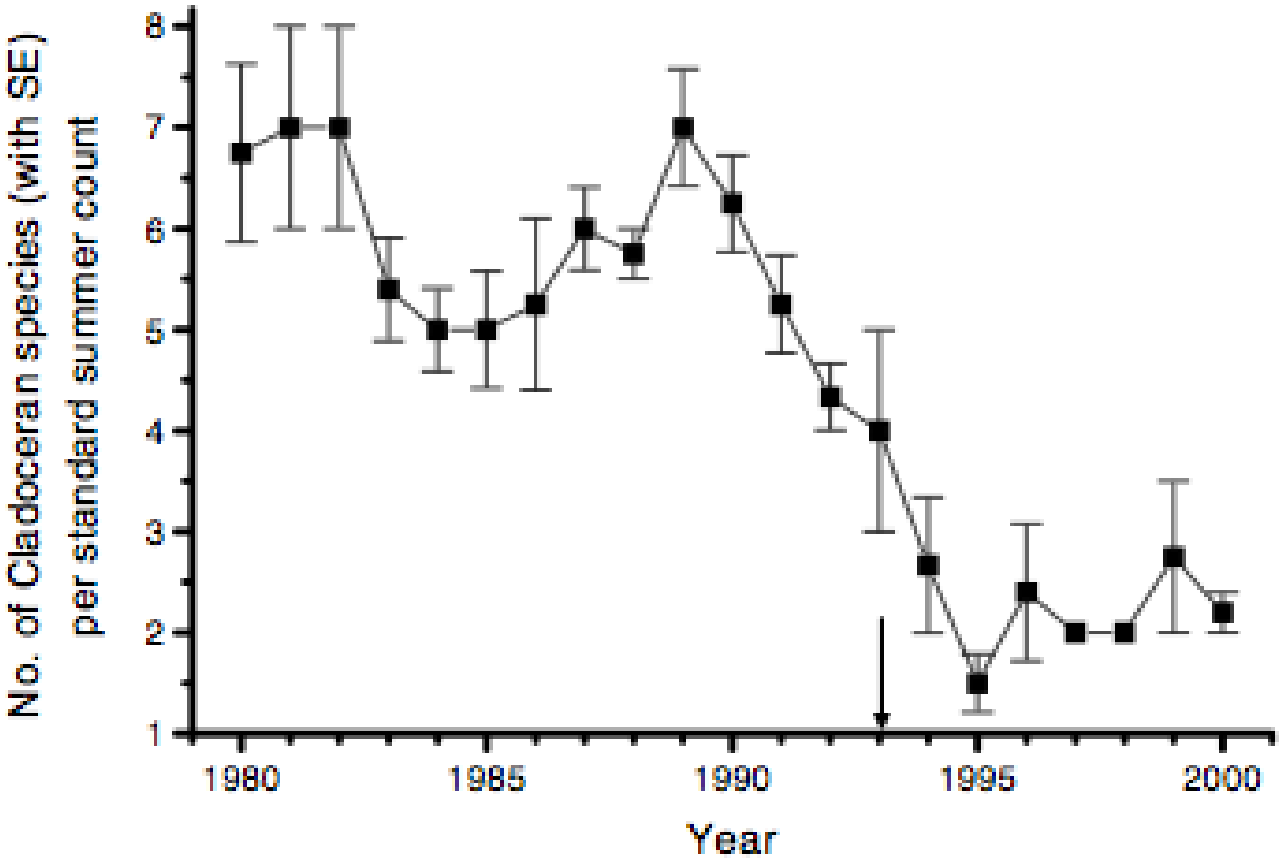
Ecological Society of America
Austin, Texas

Bythotrephes longimanus

Wisconsin Department of Natural Resources

Bythotrephes longimanus



Yan et al. (2002)

Fourth-corner

	sp 1	sp 2	sp 3	sp 4
site 1	0.1	2.1	0.1	1.5
site 2	0.7	-0.9	1.8	3.7
site 3	1.1	0.5	1.5	2.8
site 4	1.3	-2.0	3.0	-0.2
site 5	1.7	2.0	1.3	1.2
site 6	0.8	-0.1	2.0	1.1
site 7	-2.6	-1.4	1.8	4.1
site 8	-0.0	1.5	2.3	2.3

Fourth-corner

	sp 1	sp 2	sp 3	sp 4	environment
site 1	0.1	2.1	0.1	1.5	-0.3
site 2	0.7	-0.9	1.8	3.7	1.4
site 3	1.1	0.5	1.5	2.8	-0.1
site 4	1.3	-2.0	3.0	-0.2	0.4
site 5	1.7	2.0	1.3	1.2	-0.3
site 6	0.8	-0.1	2.0	1.1	-0.6
site 7	-2.6	-1.4	1.8	4.1	2.0
site 8	-0.0	1.5	2.3	2.3	0.7

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site 3	1.1	0.5	1.5	2.8	-0.1
site 4	1.3	-2.0	3.0	-0.2	0.4
site 5	1.7	2.0	1.3	1.2	-0.3
site 6	0.8	-0.1	2.0	1.1	-0.6
site 7	-2.6	-1.4	1.8	4.1	2.0
site 8	-0.0	1.5	2.3	2.3	0.7
trait	-1.0	-1.0	1.0	1.0	

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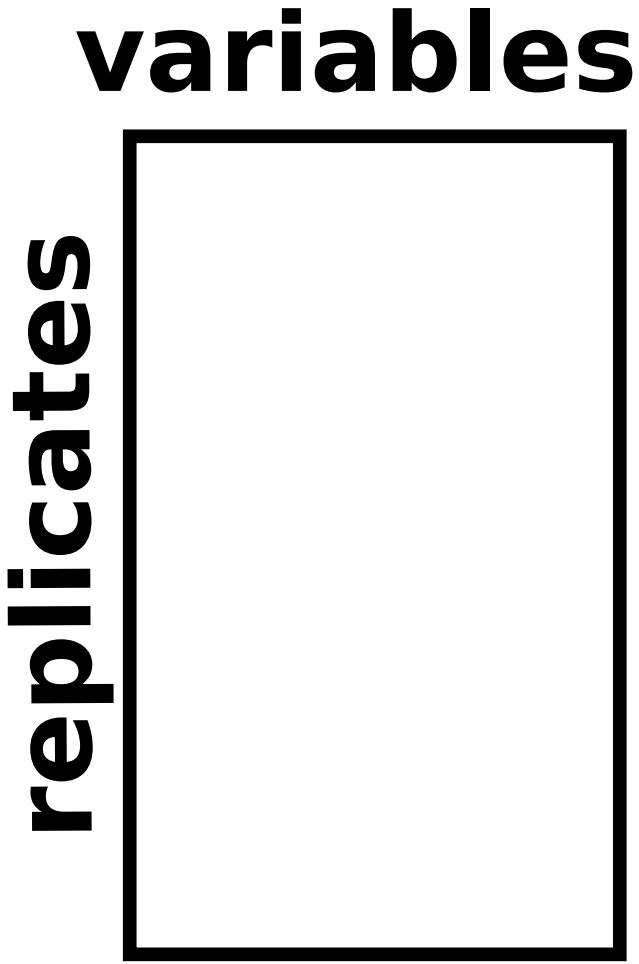
trait	-1.0	-1.0	1.0	1.0	→ **??** ←

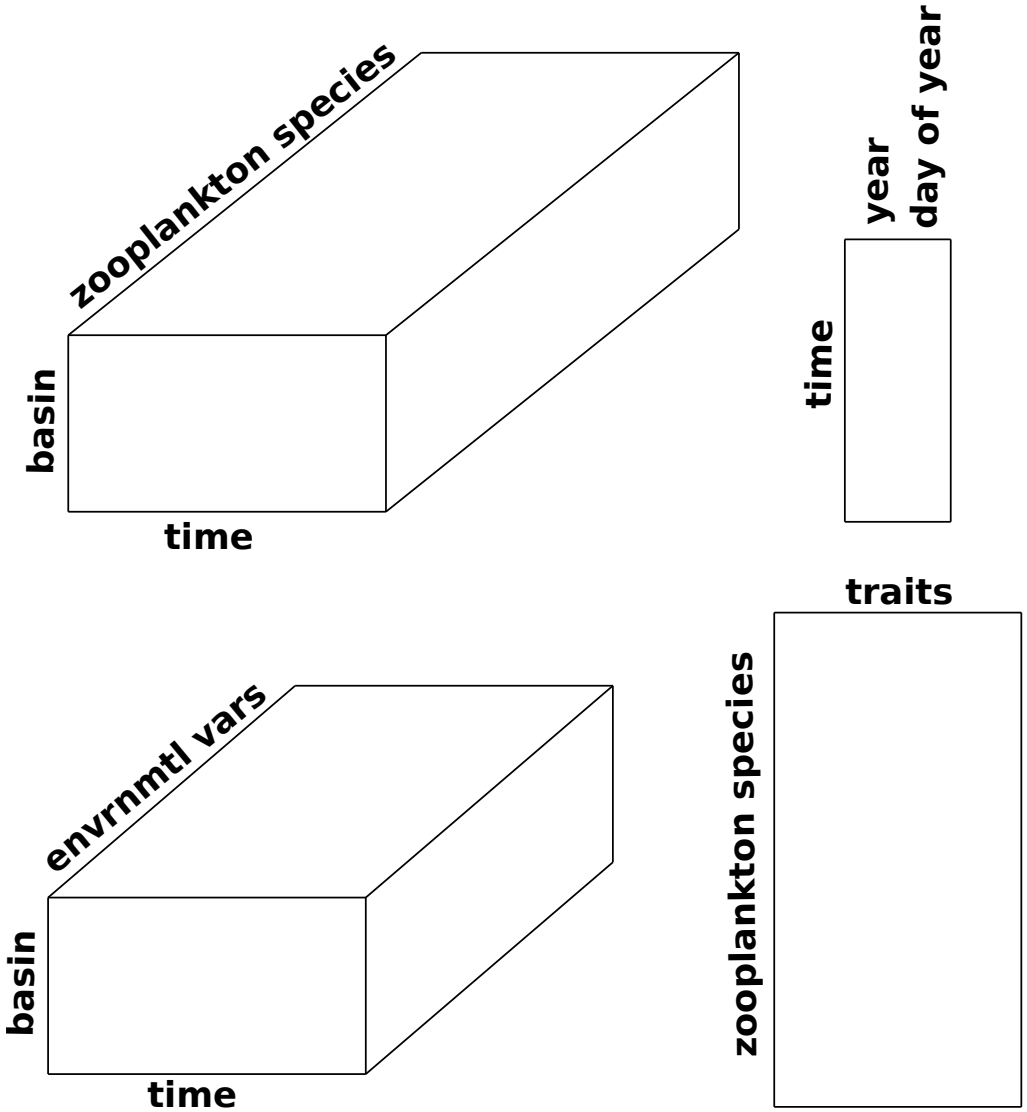
↑

Statistical methods for analyzing 'fourth-corner'-esque data

- Chessel et al. (1996) — RLQ analysis
- Legendre et al. (1997) — coined term 'fourth-corner'
- Ives and Godfray (2006) — mixed models of phylogenetically-structured foodwebs
- Dray and Legendre (2008) — extends Legendre et al.
- Pillar and Duarte (2010) — phylogenetic null models
- Leibold et al. (2010) — semi-partial correlations
- Ives and Helmus (in press) — phylogenetic generalized linear mixed models (PGLMMs)

The data frame — replicates-by-variables





Cantin et al. 2011 – Lac Croche, Québec, Canada

Linear algebra as data management

Solve for the b's

$$\begin{array}{ccccccccc} y_1 & = & b_1 x_{11} & + & b_2 x_{12} & + & \dots & + & b_m x_{1m} \\ y_2 & = & b_1 x_{21} & + & b_2 x_{22} & + & \dots & + & b_m x_{2m} \\ \vdots & & \vdots & & \vdots & & \ddots & & \vdots \\ y_n & = & b_1 x_{n1} & + & b_2 x_{n2} & + & \dots & + & b_m x_{nm} \end{array} \quad (1)$$

Linear algebra as data management

$$\mathbf{y} = \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix}, \mathbf{X} = \begin{bmatrix} x_{11} & x_{12} & \dots & x_{1m} \\ x_{21} & x_{22} & \dots & x_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ x_{n1} & x_{n2} & \dots & x_{nm} \end{bmatrix}, \mathbf{b} = \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{bmatrix} \tag{2}$$

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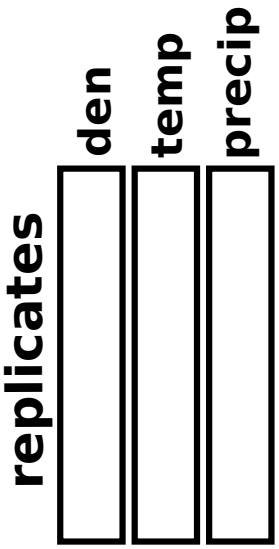
$$\begin{aligned} \mathbf{y} &= \mathbf{X}\mathbf{b} \\ \mathbf{X}^{\mathsf{T}}\mathbf{y} &= \mathbf{X}^{\mathsf{T}}\mathbf{X}\mathbf{b} \\ (\mathbf{X}^{\mathsf{T}}\mathbf{X})^{-1}\mathbf{X}^{\mathsf{T}}\mathbf{y} &= \mathbf{b} \end{aligned} \tag{2}$$

The R framework for data management



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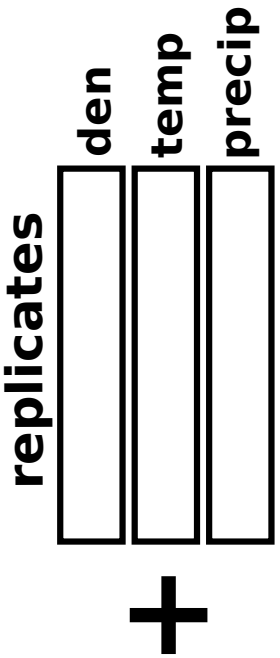
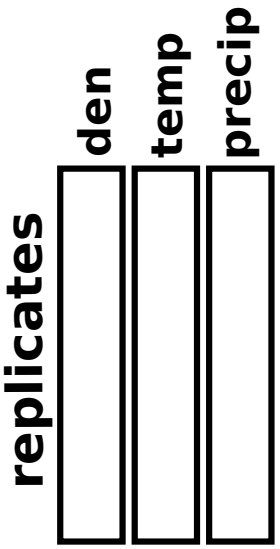


den ~ temp + precip

The R framework for data management



+

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lm / glmer / plot / xyplot

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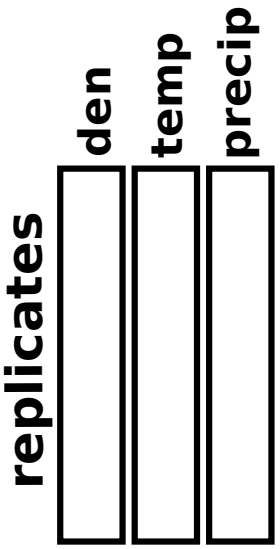

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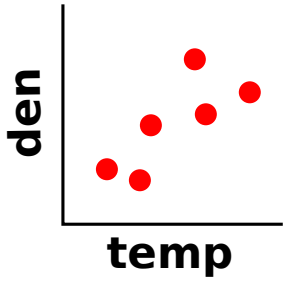

p < 0.0001

	coef	s.e.
(intcpt)	-1.2	0.4
temp	2.1	0.1
precip	-0.1	0.1

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- As new methods are developed, researchers simply pass their data frames to new functions in much the same way they would pass them to older functions.
- Thus, by separating low-level methods development from high-level data analysis, R fosters the formation of a community of researchers where both methodologists and analysts can have mutually beneficial interactions.

Goal Analyze multiple table data sets using this framework

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Goal	Analyze multiple table data sets using this framework
Problem	R doesn't do multiple tables 'out-of-the-box'
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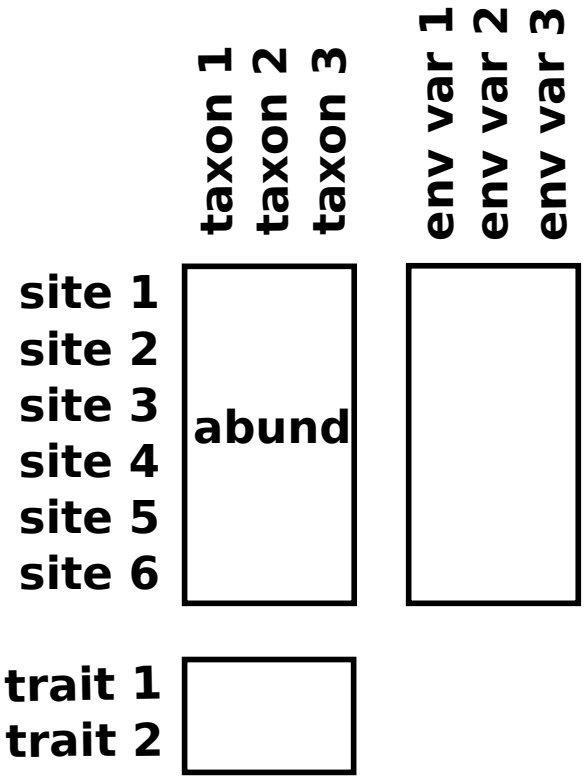
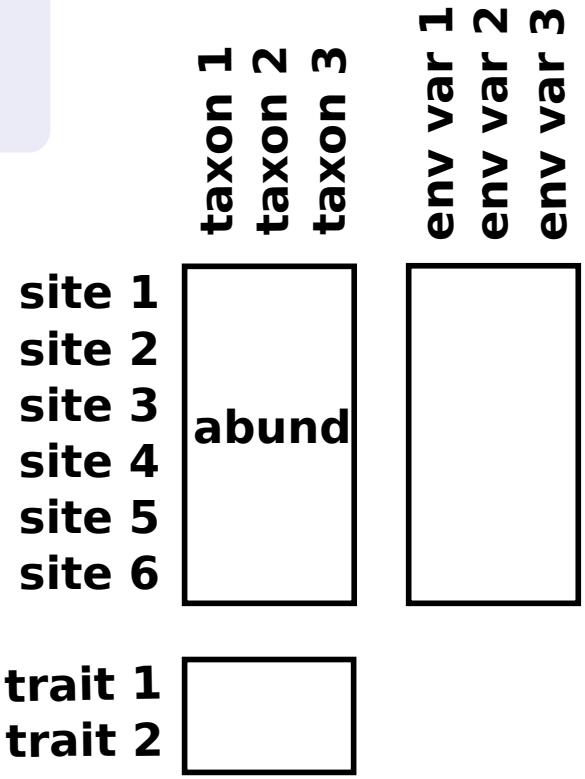
$$\begin{array}{c} \text{DATA LIST} \\ \downarrow \\ \text{DATA FRAME} + \text{FORMULA} + \text{FUNCTION} = \text{ANALYSIS} \end{array}$$

How can we convert this to a data frame?

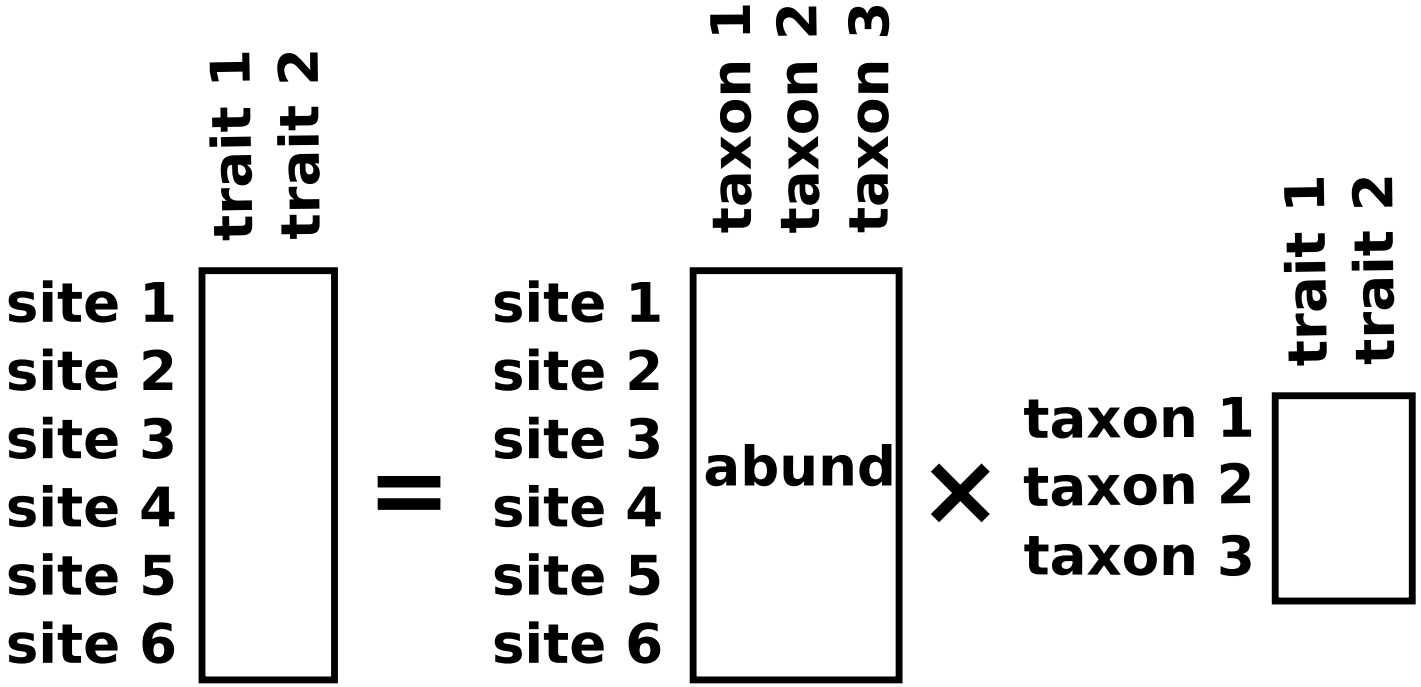


How can we convert this to a data frame?

- Lost information
- Redundant information

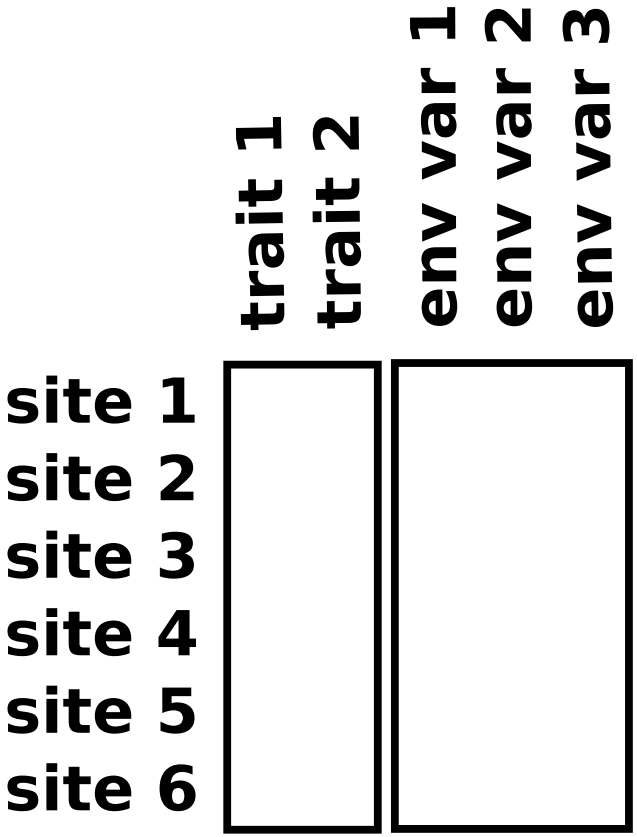


Lost information



e.g. Leibold et al. (2010)

Lost information



e.g. Leibold et al. (2010)

Redundant information

	abundance	env var 1	env var 2	env var 3	trait 1	trait 2
taxon 1, site 1						
taxon 1, site 2						
taxon 1, site 3						
taxon 1, site 4						
taxon 1, site 5						
taxon 1, site 6						
taxon 2, site 1						
taxon 2, site 2						
taxon 2, site 3						
taxon 2, site 4						
taxon 2, site 5						
taxon 2, site 6						
taxon 3, site 1						
taxon 3, site 2						
taxon 3, site 3						
taxon 3, site 4						
taxon 3, site 5						
taxon 3, site 6						

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taxon 1, site 1						
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taxon 1, site 3						
taxon 1, site 4						
taxon 1, site 5						
taxon 1, site 6						
taxon 2, site 1						
taxon 2, site 2						
taxon 2, site 3						
taxon 2, site 4						
taxon 2, site 5						
taxon 2, site 6						
taxon 3, site 1						
taxon 3, site 2						
taxon 3, site 3						
taxon 3, site 4						
taxon 3, site 5						
taxon 3, site 6						

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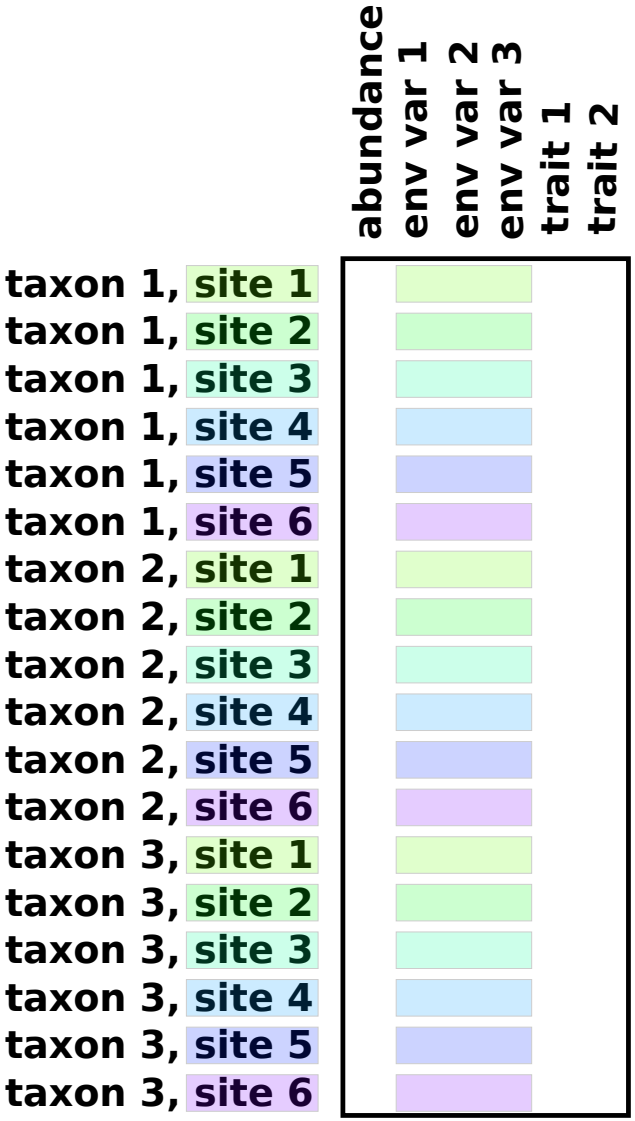

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taxon 1, site 1						
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taxon 2, site 4						
taxon 2, site 5						
taxon 2, site 6						
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taxon 3, site 5						
taxon 3, site 6						

Classifying the fourth-corner dimensions

Rules

- Dimensions that can not grow with more sampling represent groups of variables

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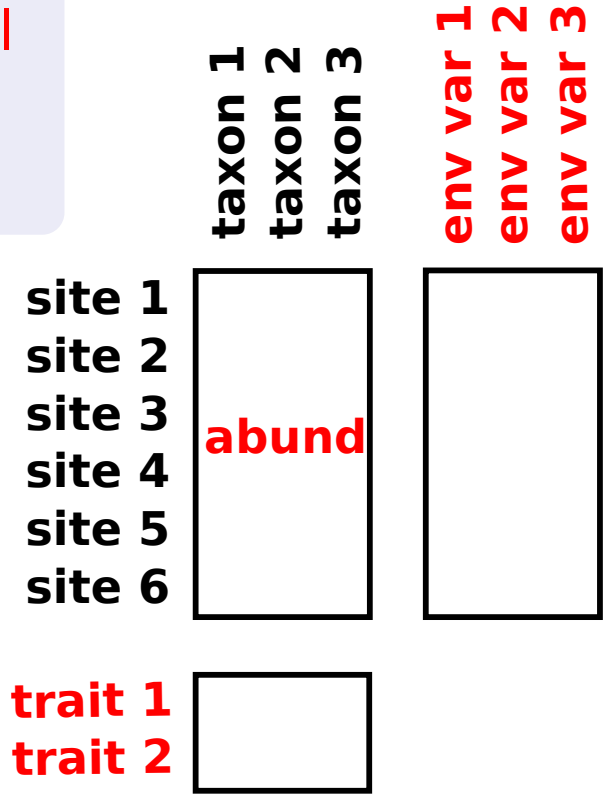
Rules

- Dimensions that can not grow with more sampling represent groups of variables
- Dimensions that can grow with more sampling represent replication

Classifying the fourth-corner dimensions

Variables

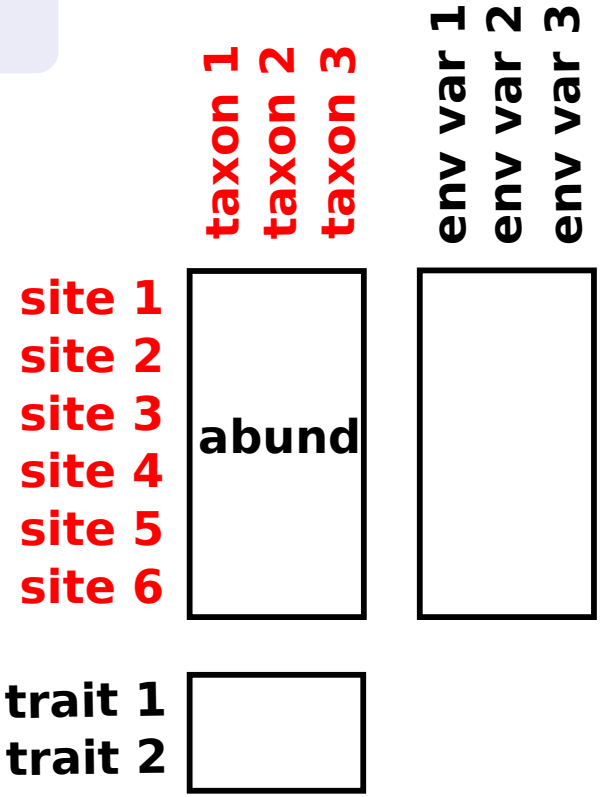
- abundance
- environmental variables
- traits



Classifying the fourth-corner dimensions

Replicates

- sites
- taxa



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	abundance	env var 1	env var 2	env var 3	trait 1	trait 2
taxon 1, site 1						
taxon 1, site 2						
taxon 1, site 3						
taxon 1, site 4						
taxon 1, site 5						
taxon 1, site 6						
taxon 2, site 1						
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taxon 2, site 4						
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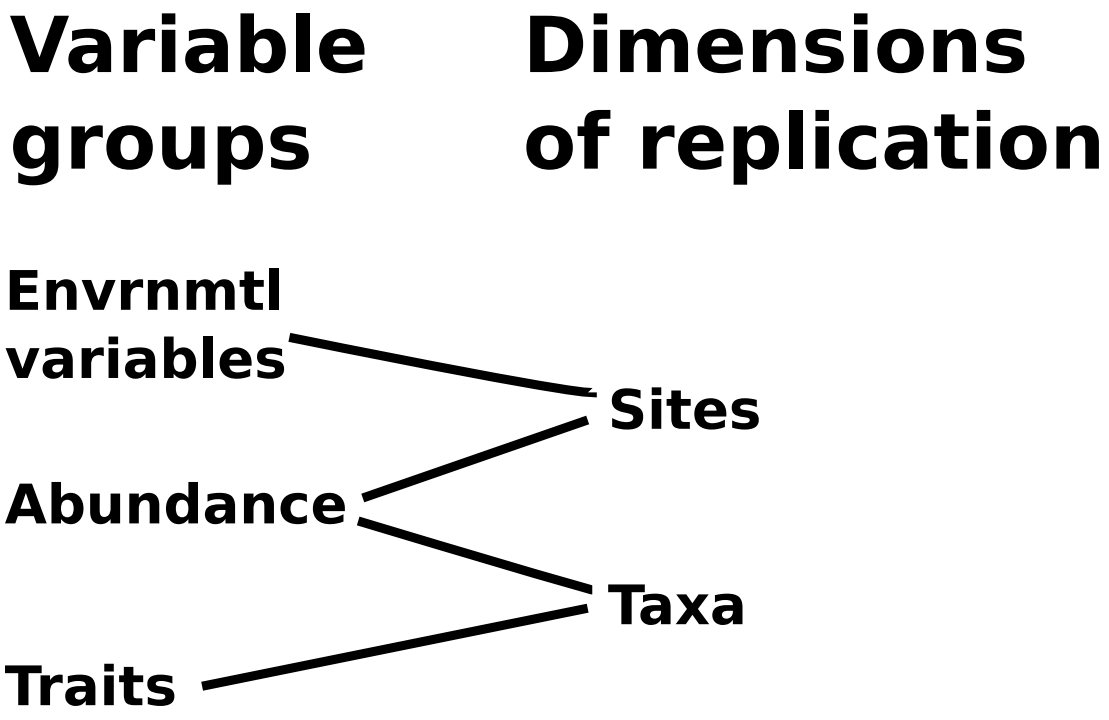
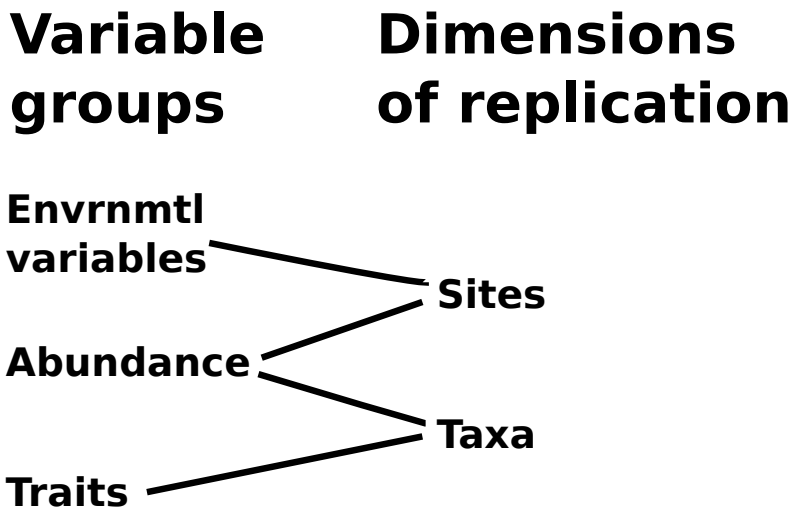
taxon 2, site 6						
taxon 3, site 1						
taxon 3, site 2						
taxon 3, site 3						
taxon 3, site 4						
taxon 3, site 5						
taxon 3, site 6						

Bipartite graphs



Biadjacency matrices



	abund.	env.	traits
sites	1	1	0
taxa	1	0	1

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Identifying data sets that are not multiple-table

If a data set has a biadjacency matrix with at least one row of all ones,

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Example

	abund.	env.	geog.	traits
space	1	1	1	1
time	1	1	0	0
taxa	1	0	0	1

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If a data set has a biadjacency matrix with at least one row of all ones, then that data set can be expressed as a single table

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time	1	1	0	0
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Biadjacency matrices

Identifying data sets that are not multiple-table

If a data set has a biadjacency matrix with at least one row of all ones, then that data set can be expressed as a single table without redundant or lost information.

Example

	abund.	env.	geog.	traits
space	1	1	1	1
time	1	1	0	0
taxa	1	0	0	1

Biadjacency matrices

Necessarily un-correlated variables

If two columns in a biadjacency matrix are orthogonal (i.e. have zero dot product)

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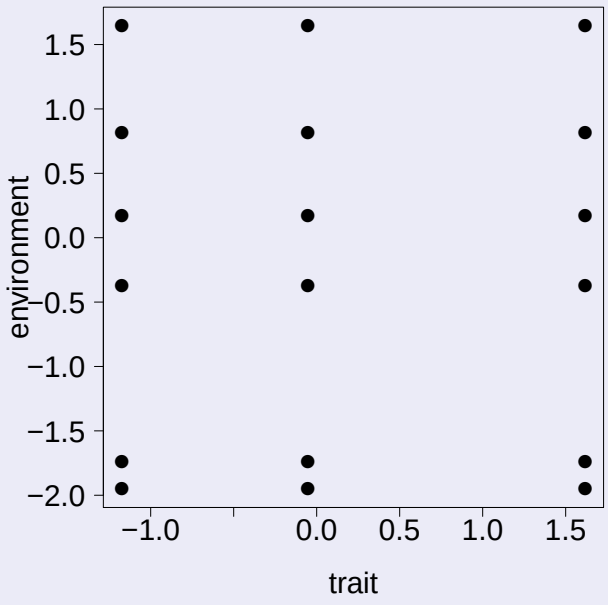

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If two columns in a biadjacency matrix are orthogonal (i.e. have zero dot product) then the associated variable groups are also orthogonal (i.e. uncorrelated),

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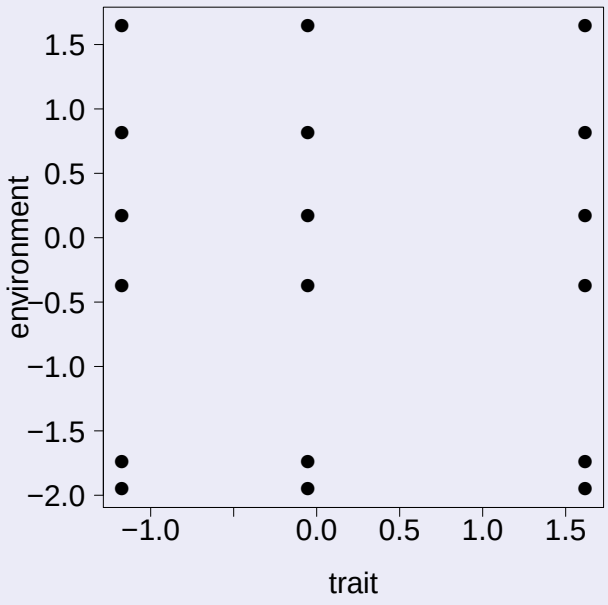

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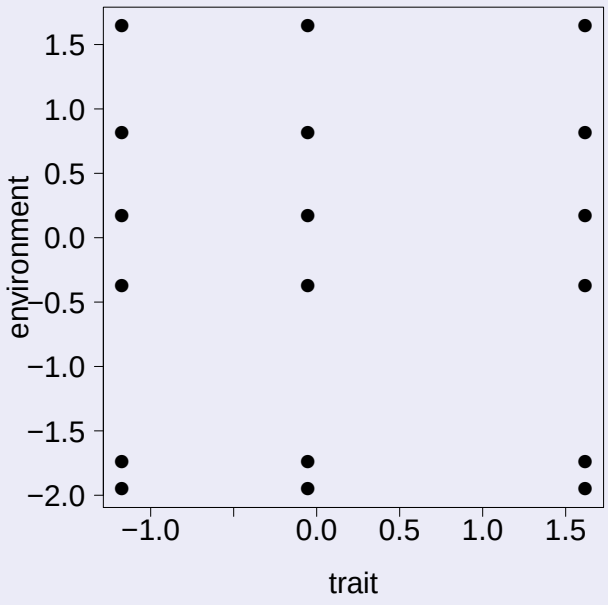
Biadjacency matrices

Necessarily un-correlated variables

If two columns in a biadjacency matrix are orthogonal (i.e. have zero dot product) then the associated variable groups are also orthogonal (i.e. uncorrelated), after the data set has been coerced to a data frame by the method of repetition.

Example



	abund.	env.	traits
sites	1	1	0
taxa	1	0	1

Biadjacency matrices

The meaning of zeros

A variable with a zero for a particular dimension of replication, is assumed (statistically) constant across that dimension.

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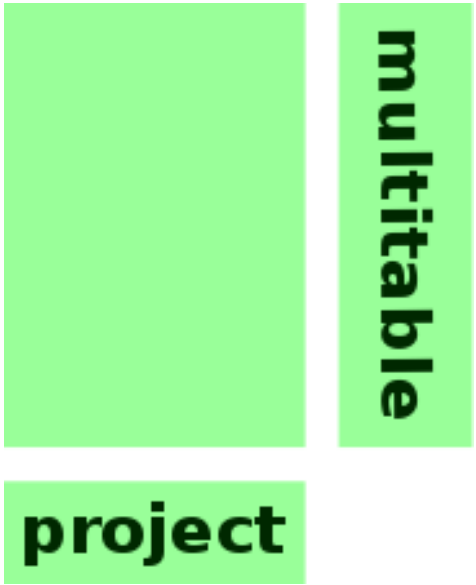
Example

	abund.	env.	traits
sites	1	1	0
taxa	1	0	1

```
> library(multitable)
```

http://multitable.r-forge.r-project.org/



```
> dl <- data.list(abundance = ab, temperature = tp,
+ bodysize = bs, dnames = c("sites", "species"))
```

```
> dl
abundance:
---------
       sppA  sppB  sppC
siteA  1.17 -0.04  0.85
siteB  0.65 -0.06 -0.37
siteC  0.51 -2.73  1.07
siteD -1.19  2.81  0.17
siteE -0.69 -0.21  0.38
Replicated along:  || sites || || species ||

temperature:
-----------
siteA siteB siteC siteD siteE
-1.04  0.77  0.82 -0.38 -0.06
Replicated along:  || sites ||
```

continued...

```
bodysize:
--------
 sppA  sppB  sppC
-0.45 -0.07  1.48
Replicated along:  || species ||


REPLICATION DIMENSIONS:
  sites species
      5       3
```

```
> dl[1:3, ]
```

```
abundance:
---------
      sppA  sppB  sppC
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siteB 0.65 -0.06 -0.37
siteC 0.51 -2.73  1.07
Replicated along:  || sites || species ||


temperature:
-----------
siteA siteB siteC
-1.04  0.77  0.82
Replicated along:  || sites ||
```
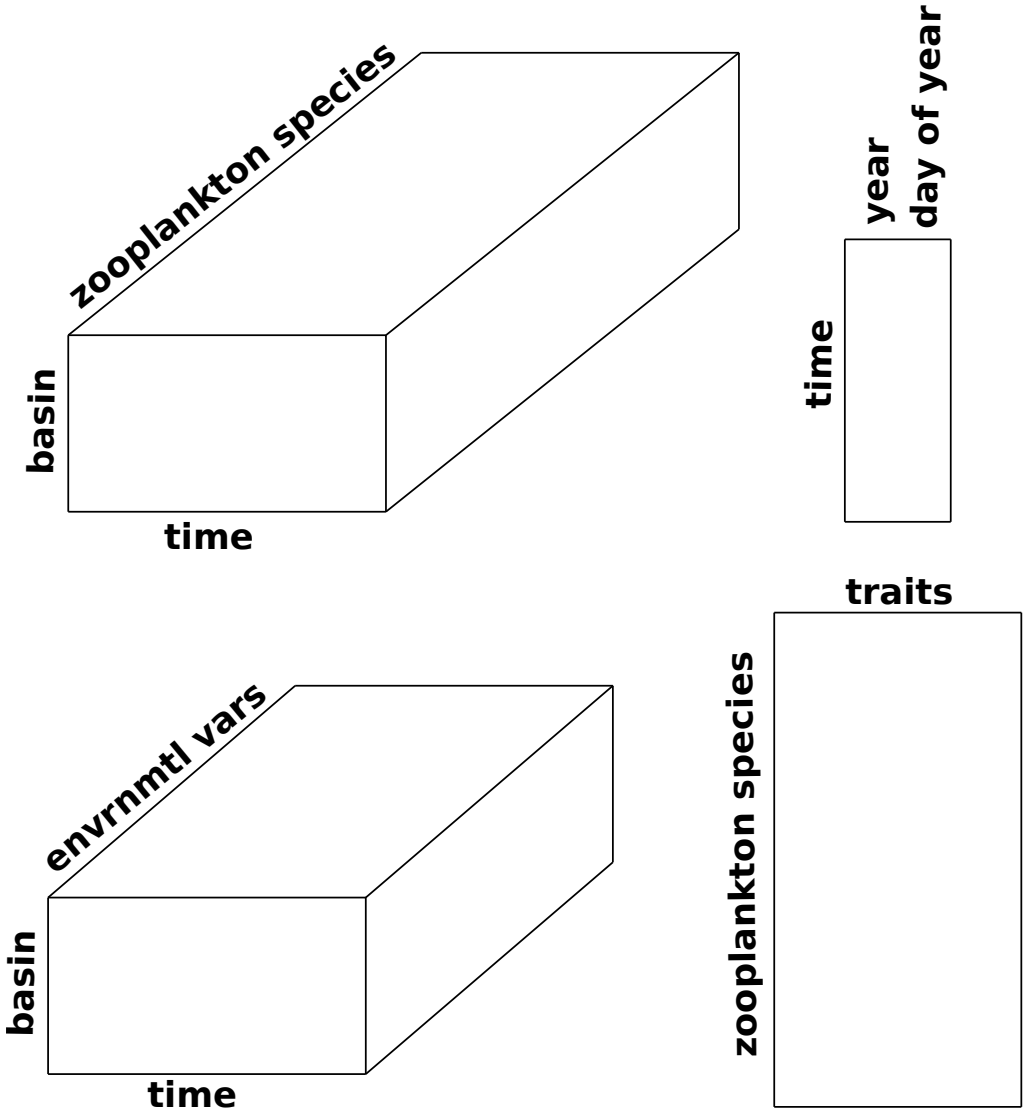

continued...

```
bodysize:
--------
 sppA  sppB  sppC
-0.45 -0.07  1.48
Replicated along:  || species ||


REPLICATION DIMENSIONS:
  sites species
      3       3
```

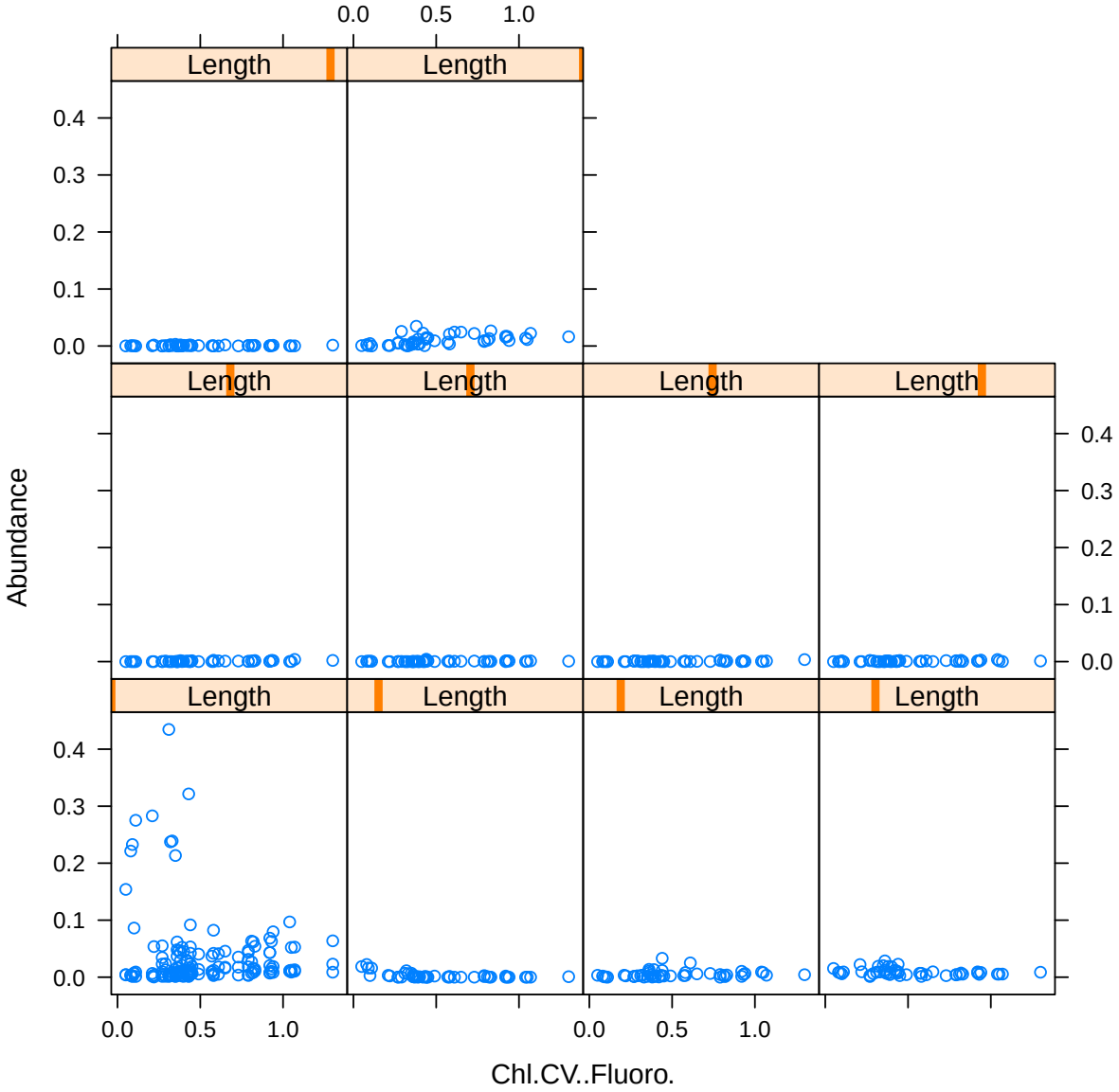
```
> lm(abundance ~ temperature * bodysize, dl)

Call:
lm(formula = abundance ~ temperature * bodysize,
data = dl)

Coefficients:
(Intercept)     temperature     bodysize
    0.08795        -0.40439      0.20848

temperature:bodysize
             0.09822
```

```
> as.data.frame(dl)
   abundance temperature bodysize
1       1.17  -1.3453605    -0.45
2       0.65   0.9475797    -0.45
3       0.51   1.0109206    -0.45
4      -1.19  -0.5092608    -0.45
5      -0.69  -0.1038791    -0.45
6      -0.04  -1.3453605    -0.07
7      -0.06   0.9475797    -0.07
8      -2.73   1.0109206    -0.07
9       2.81  -0.5092608    -0.07
10     -0.21  -0.1038791    -0.07
11      0.85  -1.3453605     1.48
12     -0.37   0.9475797     1.48
13      1.07   1.0109206     1.48
14      0.17  -0.5092608     1.48
15      0.38  -0.1038791     1.48
```



Cantin et al. 2011 – Lac Croche, Québec, Canada

```
> xyplot(Abundance ~ Chl.CV..Fluoro. | Length,
+ data = as.data.frame(dl))
```



Take-home message

Don't be scared of multiple table data sets.

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Take-home message

Don't be scared of multiple table data sets. Collect more of them! With the right data management framework, multiple table data can be modeled in much the same way that we model single table data.

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http://multitable.r-forge.r-project.org/