



De l'écologie des communautés à la génomique : apport des méthodes d'analyses multivariées

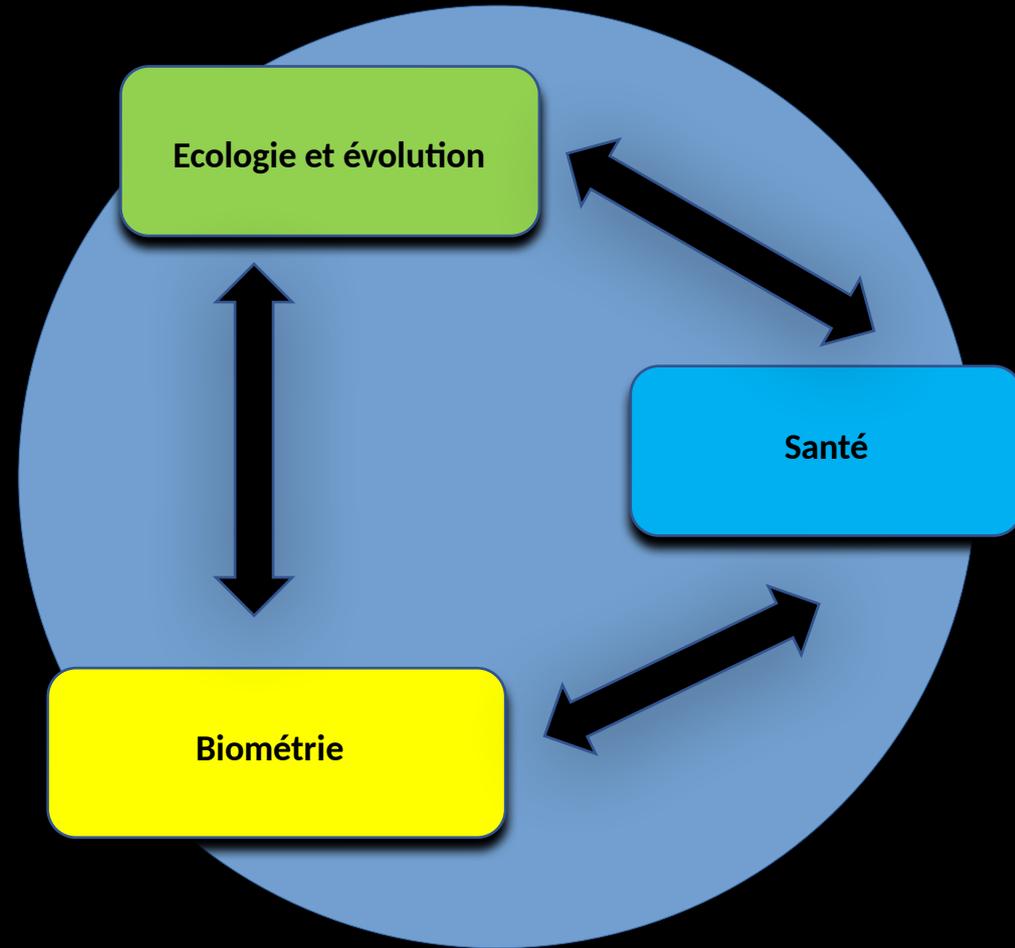
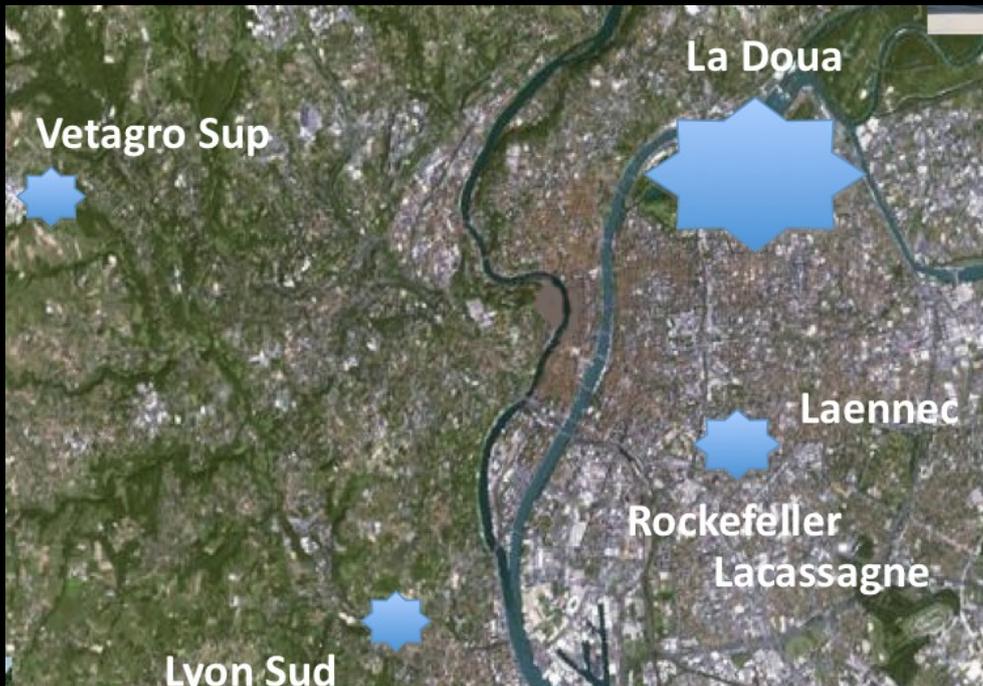
Stéphane Dray

30 mars 2023

Journée StatOmique « Analyses Factorielles »



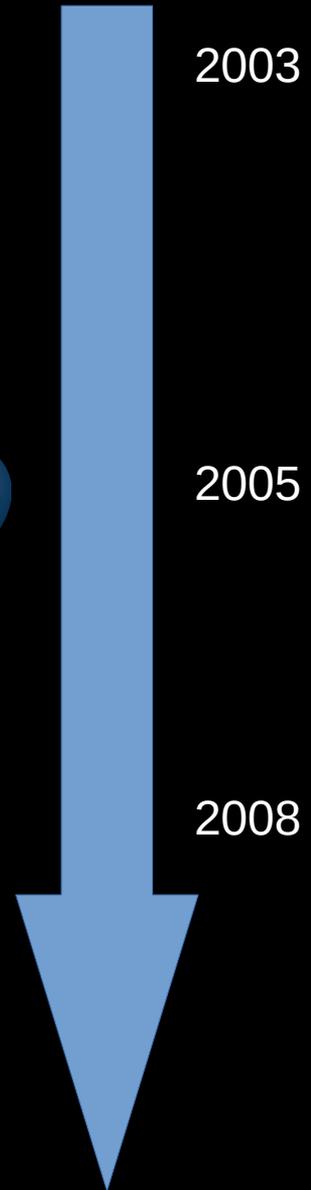
LBBE





Thibaut Jombart

Thèse : Analyses multivariées de marqueurs génétiques :
développements méthodologiques, applications et extensions



2003

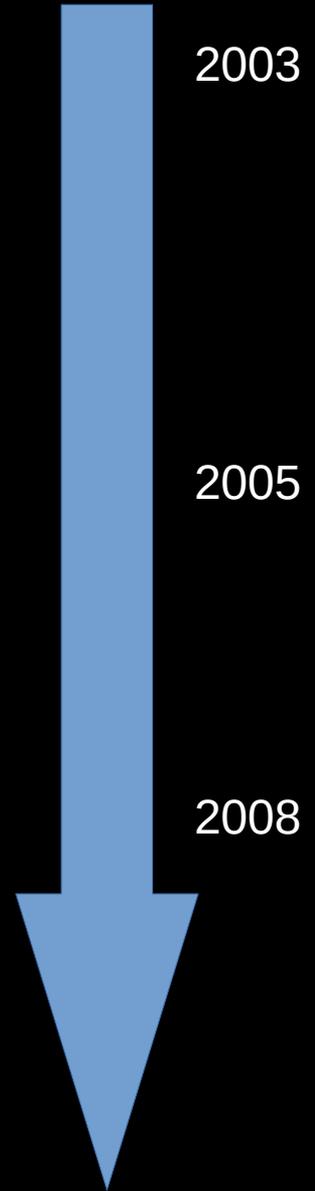
2005

2008



Thibaut Jombart

Thèse : Analyses multivariées de marqueurs génétiques :
développements méthodologiques, applications et extensions





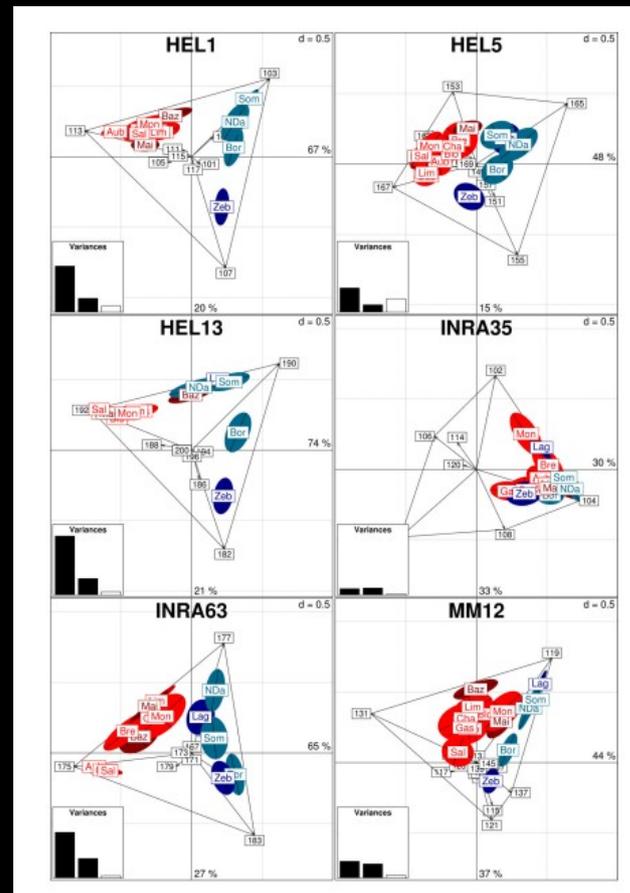
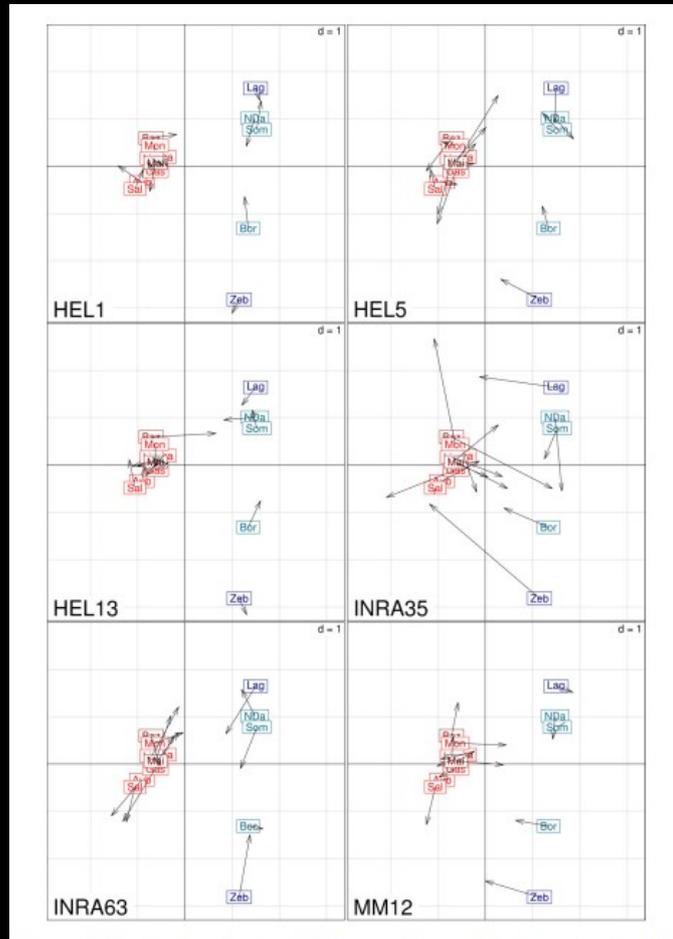
Genet. Sel. Evol. 39 (2007) 545–567
© INRA, EDP Sciences, 2007
DOI: 10.1051/gse:2007021

Available online at:
www.gse-journal.org

Original article

Consensus genetic structuring and typological value of markers using multiple co-inertia analysis

Denis LALOË^{a*}, Thibaut JOMBART^b, Anne-Béatrice DUFOUR^b,
Katayoun MOAZAMI-GOUDARZI^c



2003

2005

2008



Genet. Sel. Evol. 39 (2007) 545–567
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Consensus genetic structuring and typological value of markers using multiple co-inertia analysis

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Katayoun MOAZAMI-GOUDARZI^c

2003

BIOINFORMATICS APPLICATIONS NOTE Vol. 24 no. 11 2008, pages 1403–1405 doi:10.1093/bioinformatics/btn129

Genetics and population analysis

adegenet: a R package for the multivariate analysis of genetic markers

Thibaut Jombart*

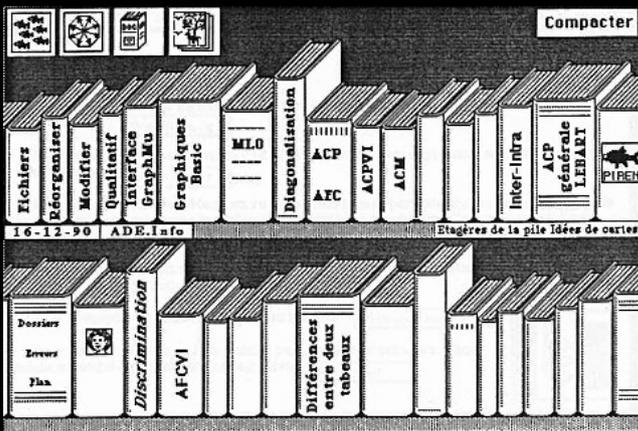
2005

ACKNOWLEDGEMENTS

The author is grateful to R-Forge for hosting *adegenet*, to P. Sólymos for his contribution and to A.-B. Dufour, S. Devillard, D. Laloë and D. Pontier for their constructive comments.

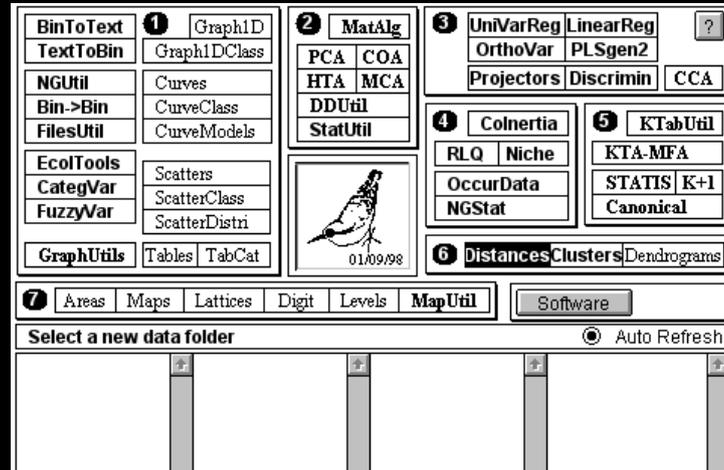
2008

grand "merci" à Stéphane Dray, Sébastien Devillard, Denis Laloë, Katayoun Moazami-Goudarzi et Sandrine Pavoine, avec qui j'ai eu le plaisir de collaborer. En particulier, merci à Stéphane pour m'avoir fait participer au SEDAR, et à Sébastien et Denis pour avoir servi de beta-testeurs à adegenet. Merci également à Hilmar Lapp et aux organisateurs et aux participants du 'R



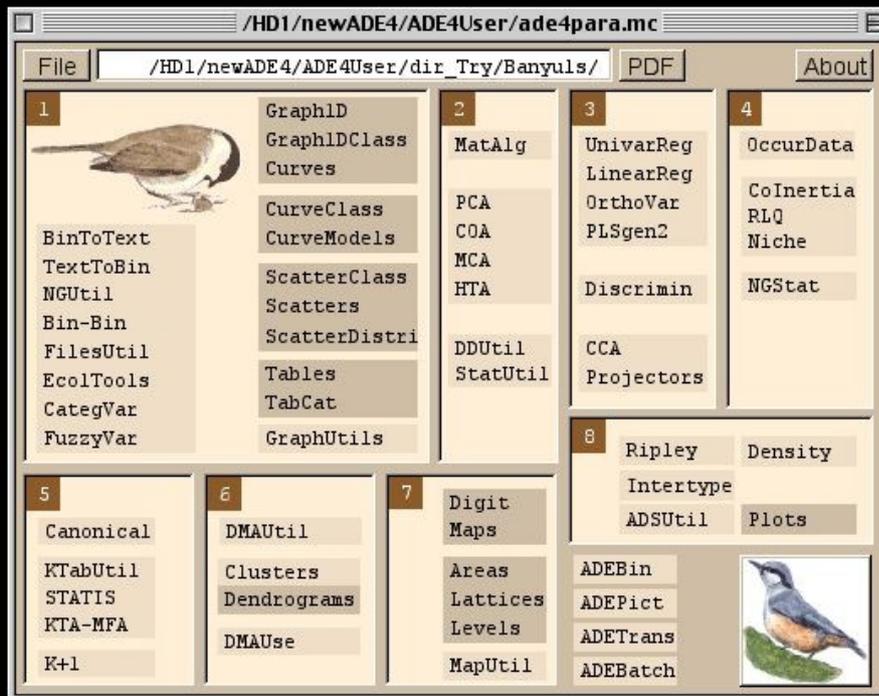
ADECO (1989)

- modules in Microsoft QuickBasic
- Hypercard interface



ADE-4 (1995)

- modules in C
- Hypercard and Winplus interfaces



ADE-4 (2000)

- Metacard interface
- batch mode







The ade4 Package — II: Two-table and K-table Methods

by Stéphane Dray, Anne B. Dufour and Daniel Chessel



Journal of Statistical Software

August 2018, Volume 86, Issue 1.

doi: 10.18637/jss.v086.i01

Supervised Multiblock Analysis in R with the ade4 Package

The ade4 package - I : One-table methods

by Daniel Chessel, Anne B Dufour and Jean Thioulouse

For example, if X is a table containing normalized quantitative variables, if Q is the identity matrix I_p



Journal of Statistical Software

September 2007, Volume 22, Issue 5.

<http://www.jstatsoft.org/>

Interactive Multivariate Data Analysis in R with the ade4 and ade4TkGUI Packages



Journal of Statistical Software

September 2007, Volume 22, Issue 4.

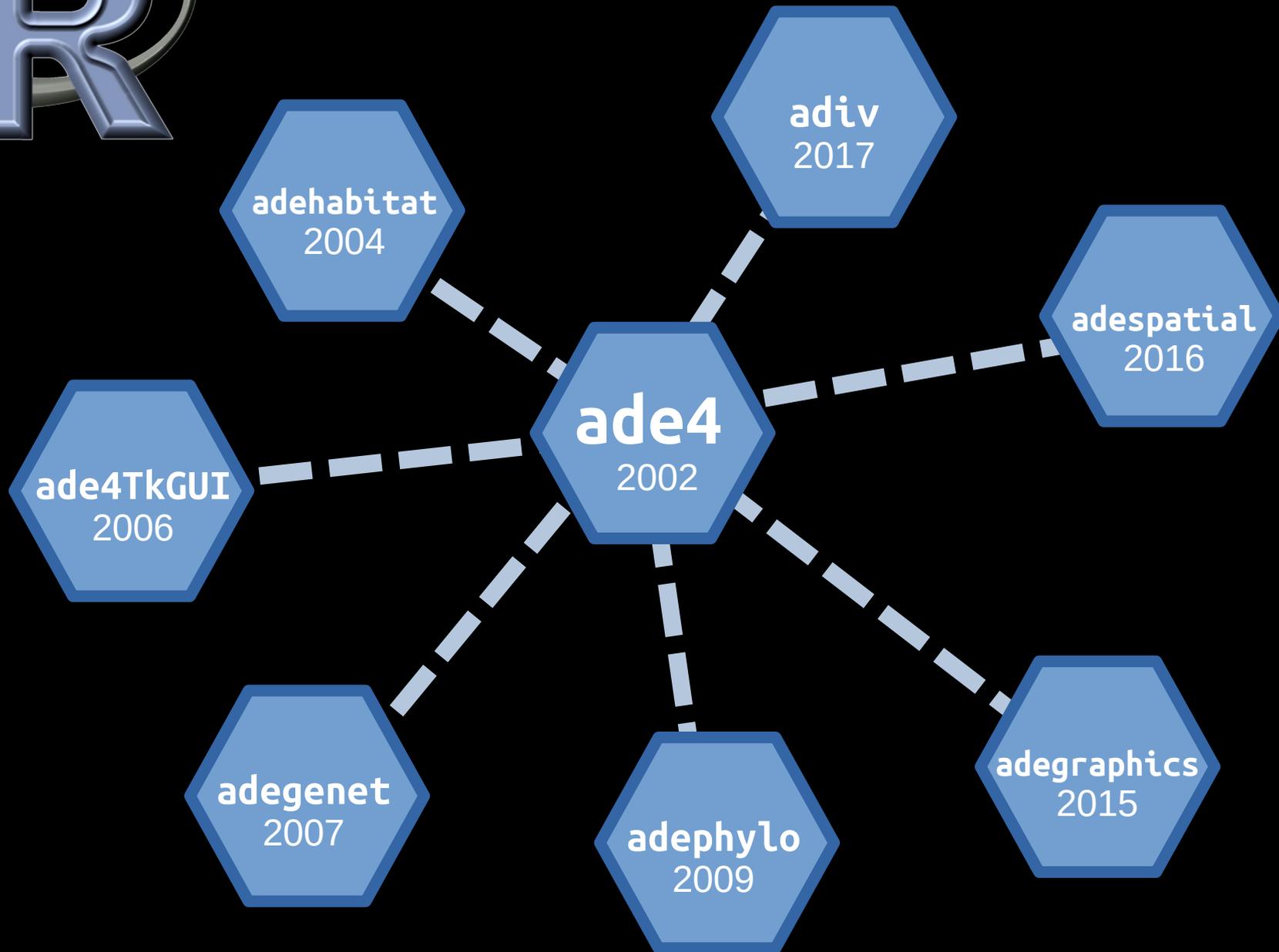
<http://www.jstatsoft.org/>

The ade4 Package: Implementing the Duality Diagram for Ecologists

Jean Thioulouse · Stéphane Dray
Anne-Béatrice Dufour · Aurélie Siberchicot
Thibaut Jombart · Sandrine Pavoine

Multivariate
Analysis of
Ecological Data
with ade4

Springer



Ecologie des communautés et analyses multivariées

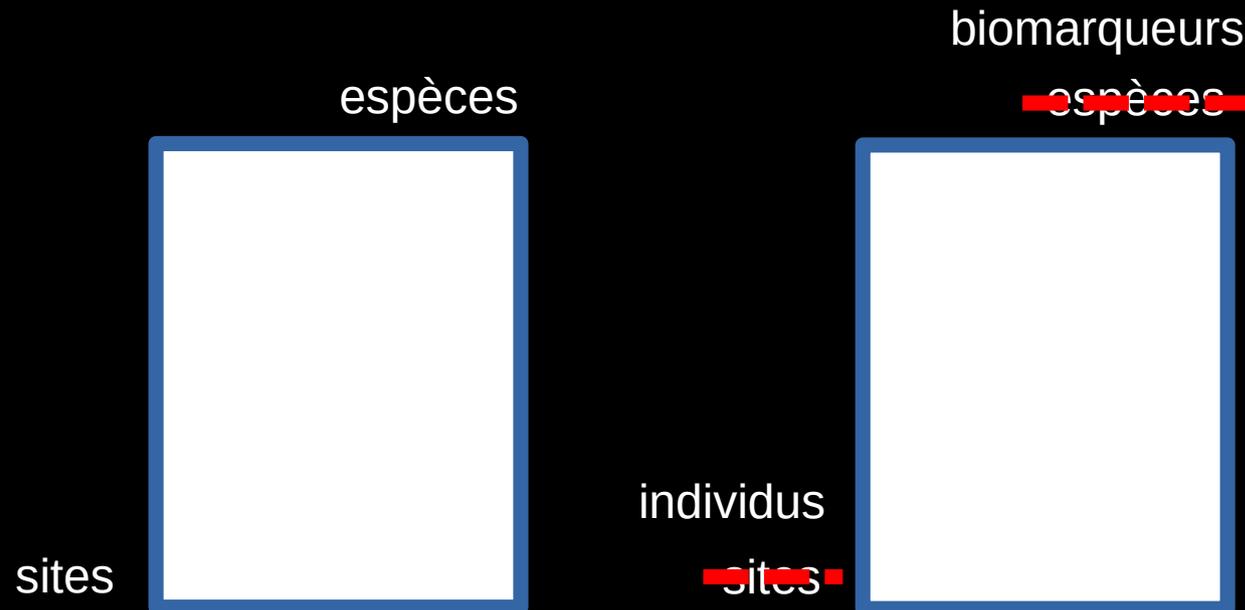
- quelles questions ?
- quelles données ?
- quelles méthodes ?

De l'écologie des communautés à la génomique ...

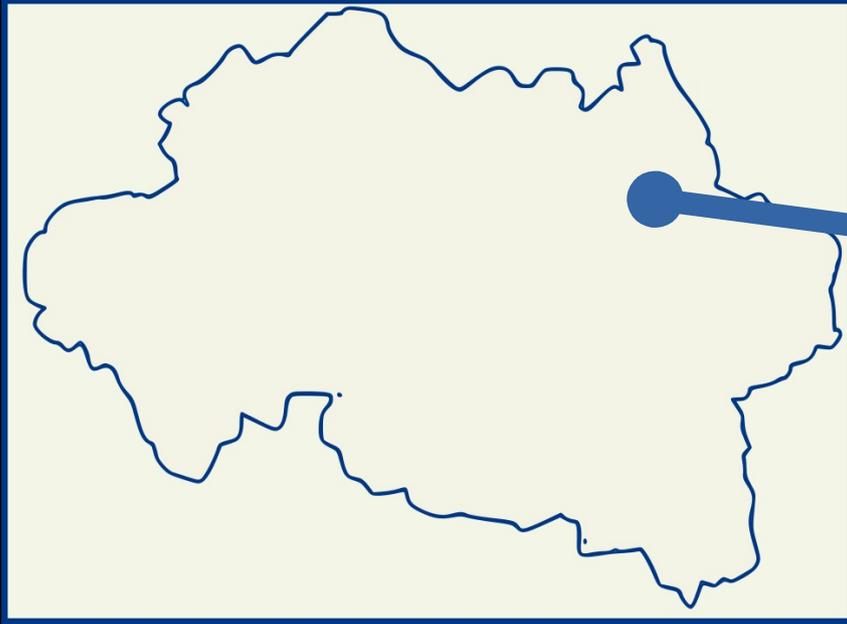
Ecologie des communautés et analyses multivariées

- quelles questions ?
- quelles données ?
- quelles méthodes ?

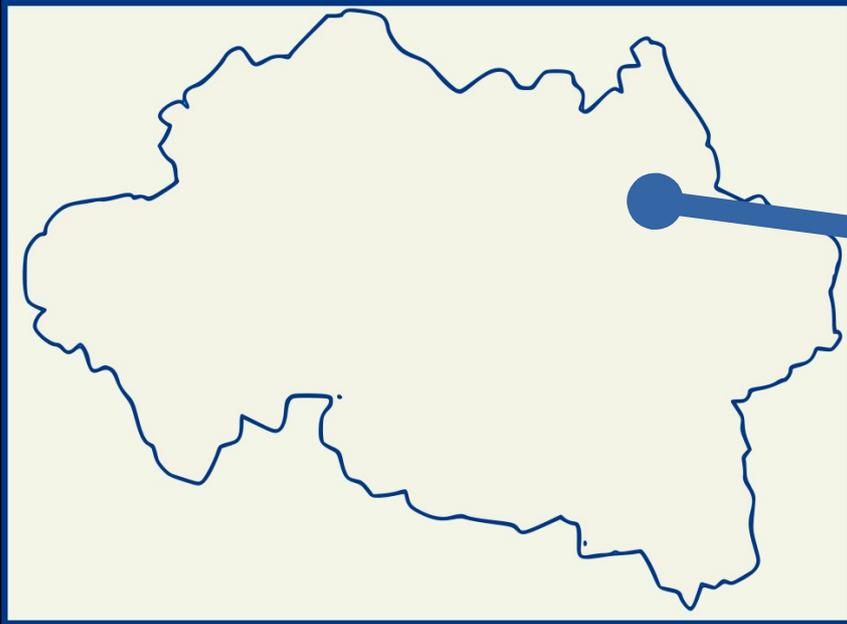
De l'écologie des communautés à la génomique ...



Une communauté



Une communauté

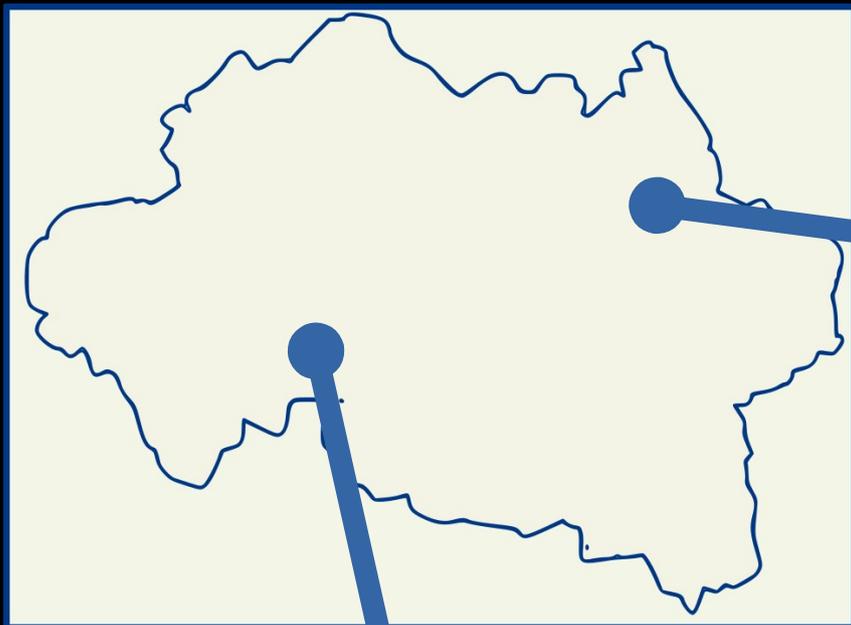


Un vecteur :



Diversité α

Deux communautés



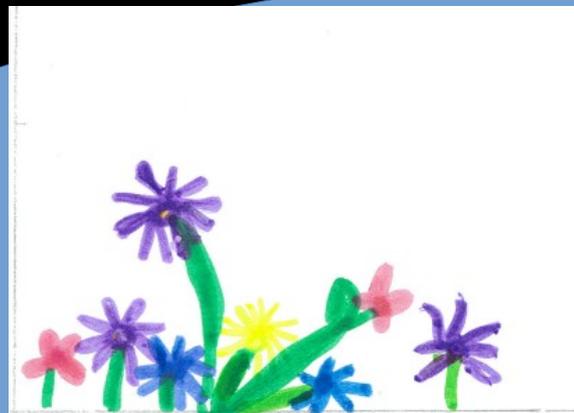
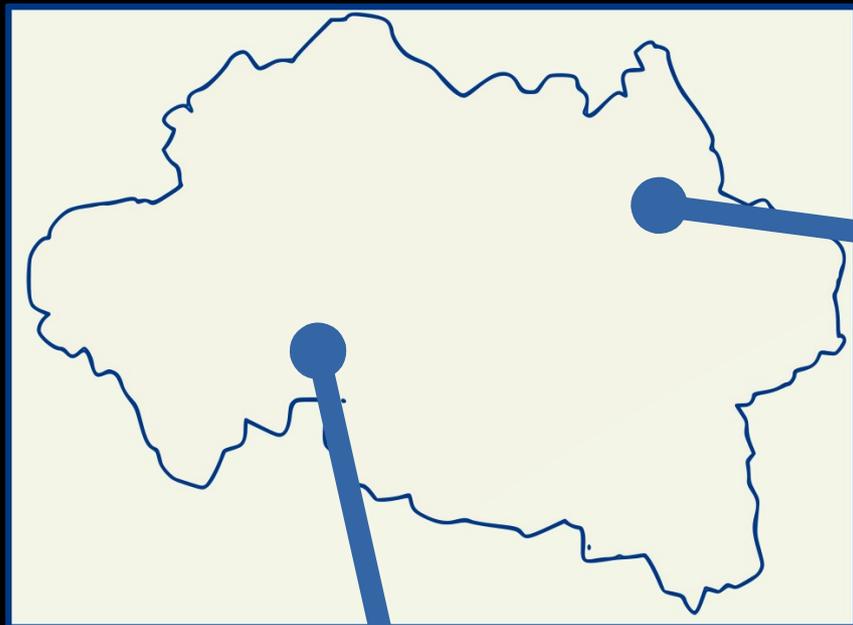
Diversité α_1



Diversité α_2

Tree	Purple flower	Pink flower	Yellow flower	Blue flower
0	3	2	1	2
4	1	1	0	0

Deux communautés



Diversité α_1



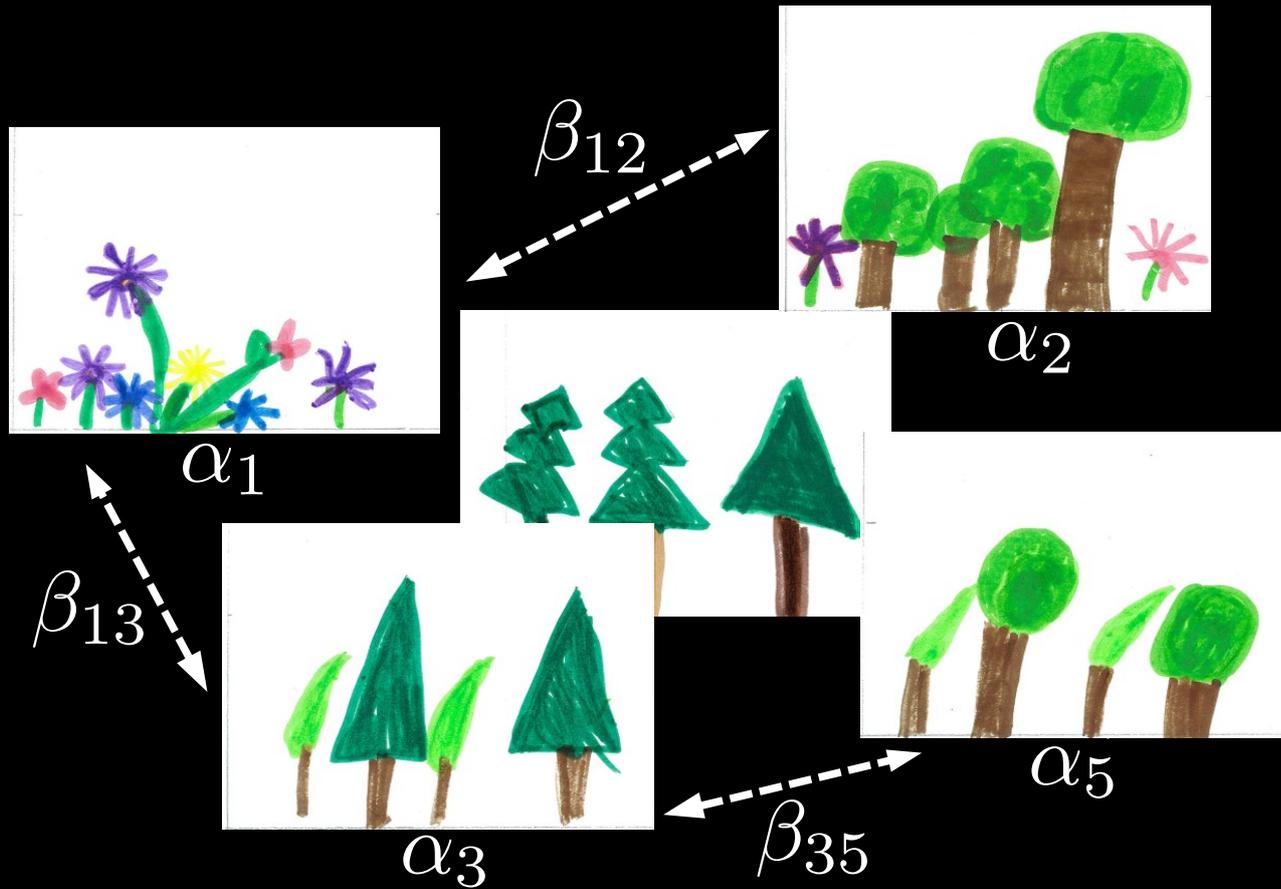
Diversité α_2

Diversité β_{12}

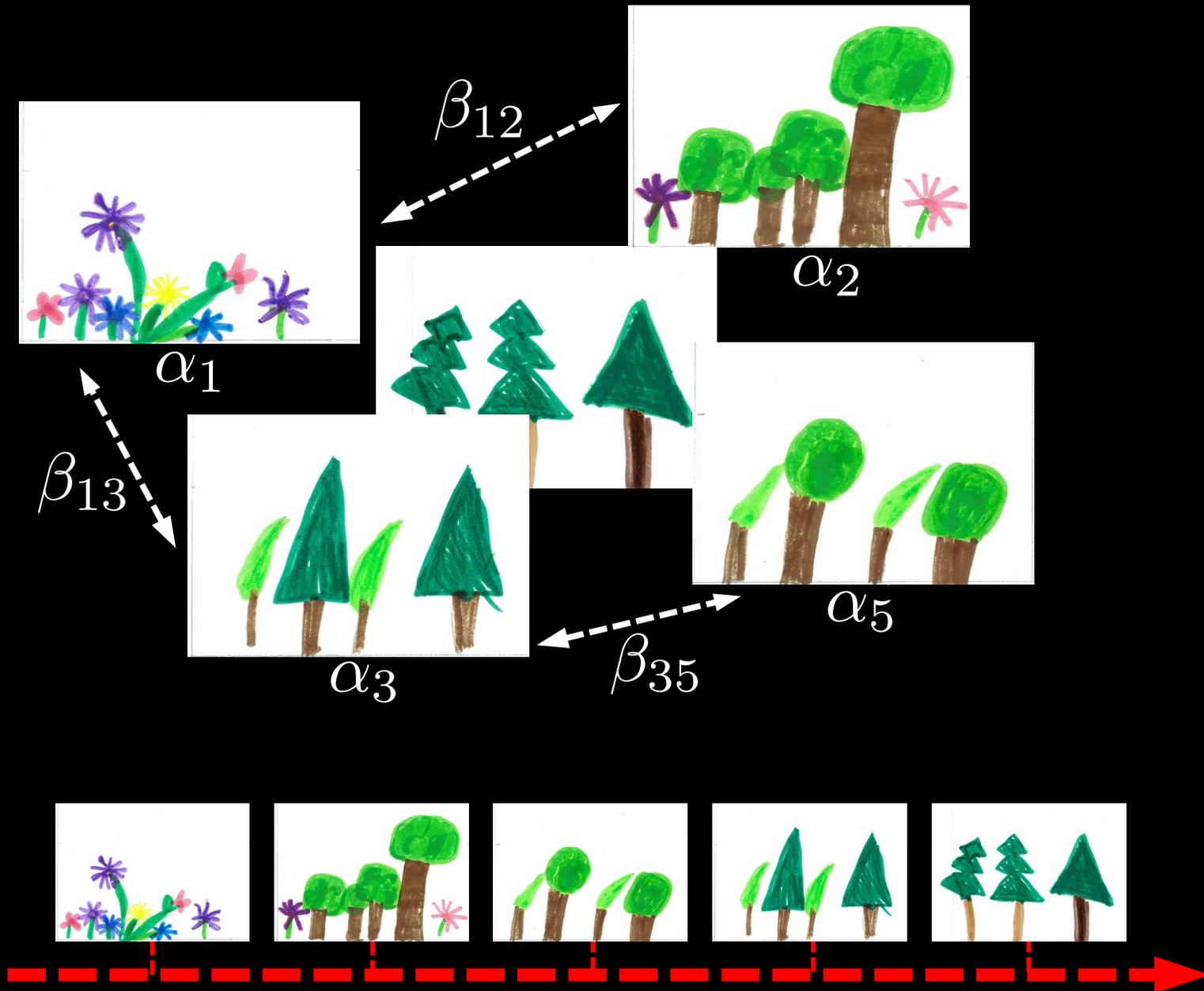
Diversité γ

Tree	Purple flower	Pink flower	Yellow flower	Blue flower
0	3	2	1	2
4	1	1	0	0

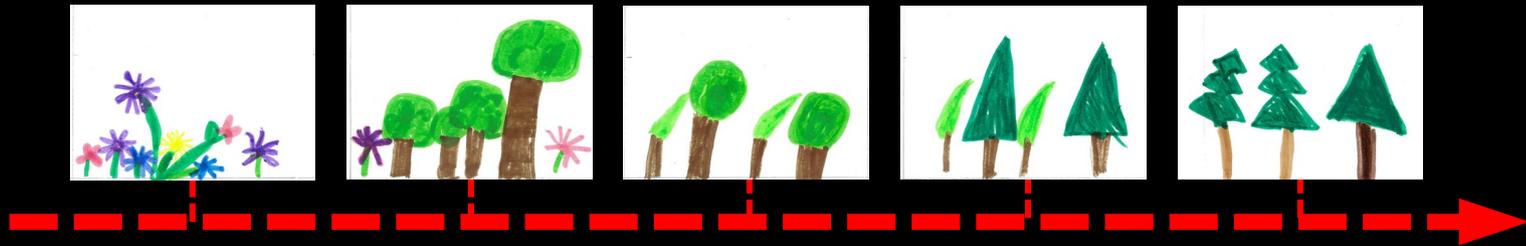
Ordination des communautés



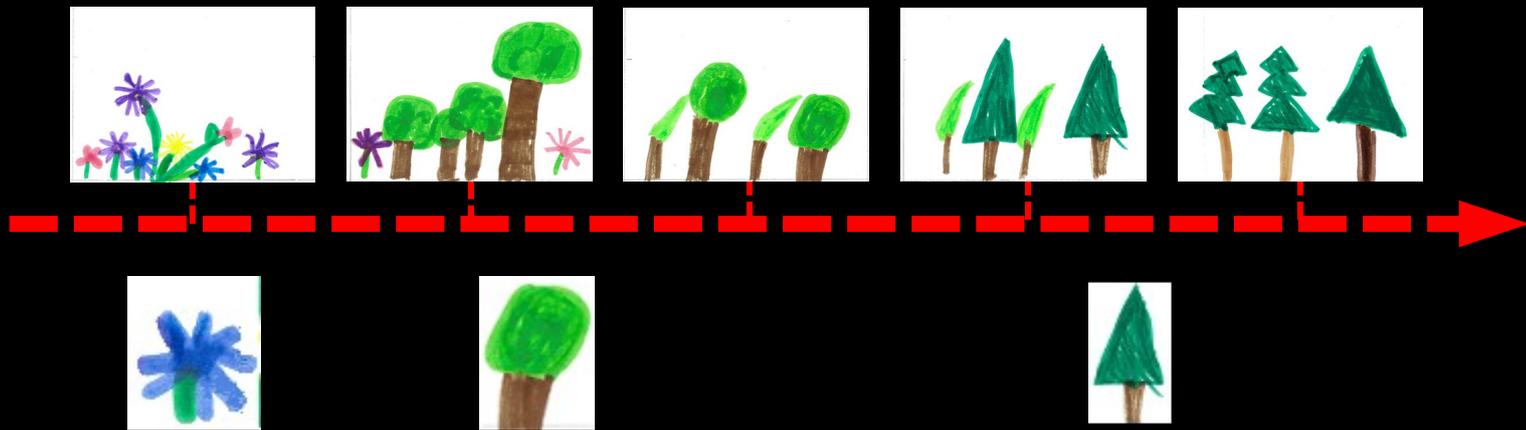
Ordination des communautés



Ordination simultanée

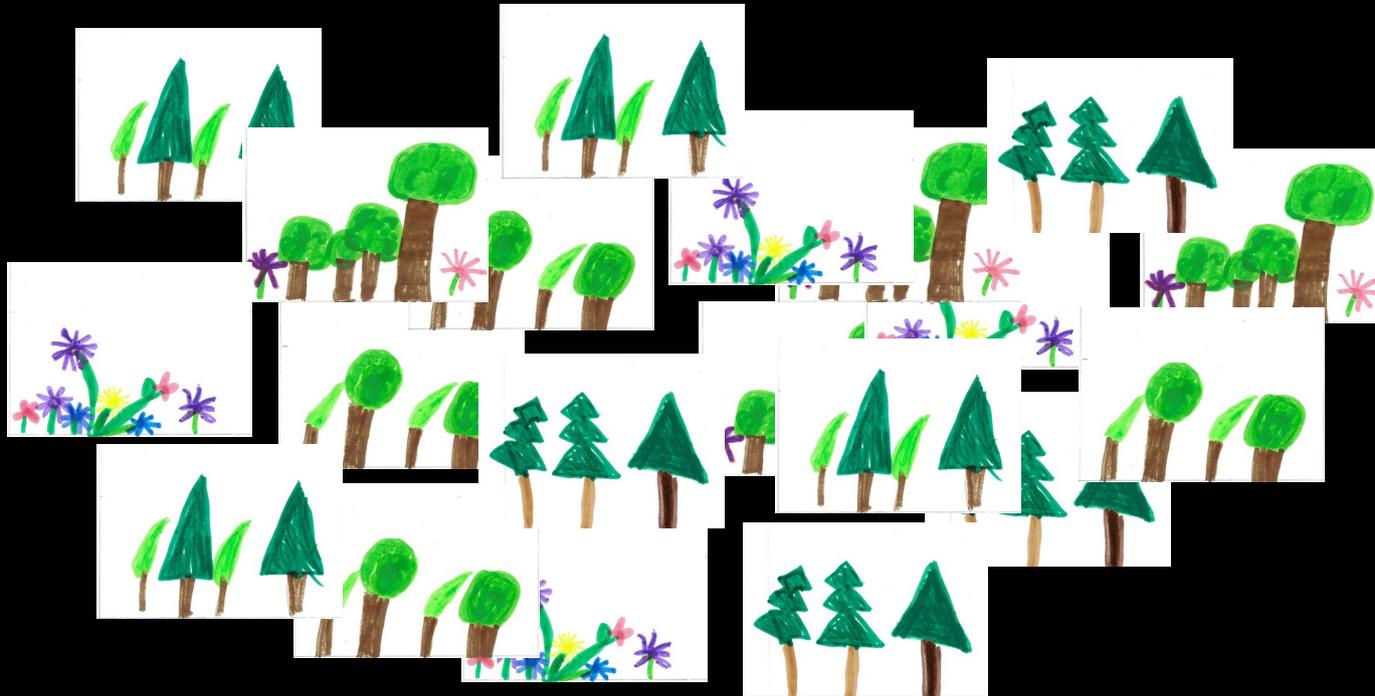


Ordination simultanée

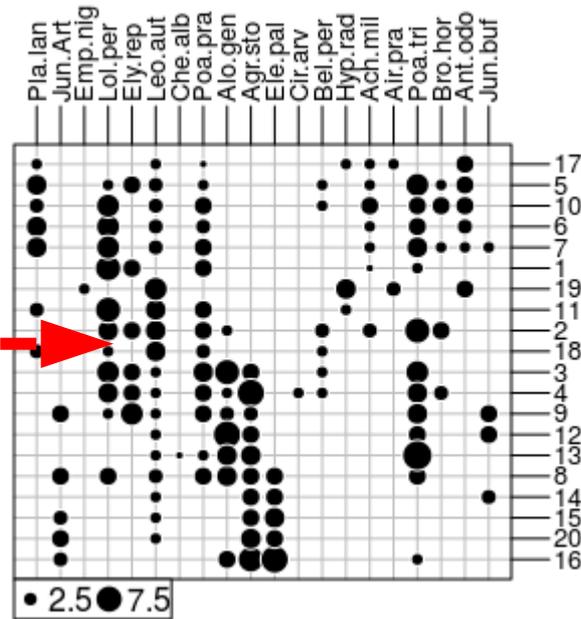
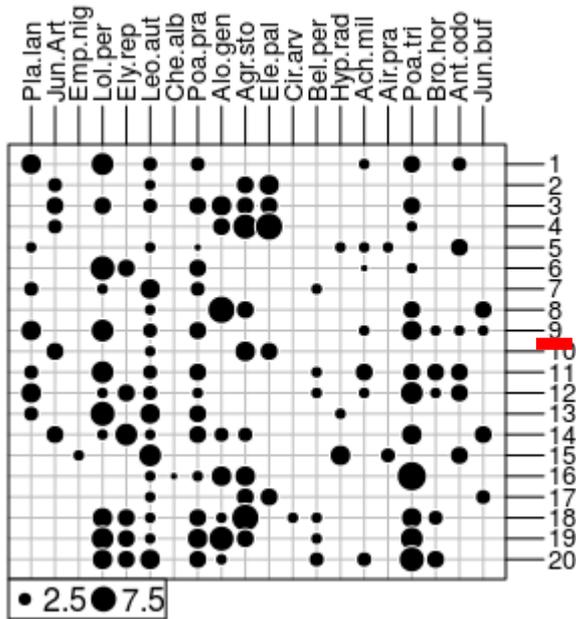


Moyenne pondérée
(*weighted averaging*)

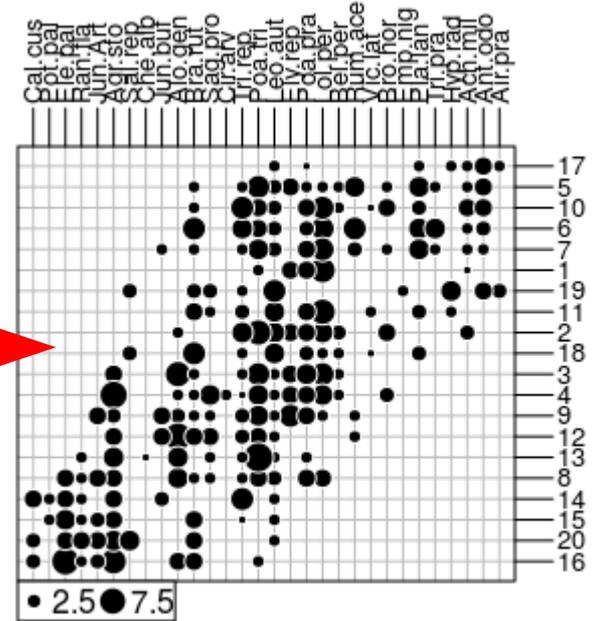
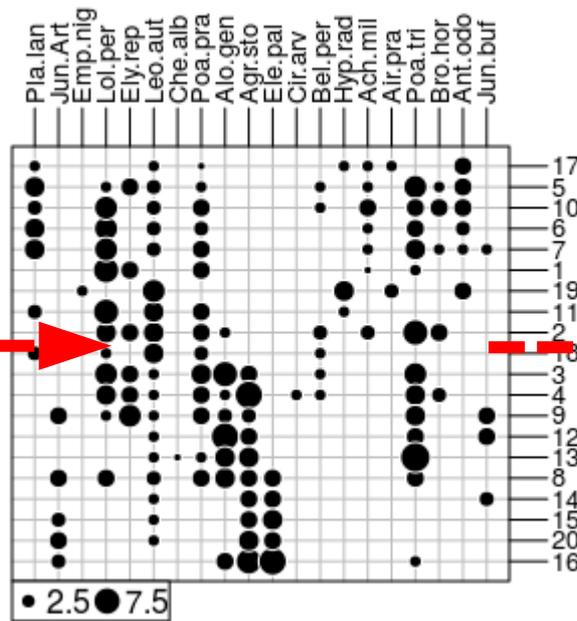
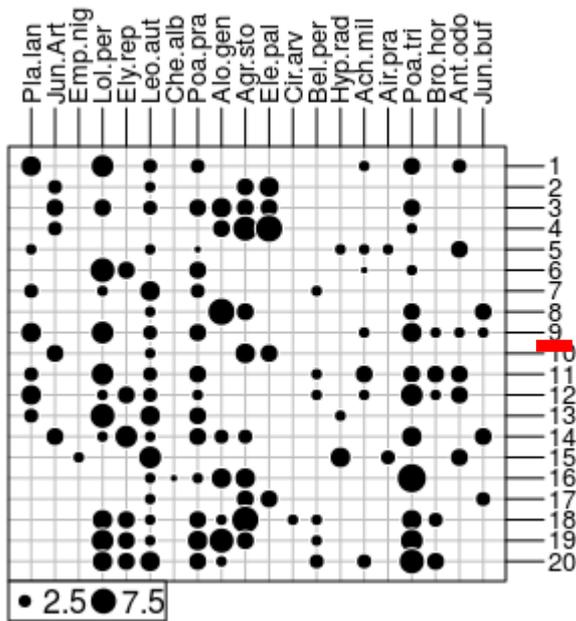
Un casse-tête



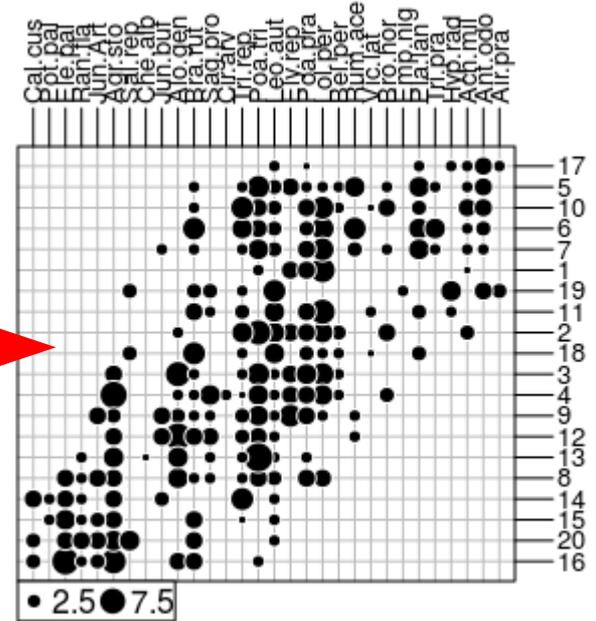
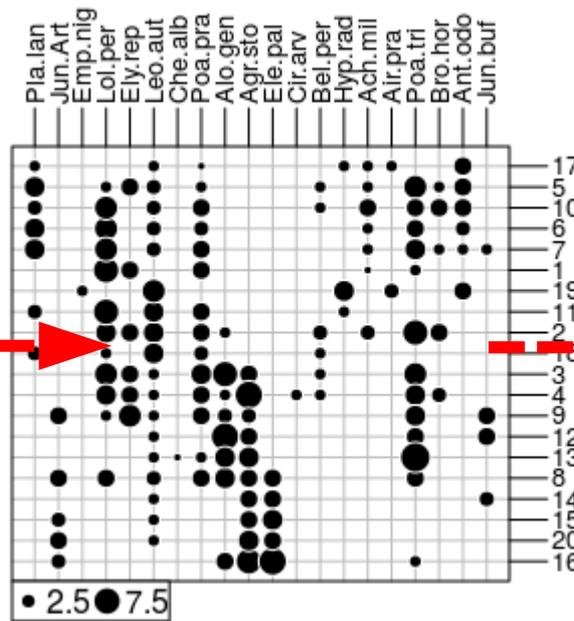
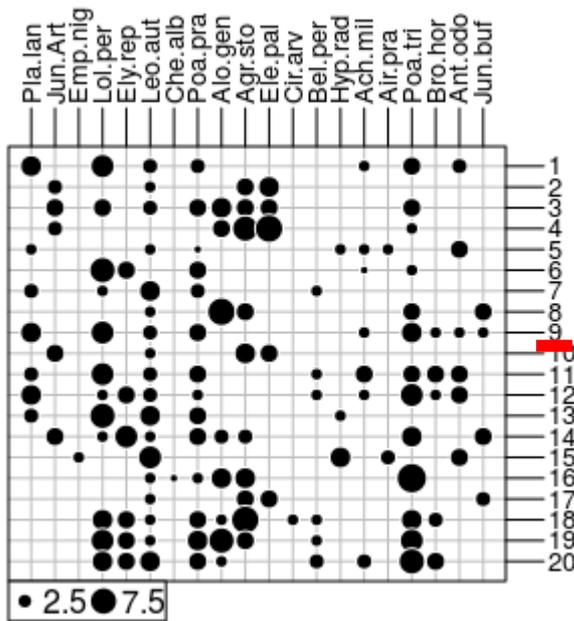
Ordonner un tableau



Ordonner un tableau



Ordonner un tableau



Besoin de méthodes objectives permettant d'ordonner les sites et les espèces et d'identifier les principaux axes de variation de diversité.

D'une question écologique à une problématique méthodologique

OBJECTIVE METHODS FOR THE CLASSIFICATION OF
VEGETATION

III. AN ESSAY IN THE USE OF FACTOR ANALYSIS*

By D. W. GOODALL†

(Manuscript received April 5, 1954)

GRADIENT ANALYSIS OF VEGETATION*

By

R. H. WHITTAKER

AN ORDINATION STUDY OF
A CHALK GRASSLAND COMMUNITY

By M. P. AUSTIN*

AN ORDINATION OF THE UPLAND FOREST COMMUNITIES OF
SOUTHERN WISCONSIN*

J. ROGER BRAY† AND J. T. CURTIS

Department of Botany, University of Minnesota, Minneapolis, Minnesota

Department of Botany, University of Wisconsin, Madison, Wisconsin

GEOMETRIC MODELS IN ECOLOGY

I. THE THEORY AND APPLICATION OF SOME ORDINATION METHODS

By L. ORLOCI

PRINCIPAL COMPONENT ORDINATION AND SIMULATED
VEGETATIONAL DATA¹

I. NOY-MEIR

*Department of Biogeography and Geomorphology, Research School of Pacific Studies
Australian National University, Canberra, Australia*

AND

M. P. AUSTIN

Division of Land Research, CSIRO, Canberra, Australia

THE APPLICATION OF QUANTITATIVE METHODS TO
VEGETATION SURVEY

II. SOME METHODOLOGICAL PROBLEMS OF DATA
FROM RAIN FOREST

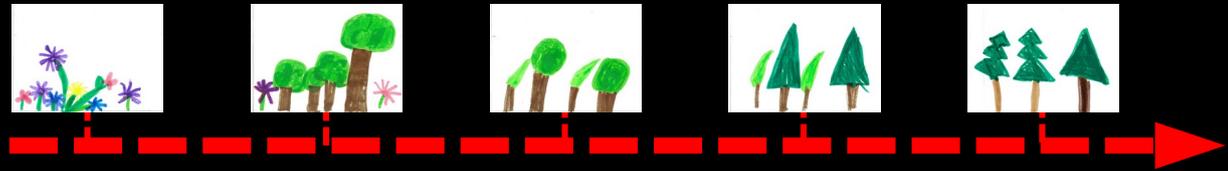
By M. P. AUSTIN* AND P. GREIG-SMITH

GEOMETRIC MODELS IN ECOLOGY

II. AN EVALUATION OF SOME ORDINATION TECHNIQUES

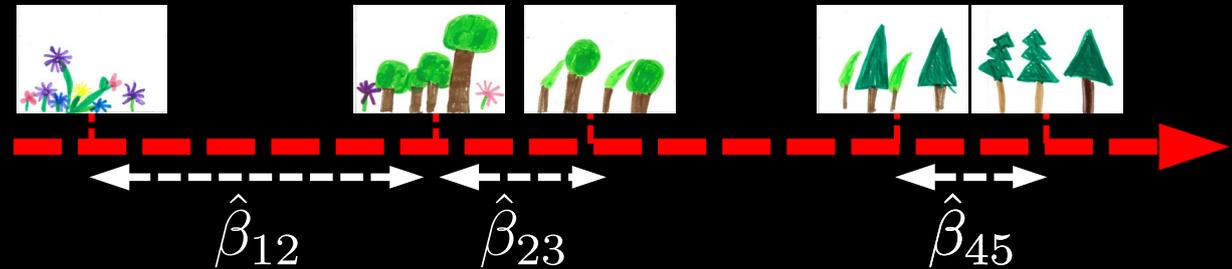
By M. P. AUSTIN AND L. ORLOCI*

L'ordination des tableaux écologiques



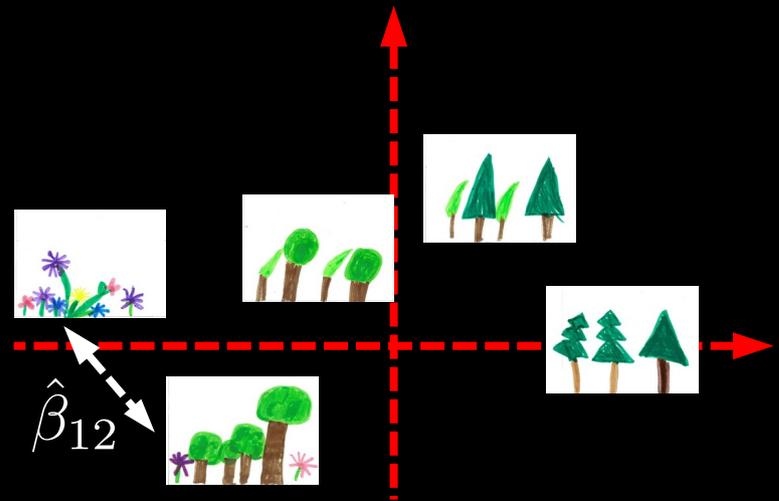
L'ordination des tableaux écologiques

- Scoring



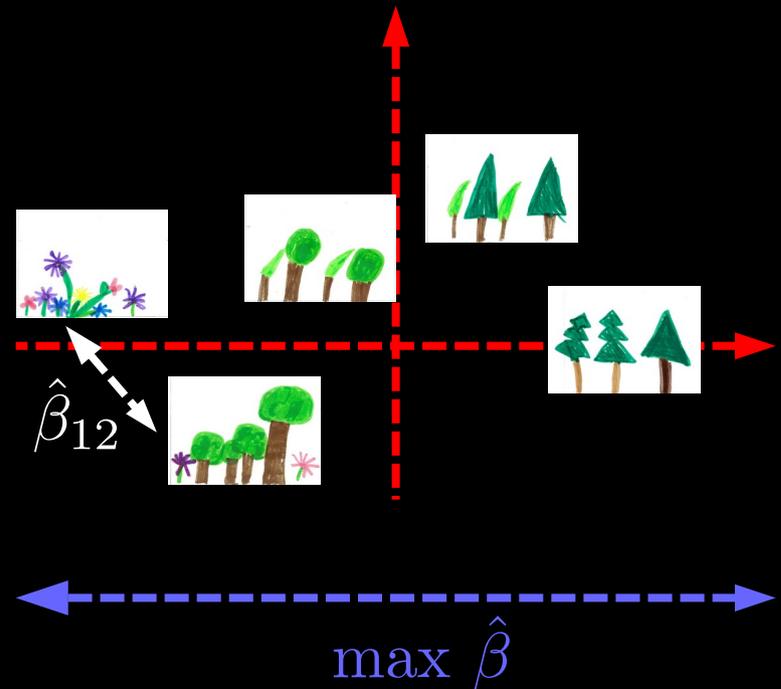
L'ordination des tableaux écologiques

- Scoring
- Multi-dimensionnel



L'ordination des tableaux écologiques

- Scoring
- Multi-dimensionnel
- Maximise la diversité



Analyses multivariées

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VEGETATION

III. AN ESSAY IN THE USE OF FACTOR ANALYSIS*

By D. W. GOODALL†

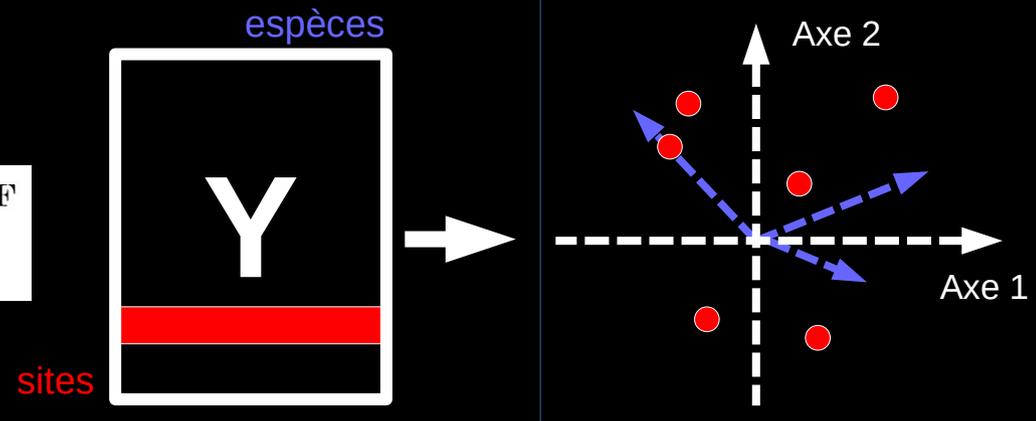
(Manuscript received April 5, 1954)

ACP (1954)

AN ORDINATION OF THE UPLAND FOREST COMMUNITIES OF
SOUTHERN WISCONSIN*

J. ROGER BRAY† AND J. T. CURTIS

PCoA (1957)



RECIPROCAL AVERAGING: AN EIGENVECTOR METHOD OF
ORDINATION

By M. O. HILL*

AFC (1973)

Analyses multivariées...

OBJECTIVE METHODS FOR THE CLASSIFICATION OF
VEGETATION

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(Manuscript received April 5, 1954)

ACP (1954)

... et diversité

PRINCIPAL COMPONENTS BIPLOTS AND ALPHA
AND BETA DIVERSITY¹

CAJO J. F. TER BRAAK

ACP et α -Simpson (1983)

AN ORDINATION OF THE UPLAND FOREST COMMUNITIES OF
SOUTHERN WISCONSIN*

J. ROGER BRAY† AND J. T. CURTIS

PCoA (1957)

CONSISTENCY BETWEEN ORDINATION TECHNIQUES AND DIVERSITY
MEASUREMENTS: TWO STRATEGIES FOR SPECIES OCCURRENCE DATA

RAPHAËL PÉLISSIER,^{1,4} PIERRE COUTERON,² STÉPHANE DRAY,³ AND DANIEL SABATIER¹

RECIPROCAL AVERAGING: AN EIGENVECTOR METHOD OF
ORDINATION

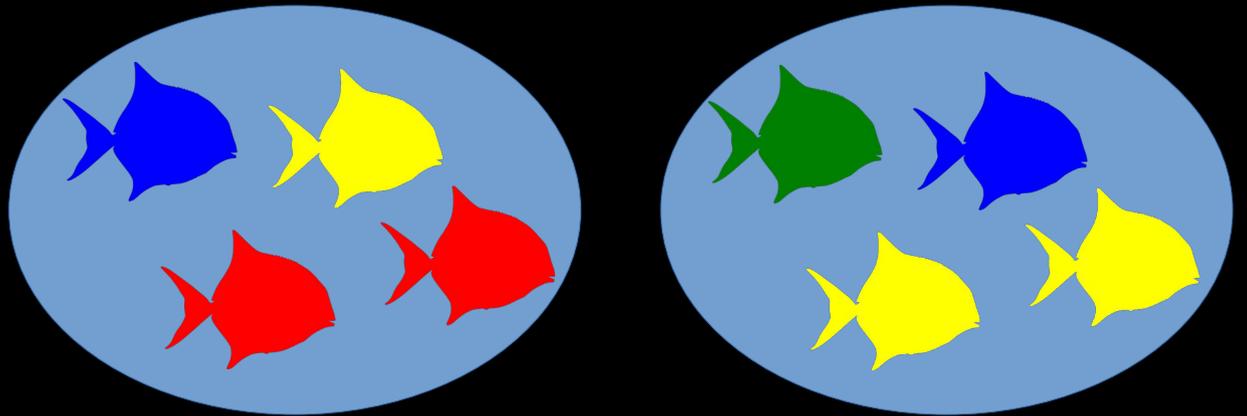
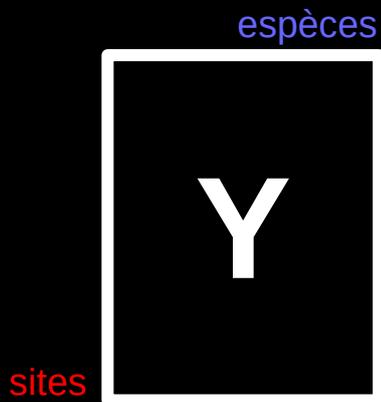
By M. O. HILL*

AFC (1973)

AFC / ANSC et α, β, γ -
Richesse / Simpson (2003)

Diversités

Diversité spécifique

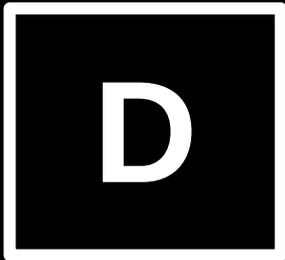


Indice de Simpson

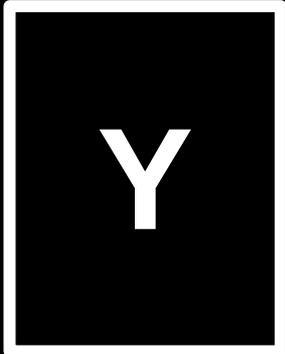
$$Q = 1 - \sum p_i^2$$

Diversités

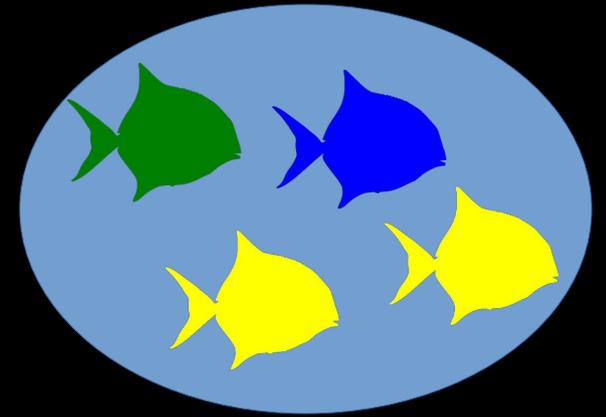
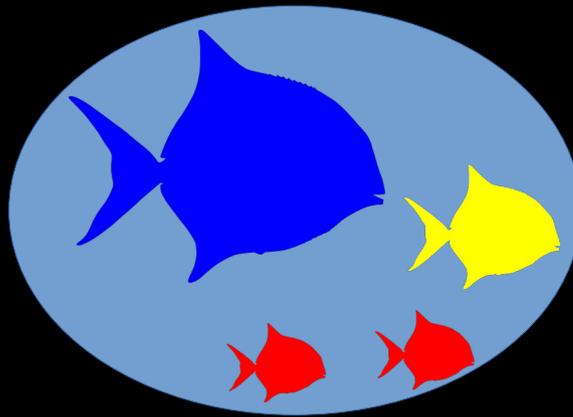
Diversité fonctionnelle



espèces



sites

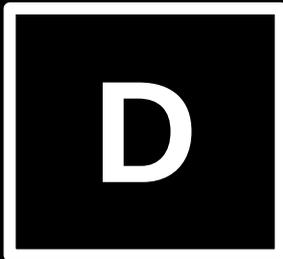


Indice de Rao

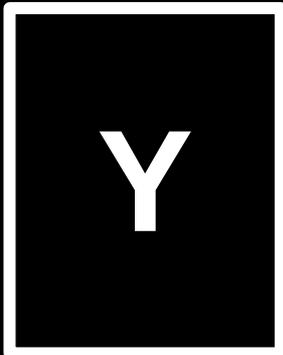
$$Q = \sum \sum p_i p_j d_{ij}^2$$

Analyse multivariées et diversité

DPCoA



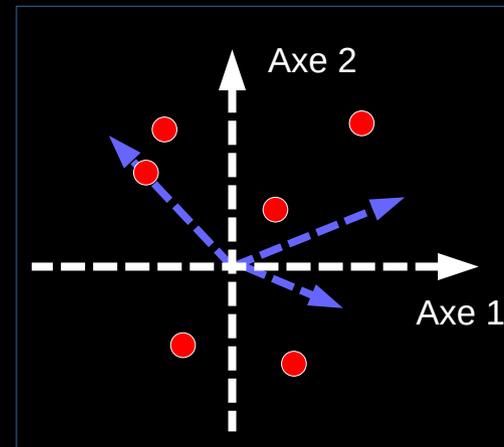
espèces



sites

From dissimilarities among species to dissimilarities among communities: a double principal coordinate analysis

Sandrine Pavoine^{*,*}, Anne-Béatrice Dufour^{*}, Daniel Chessel^{*}



Inertie totale = indice de Rao

Réconcilier statistiques et écologie

« *A major purpose is **interpretation** [...]*

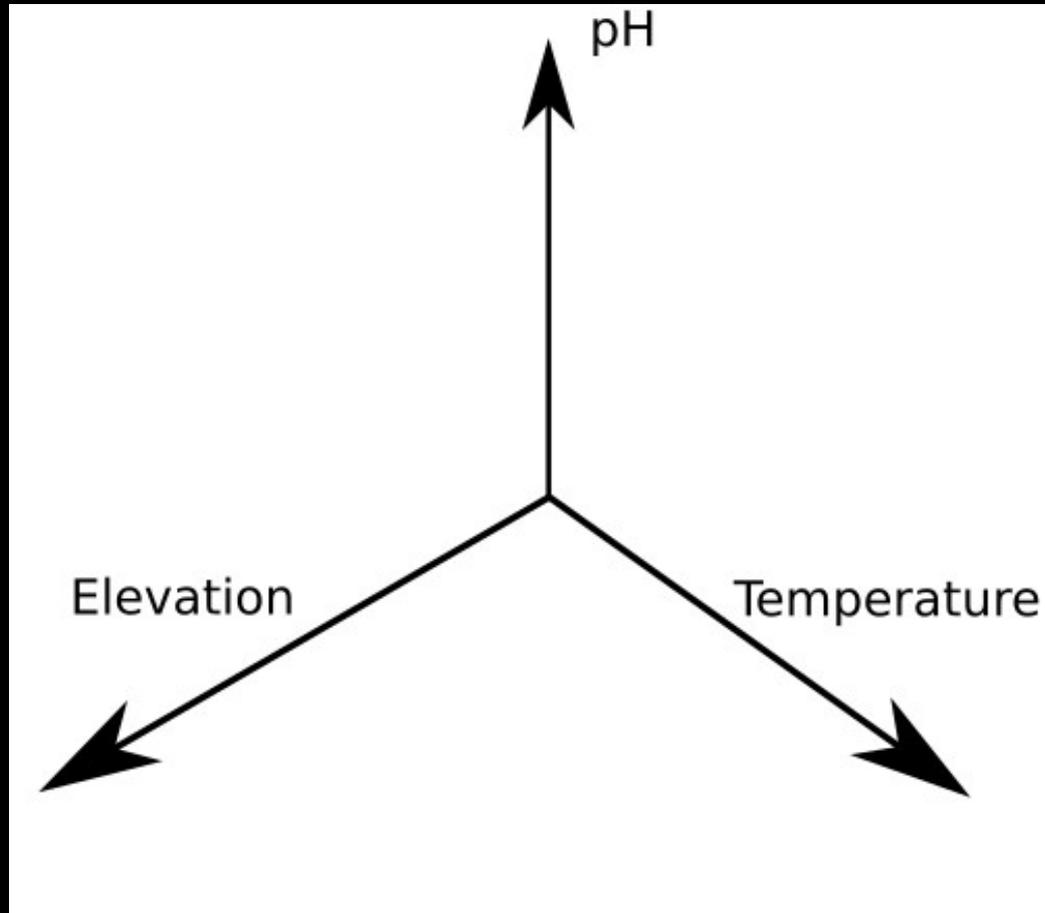
and not simply the representation of numerical relationships among samples or species in a hyperspace with a limited number of axes. »

Patrons ↔ Facteurs / Processus

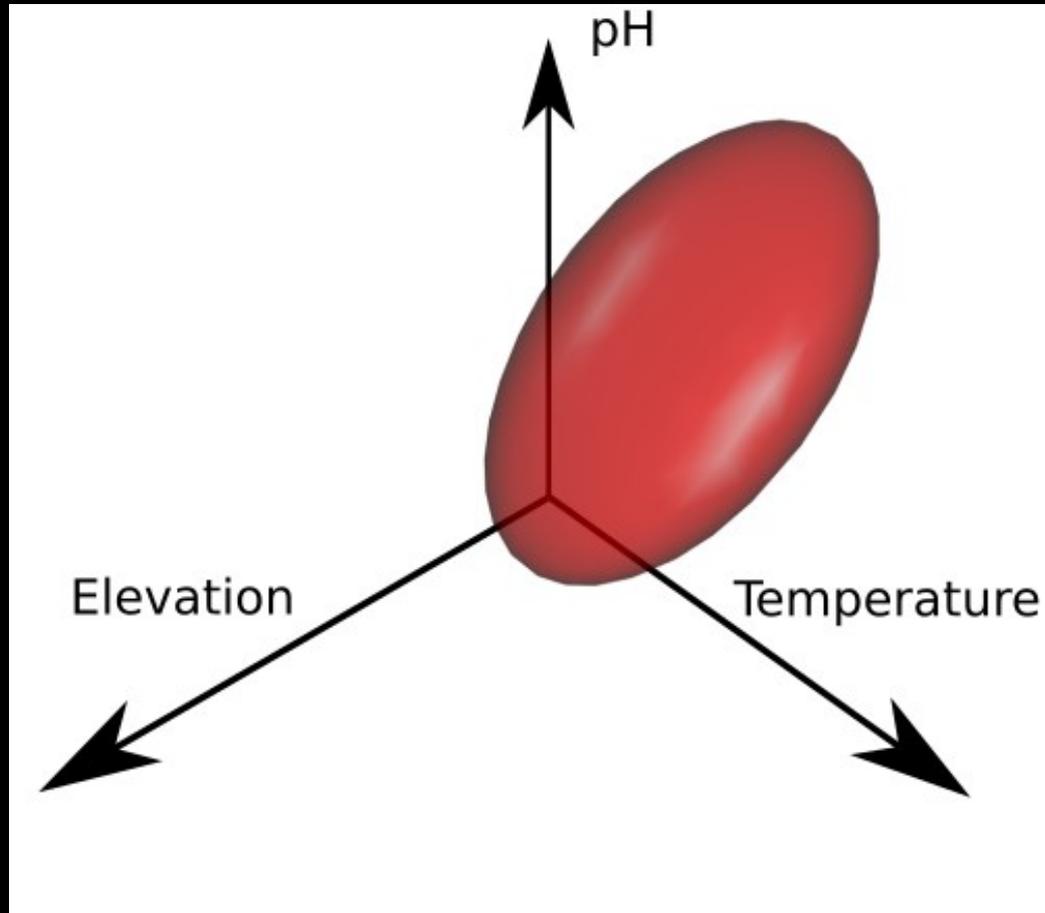
Réconcilier statistiques et écologie

« A major purpose is interpretation of community relationships to environment, and not simply the representation of numerical relationships among samples or species in a hyperspace with a limited number of axes. »

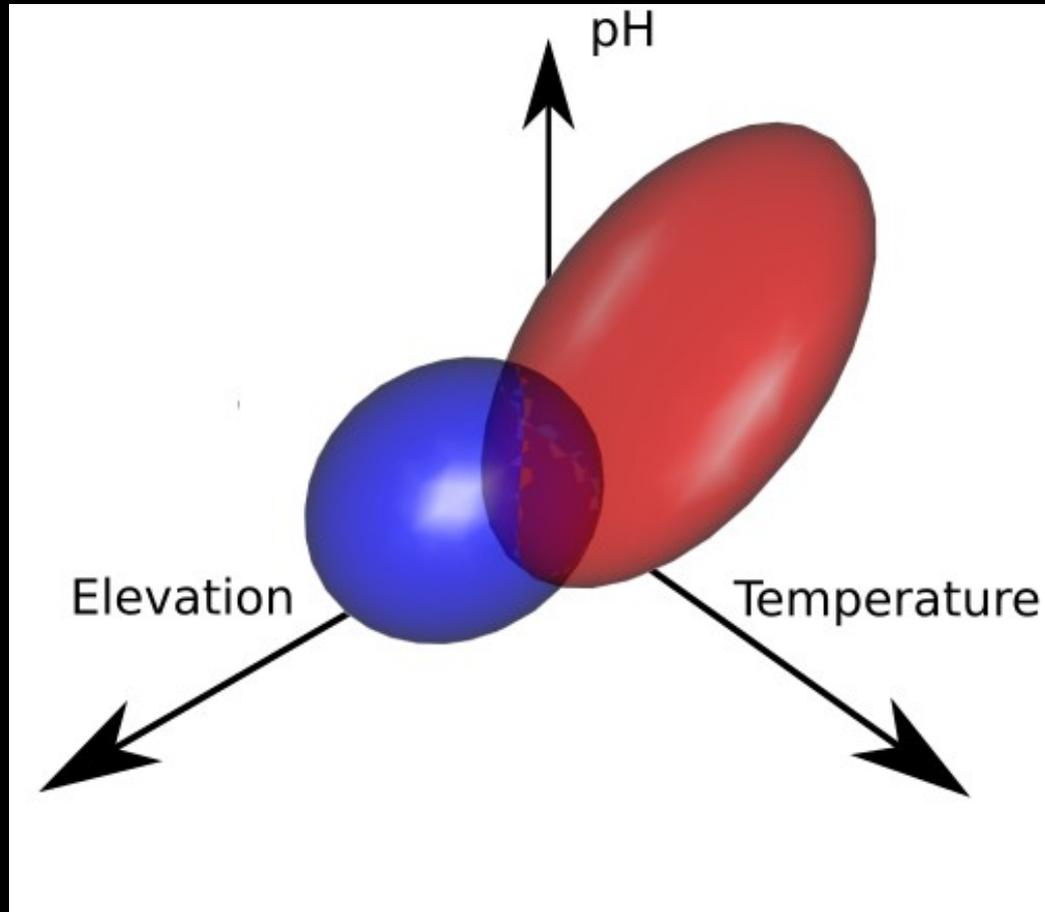
The niche theory



The niche theory



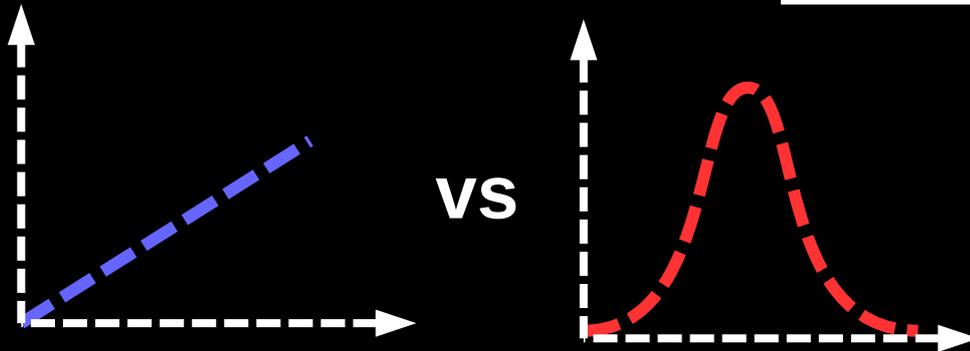
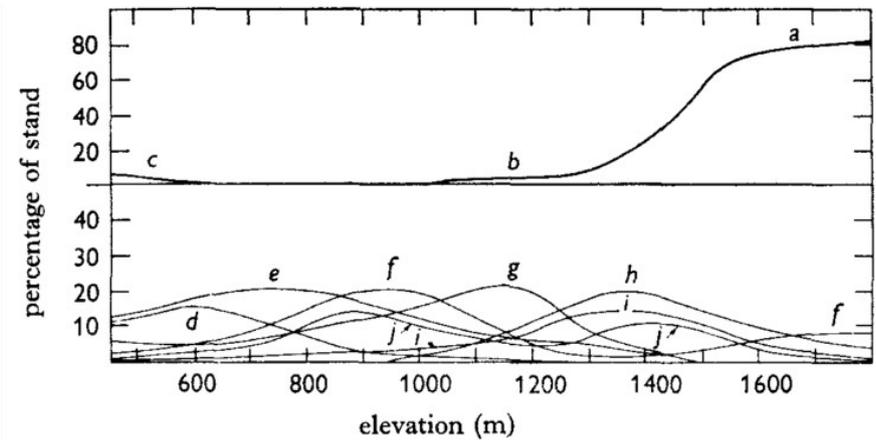
The niche theory



Gradient sous-jacent

GRADIENT ANALYSIS OF VEGETATION*

By
R. H. WHITTAKER



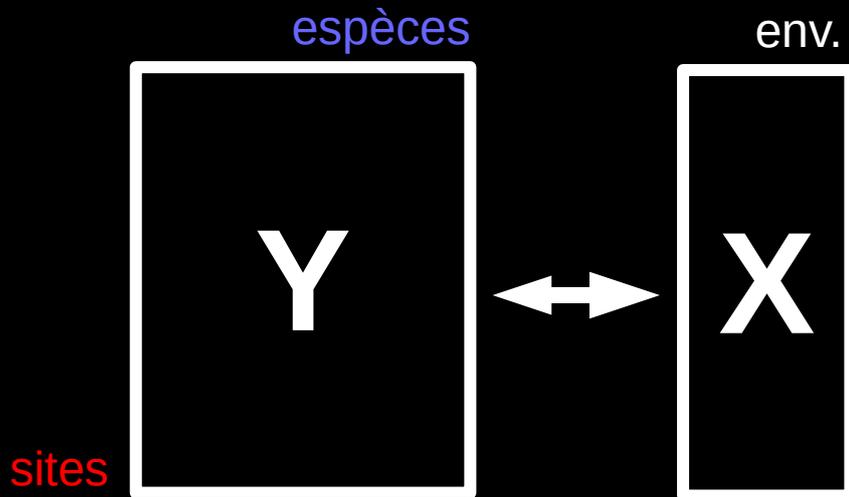
Vers une ordination optimale

*« Ecologists would welcome a technique that could (a) extract **main directions of community-and-environmental variation** on the basis of **simultaneous consideration** of vegetational and environmental data and (b) yield, in the axes extracted, an effective and **interpretable** ordination without the vulnerability to distortion that affects some other techniques. »*

Ordination directe

CANONICAL CORRESPONDENCE ANALYSIS:
A NEW EIGENVECTOR TECHNIQUE FOR MULTIVARIATE
DIRECT GRADIENT ANALYSIS¹

CAJO J. F. TER BRAAK



Ordination directe

CANONICAL CORRESPONDENCE ANALYSIS:
A NEW EIGENVECTOR TECHNIQUE FOR MULTIVARIATE
DIRECT GRADIENT ANALYSIS¹

CAJO J. F. TER BRAAK

Contrainte environnementale

$$z = f(\mathbf{X}) = a_1 x_1 + a_2 x_2 + \dots + a_p x_p$$



espèces

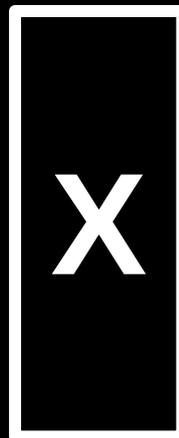
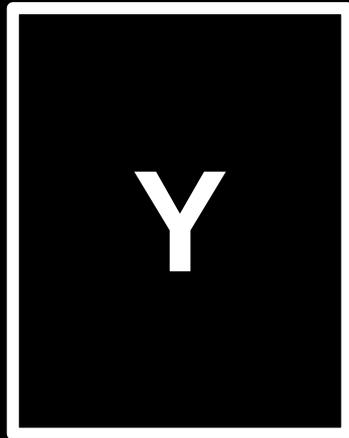
env.

Y

X



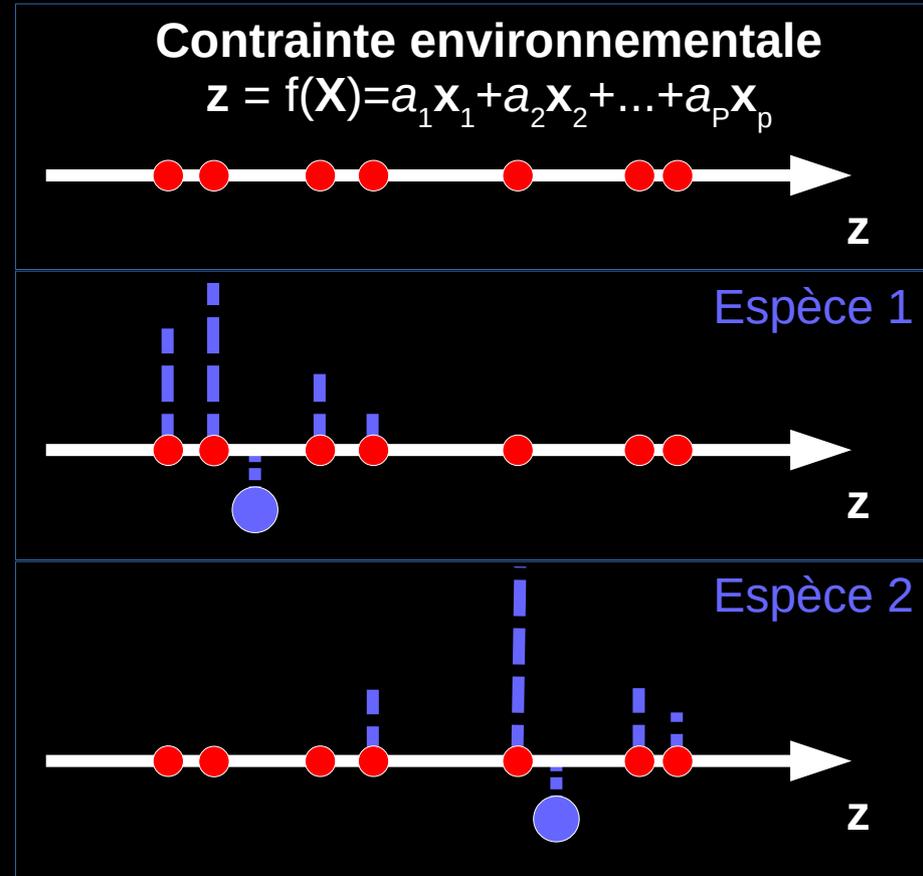
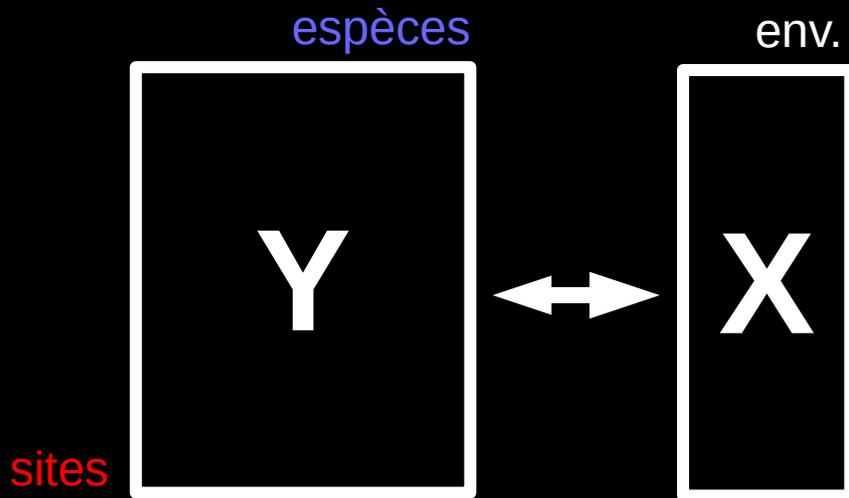
sites



Ordination directe

CANONICAL CORRESPONDENCE ANALYSIS:
A NEW EIGENVECTOR TECHNIQUE FOR MULTIVARIATE
DIRECT GRADIENT ANALYSIS¹

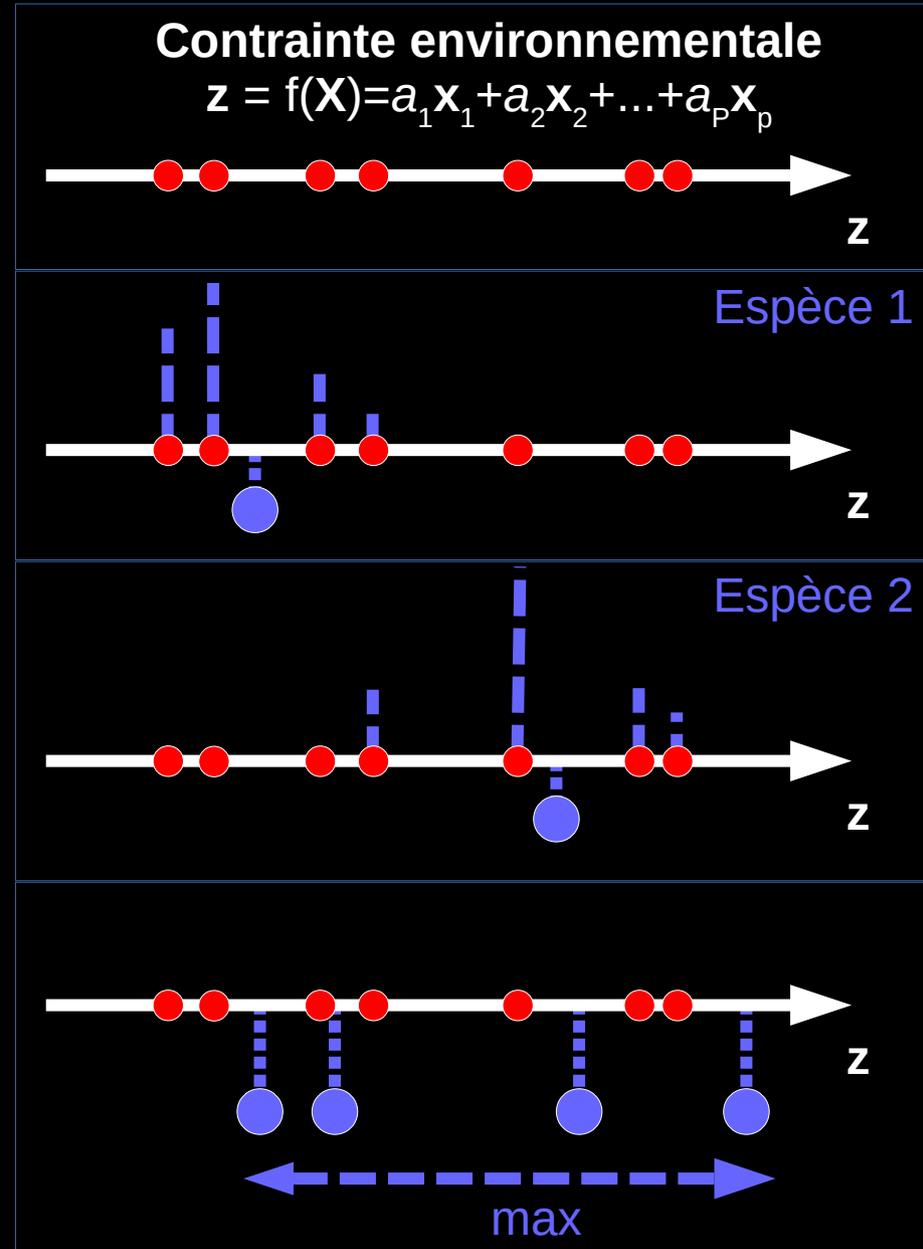
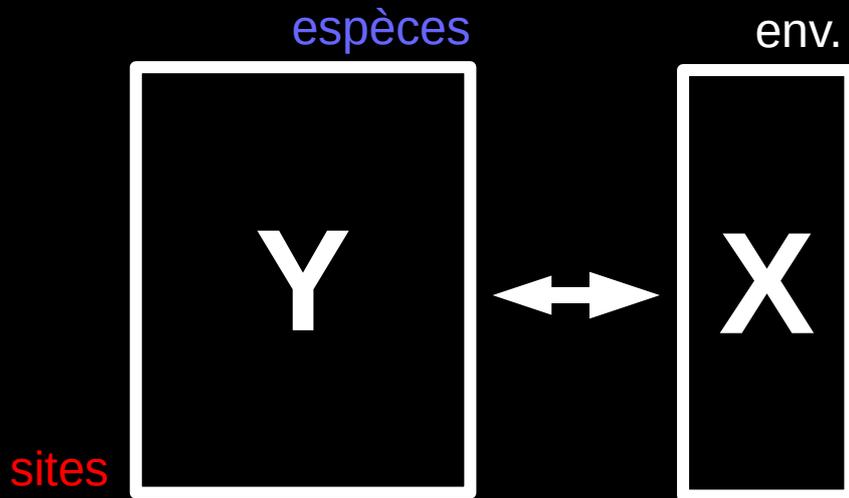
CAJO J. F. TER BRAAK



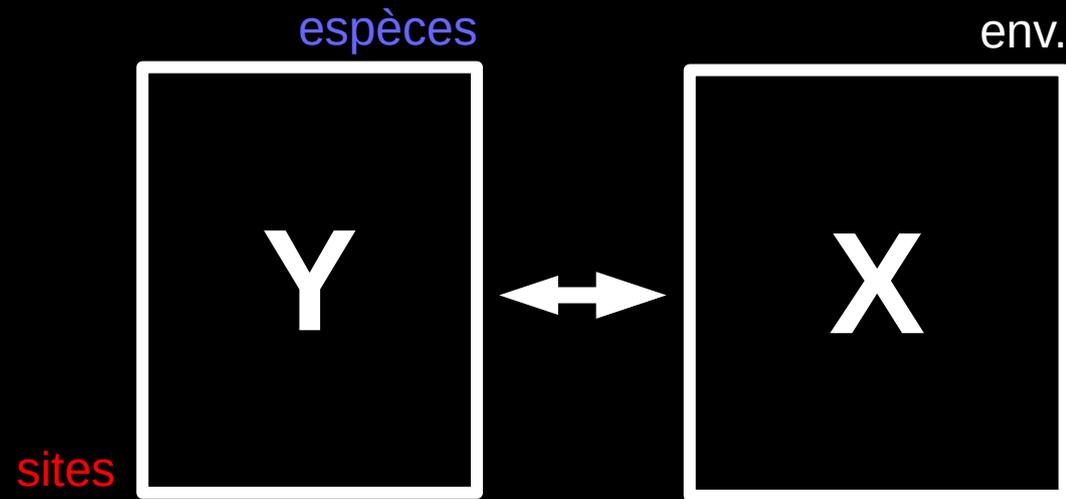
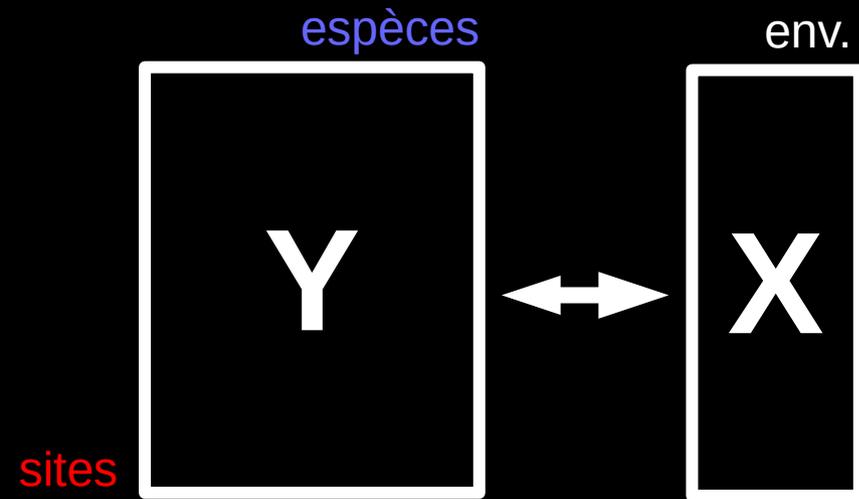
Ordination directe

CANONICAL CORRESPONDENCE ANALYSIS:
A NEW EIGENVECTOR TECHNIQUE FOR MULTIVARIATE
DIRECT GRADIENT ANALYSIS¹

CAJO J. F. TER BRAAK



Régression ou co-variation



ACPVI

- analyse des redondances
- analyse canonique des correspondances

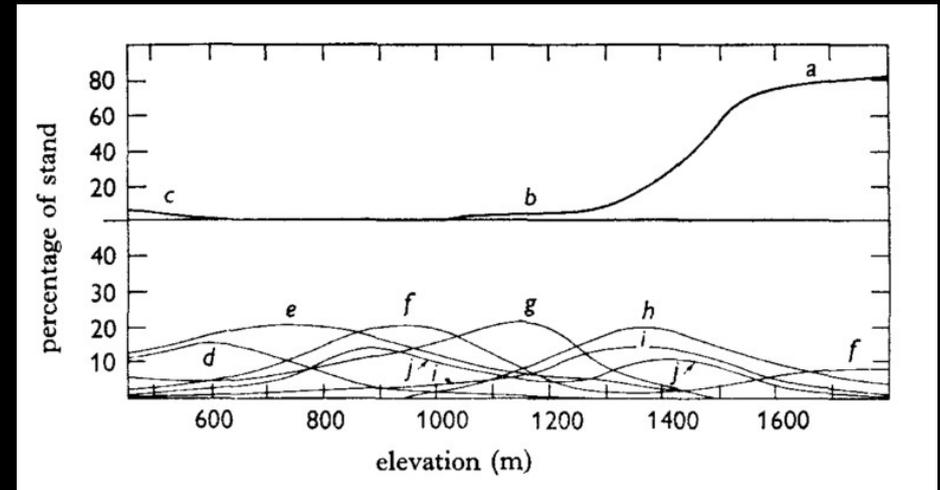
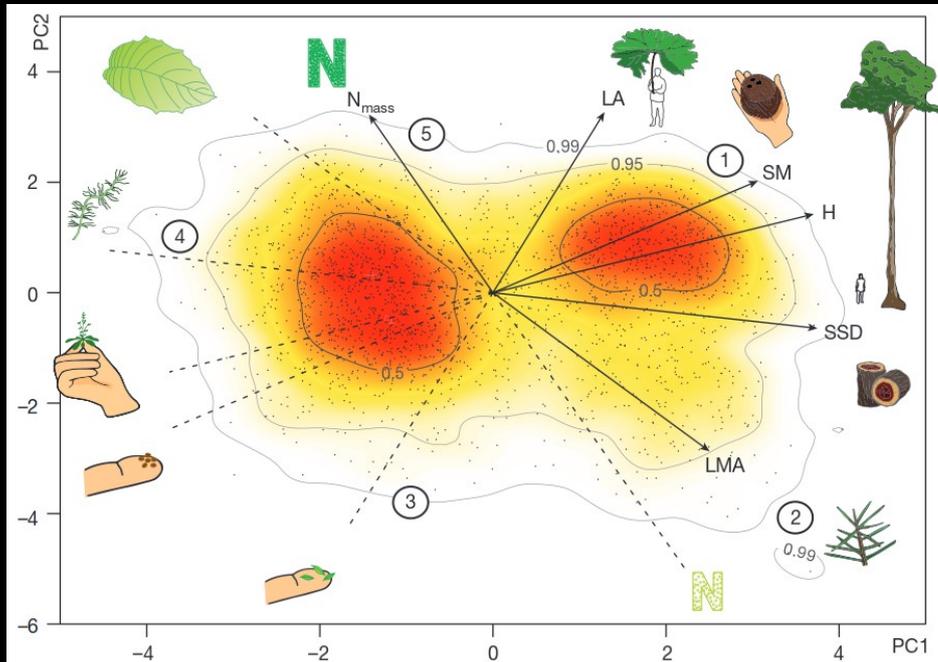
Co-inertia analysis: an alternative method for studying species–environment relationships

SYLVAIN DOLÉDEC* AND DANIEL CHESSEL

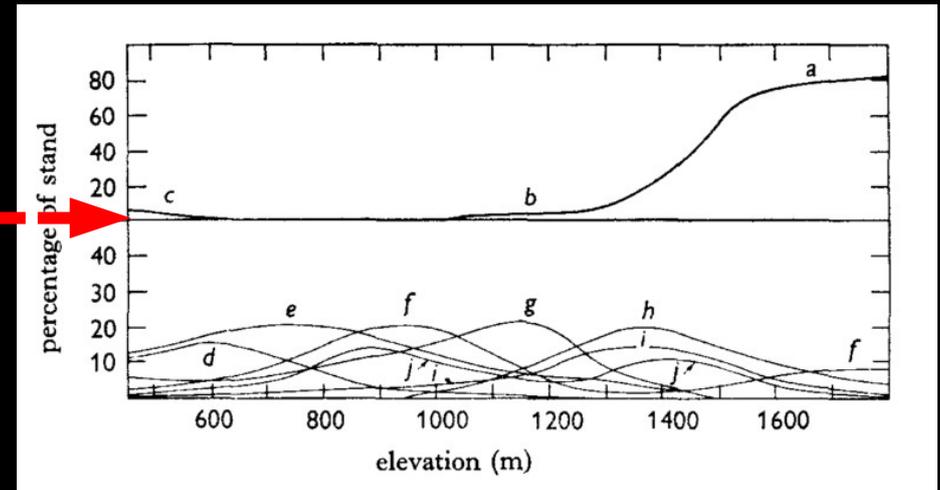
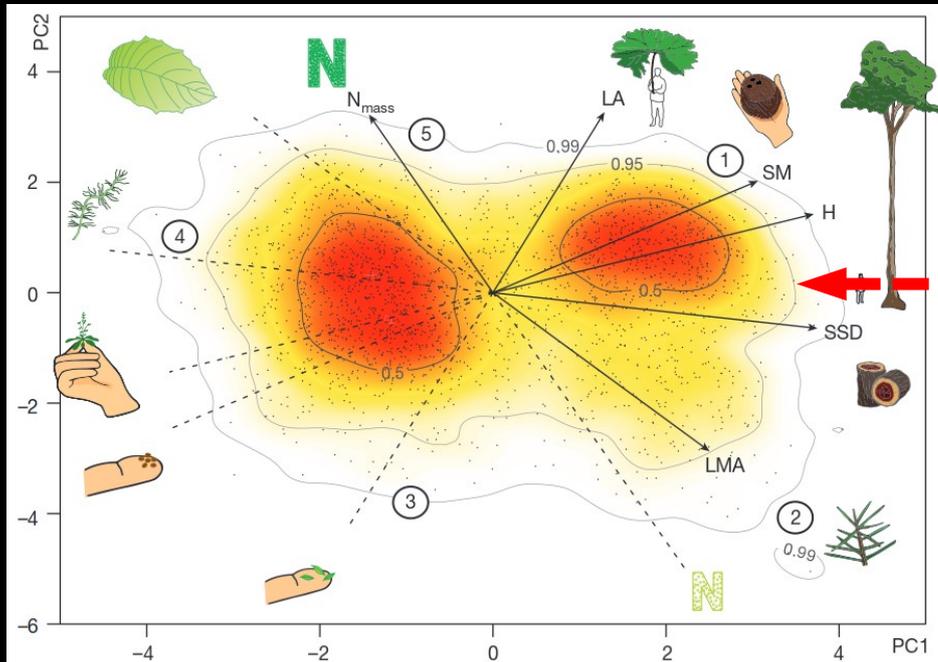
$$\max R^2_{Y/X}$$

$$\max \text{cov}^2 (Y_a, X_b)$$

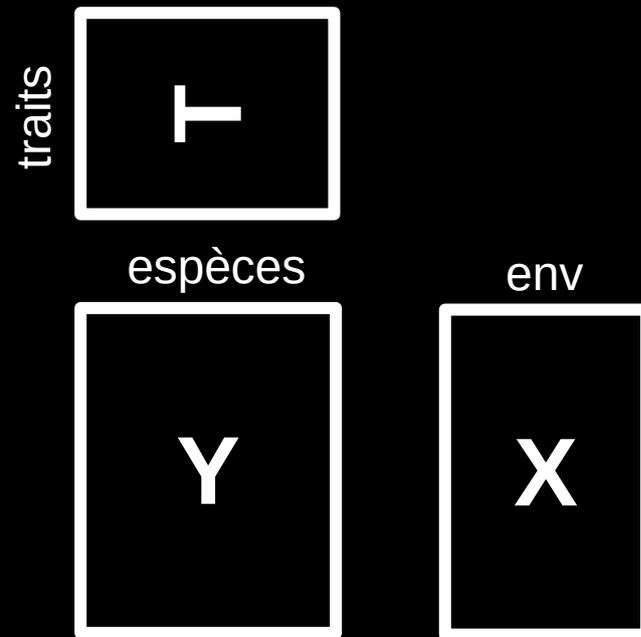
Lien traits-environnement



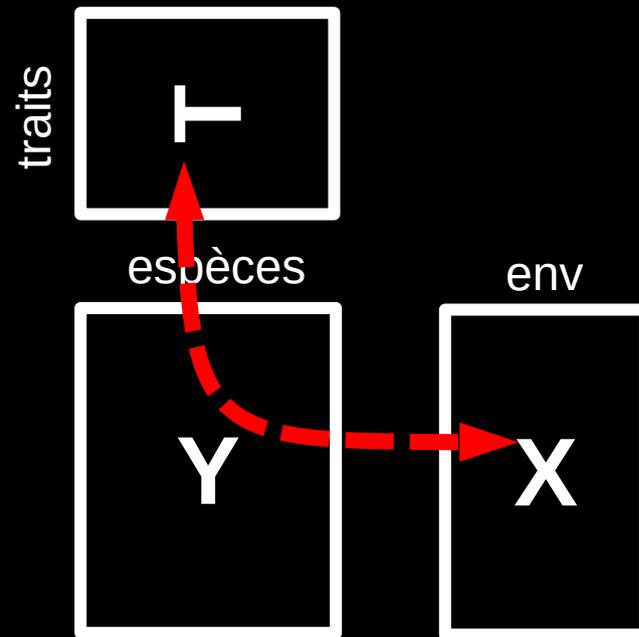
Lien traits-environnement



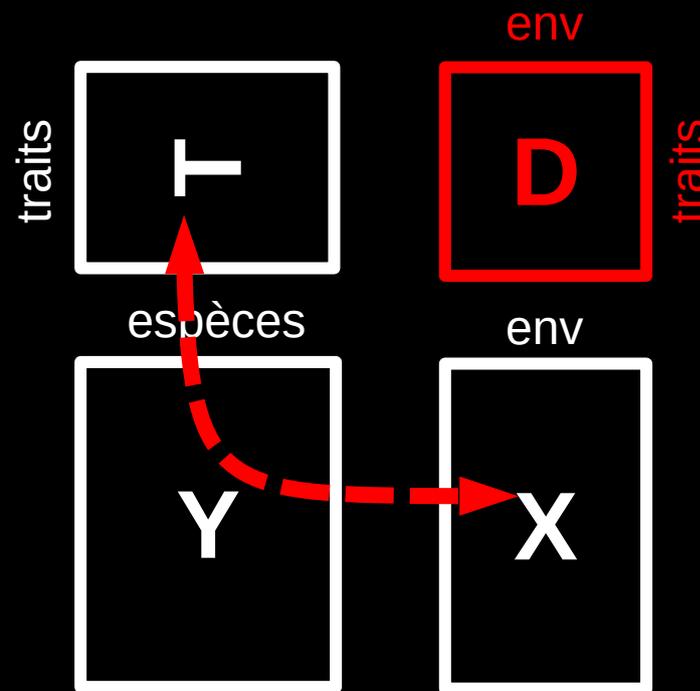
Le quatrième coin



Le quatrième coin



Le quatrième coin



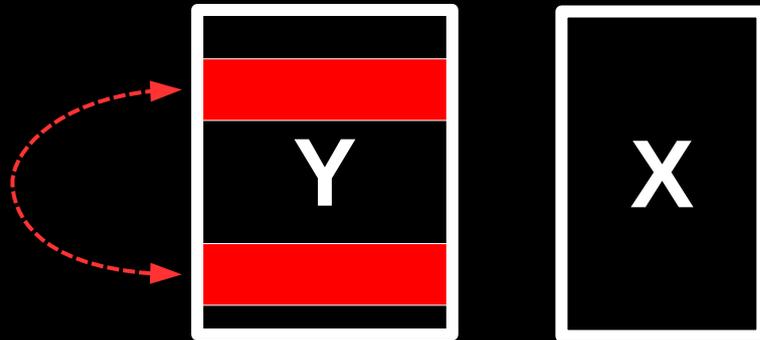
Le quatrième coin :

$$D = T^T Y^T X$$

- Ordination : analyse RLQ
- Test d'hypothèses par permutation

Test d'hypothèses

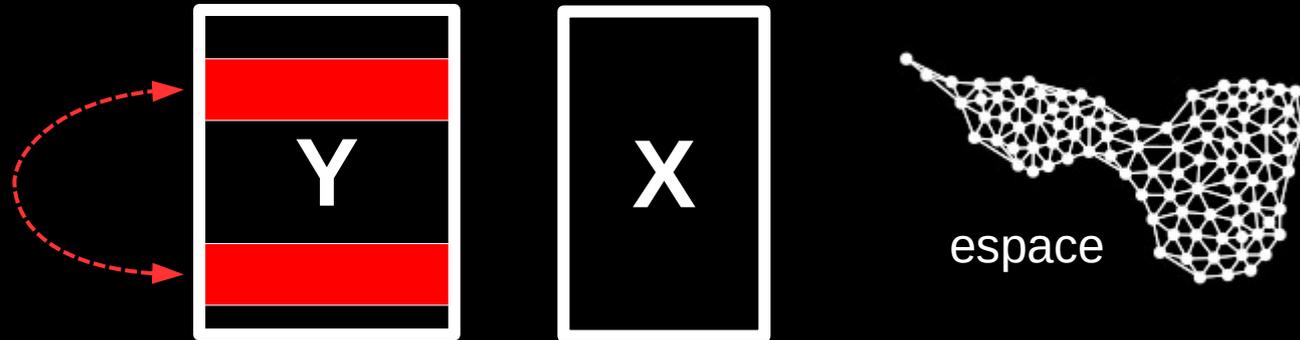
$H_0 : Y \not\leftrightarrow X$
 $H_1 : Y \leftrightarrow X$



- Compute a statistic S_{obs} on observed data (e.g., total inertia)
- Randomize data (e.g., permutations)
- Compute S_{sim} on randomized data
- Repeat 2-3 a number of times (e.g., 999)
- Compare S_{obs} to the distribution of S_{sim} and take the appropriate decision

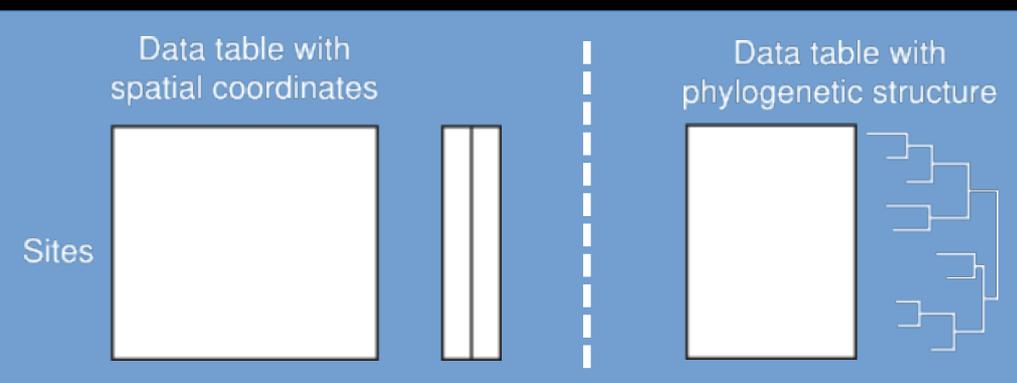
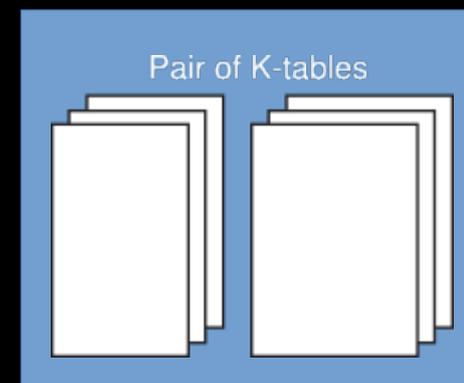
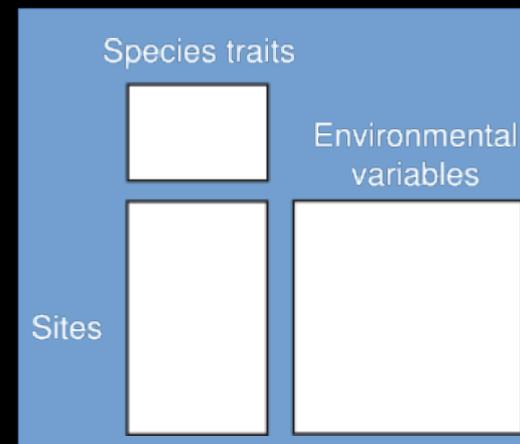
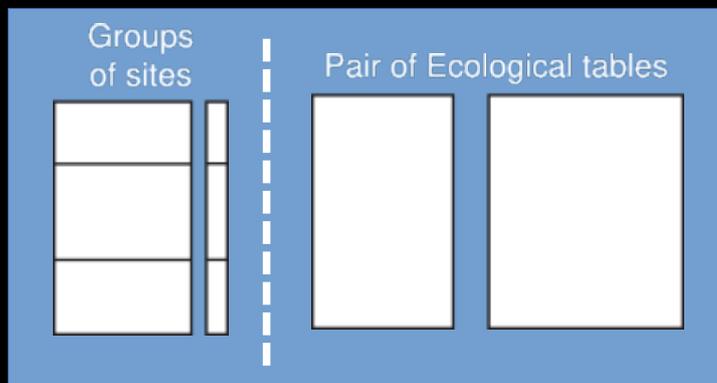
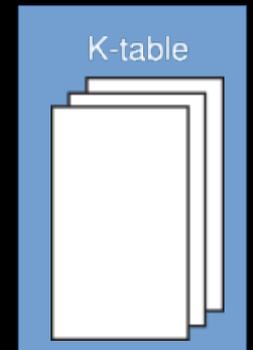
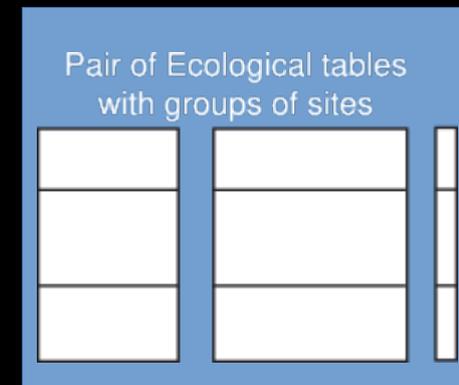
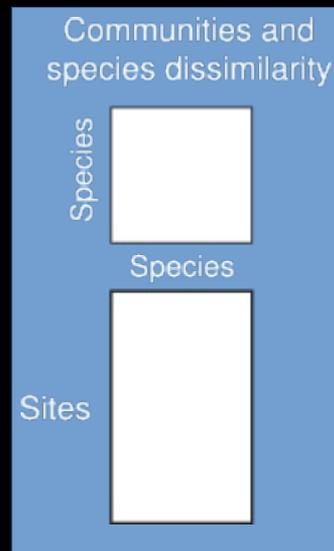
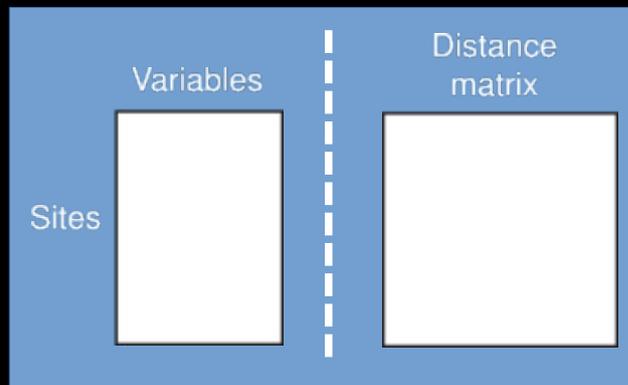
Test d'hypothèses

$H_0 : Y \not\leftrightarrow X$
 $H_1 : Y \leftrightarrow X$



- Compute a statistic S_{obs} on observed data (e.g., total inertia)
- Randomize data (e.g., **constrained** permutations)
- Compute S_{sim} on randomized data
- Repeat 2-3 a number of times (e.g., 999)
- Compare S_{obs} to the distribution of S_{sim} and take the appropriate decision

Plus de structures de données variées, plus de méthodes



Plus de questions, plus de données

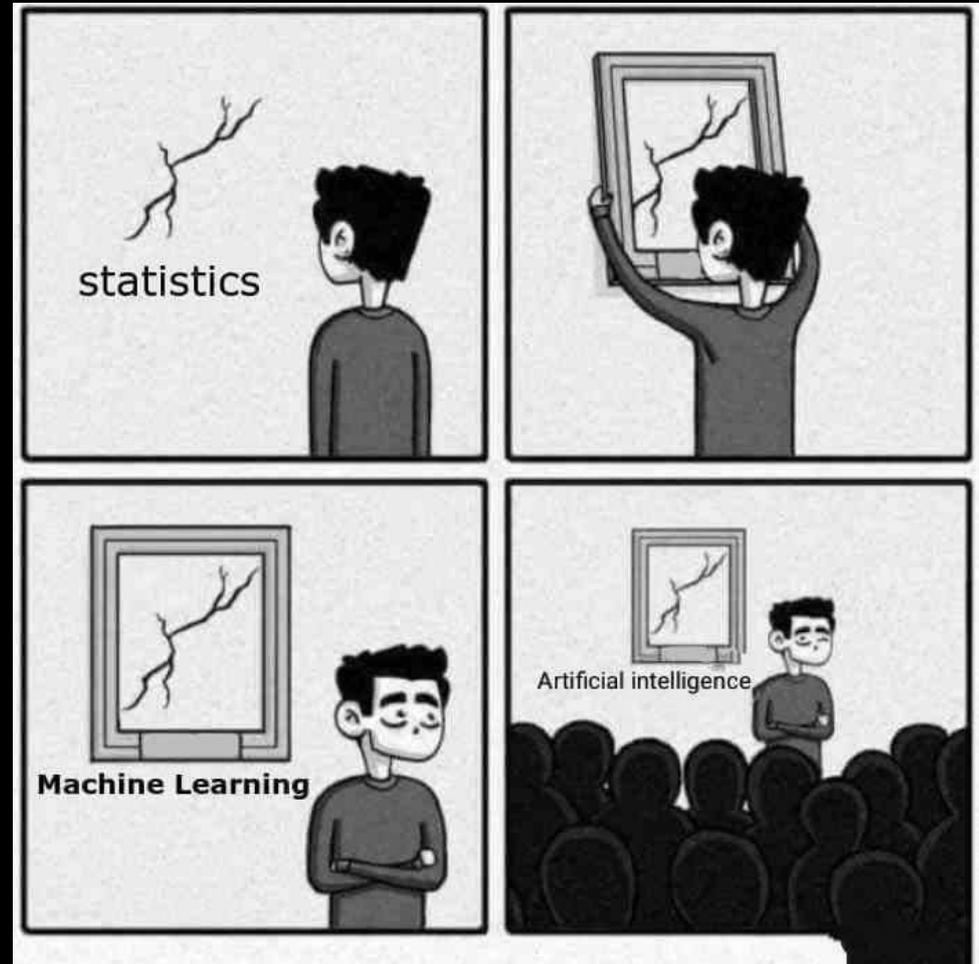


Données massives,
hétérogènes, spatio-
temporelle, etc.



En résumé

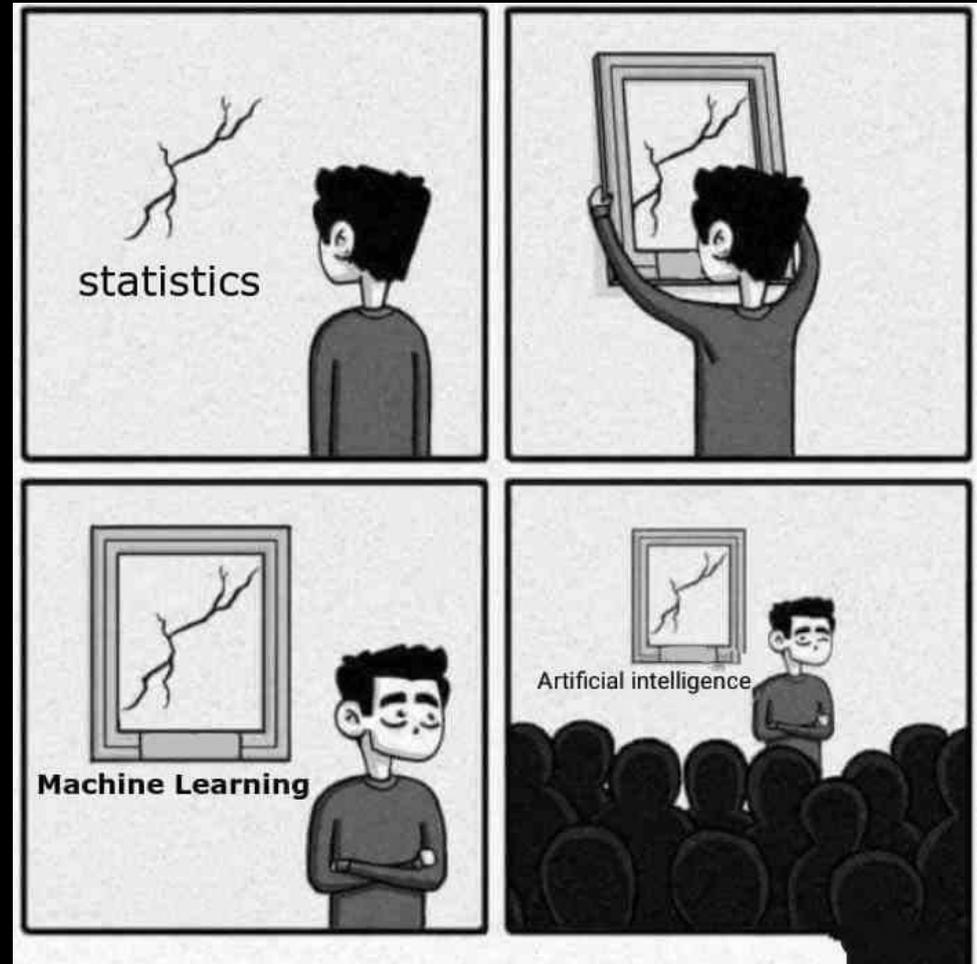
Des approches anciennes



En résumé

Des approches anciennes **mais**

- lien fort avec les théories en écologie
- simplicité de mise en œuvre
- grande diversité d'outils disponibles
- encore des développements



De l'écologie à la génomique

Considering external information to improve the phylogenetic comparison of microbial communities: a new approach based on constrained Double Principal Coordinates Analysis (cDPCoA)

S. DRAY,*† S. PAVOINE‡§ and D. AGUIRRE DE CÁRCER¶

D

espèces

Y

sites

DPCoA

Application en métagénomique

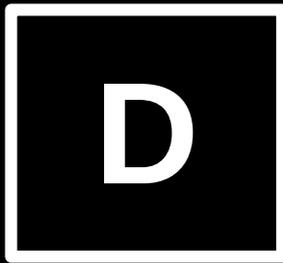
Y : échantillons de sol x OTUs

D : matrice de distances entre OTUs

De l'écologie à la génomique

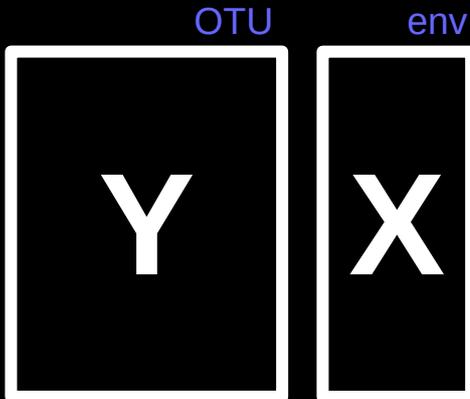
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S. DRAY,*† S. PAVOINE‡§ and D. AGUIRRE DE CÁRCER¶



DPCoA

Application en métagénomique



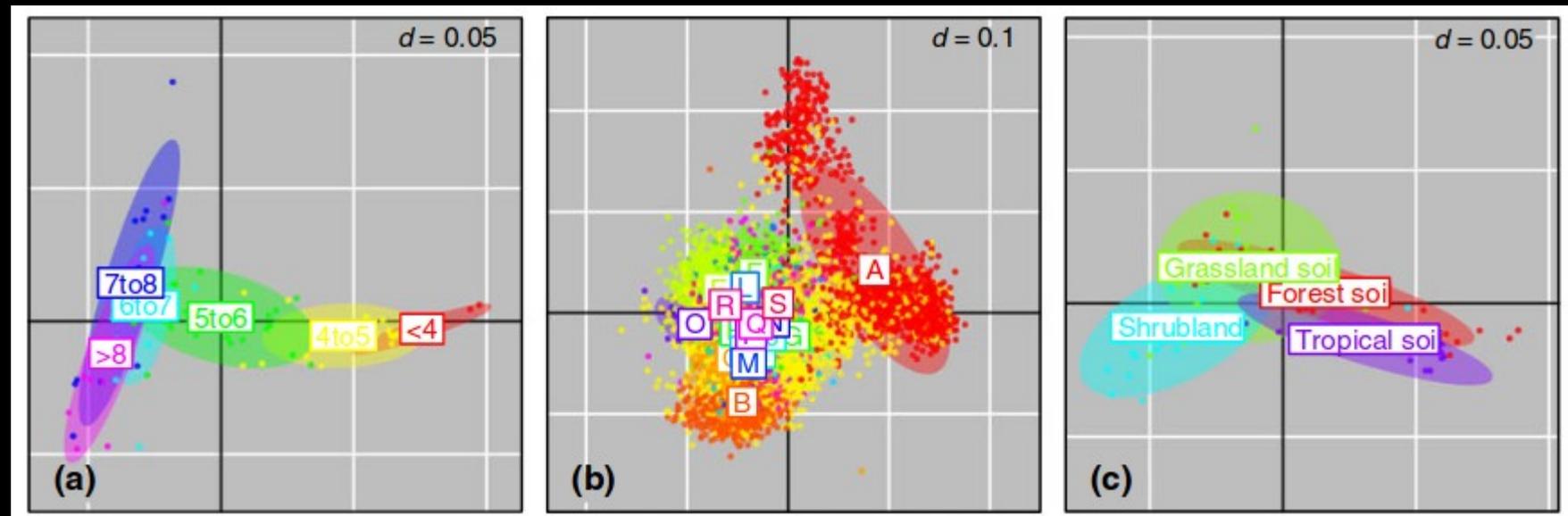
Y : échantillons de sol x OTUs

D : matrice de distances entre OTUs

X : pH et type de végétation

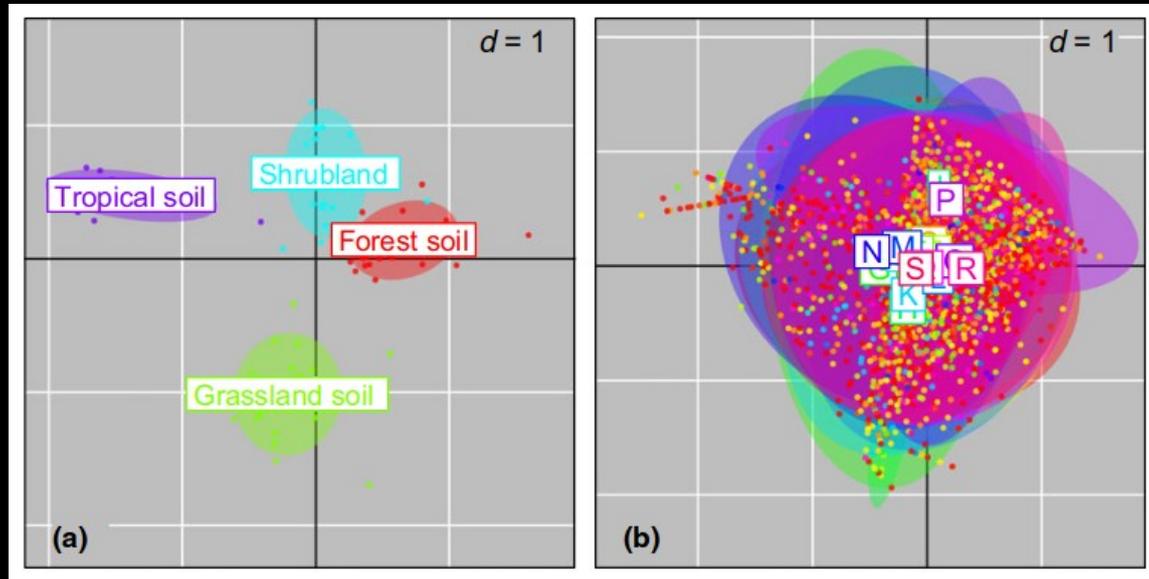
Diversité phylogénétique des communautés microbiennes du sol

DPCoA



Les différences de composition des communautés entre types (21.5 %) sont essentiellement dues aux différences de pH

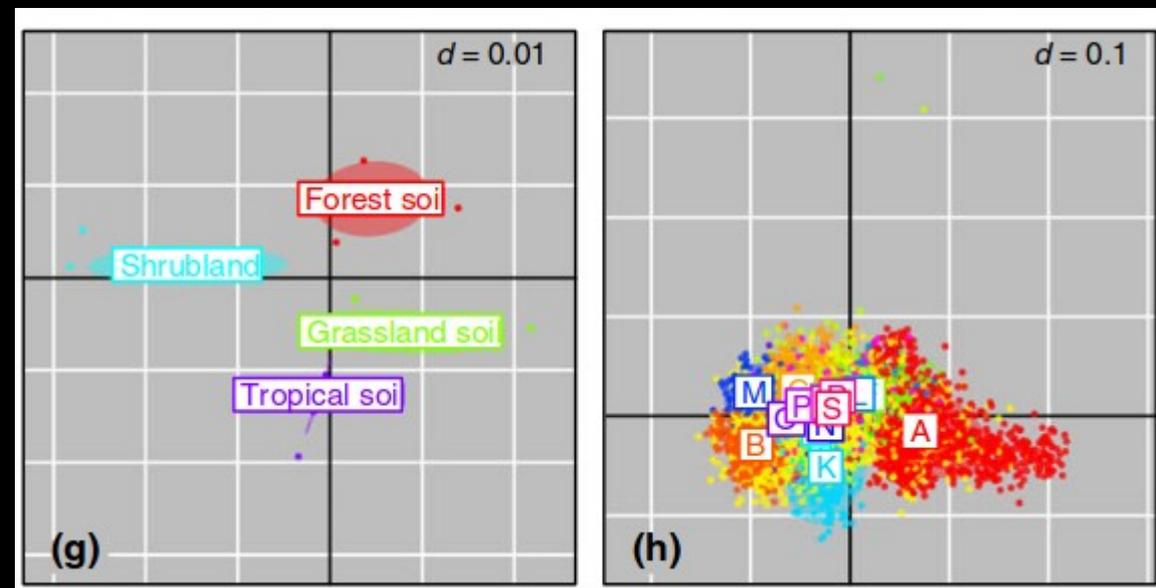
Diversité phylogénétique des communautés microbiennes du sol



AFC
intra pH
inter types

DPCoA
intra pH
inter types

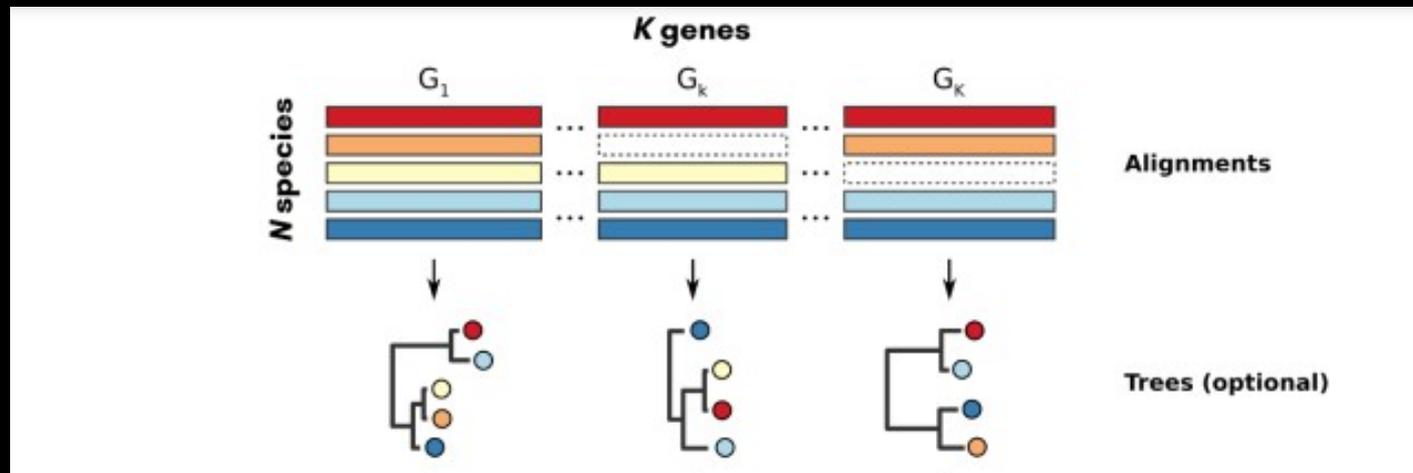
54.5 % non expliquée par le pH
5.45 % non expliquée par le pH mais
expliquée par le type



Congruence d'arbres de gènes

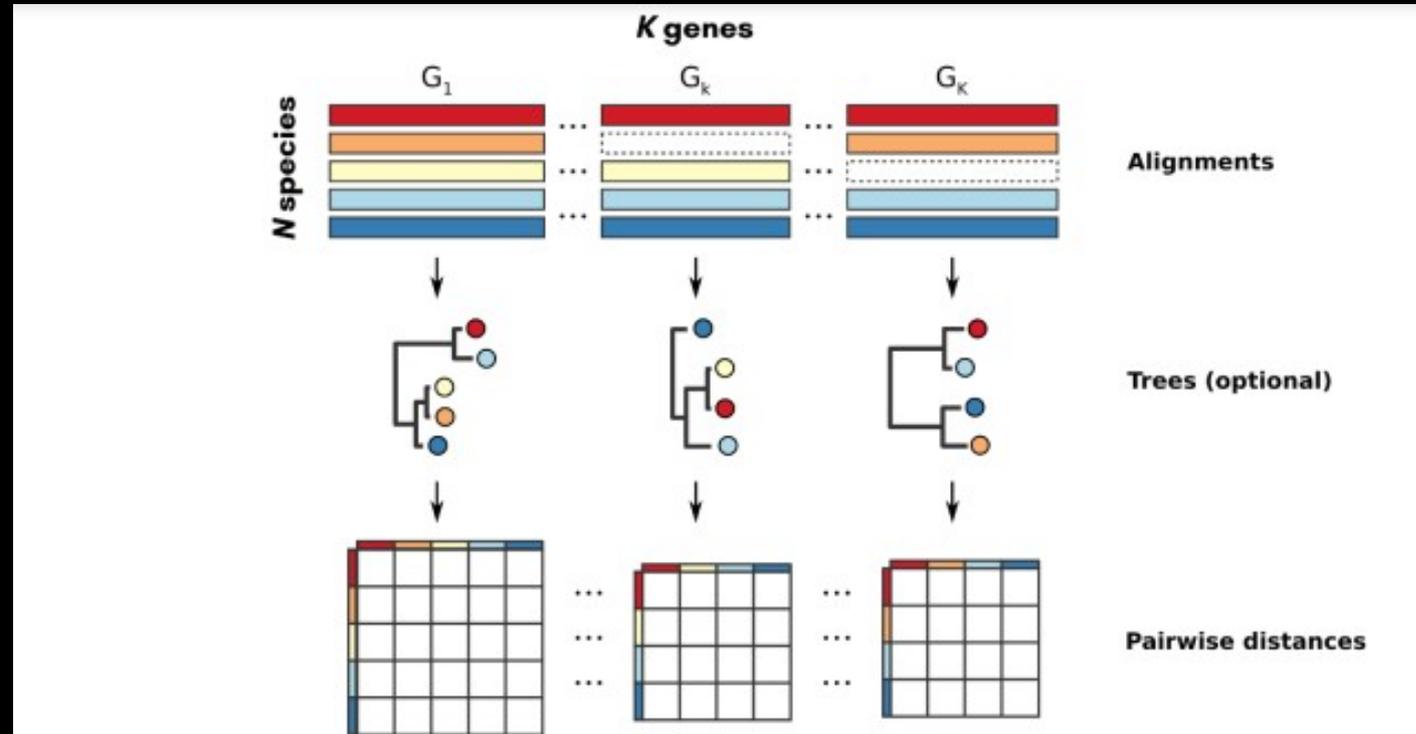
PhylteR: efficient identification of outlier sequences
in phylogenomic datasets

Aurore Comte^{1,2,†}, Théo Tricou^{3,†}, Eric Tannier^{3,4}, Julien Joseph³, Aurélie Siberchicot³,
Simon Penel³, Rémi Allio⁵, Frédéric Delsuc⁶, Stéphane Dray³, Damien M. de Vienne^{3,4}

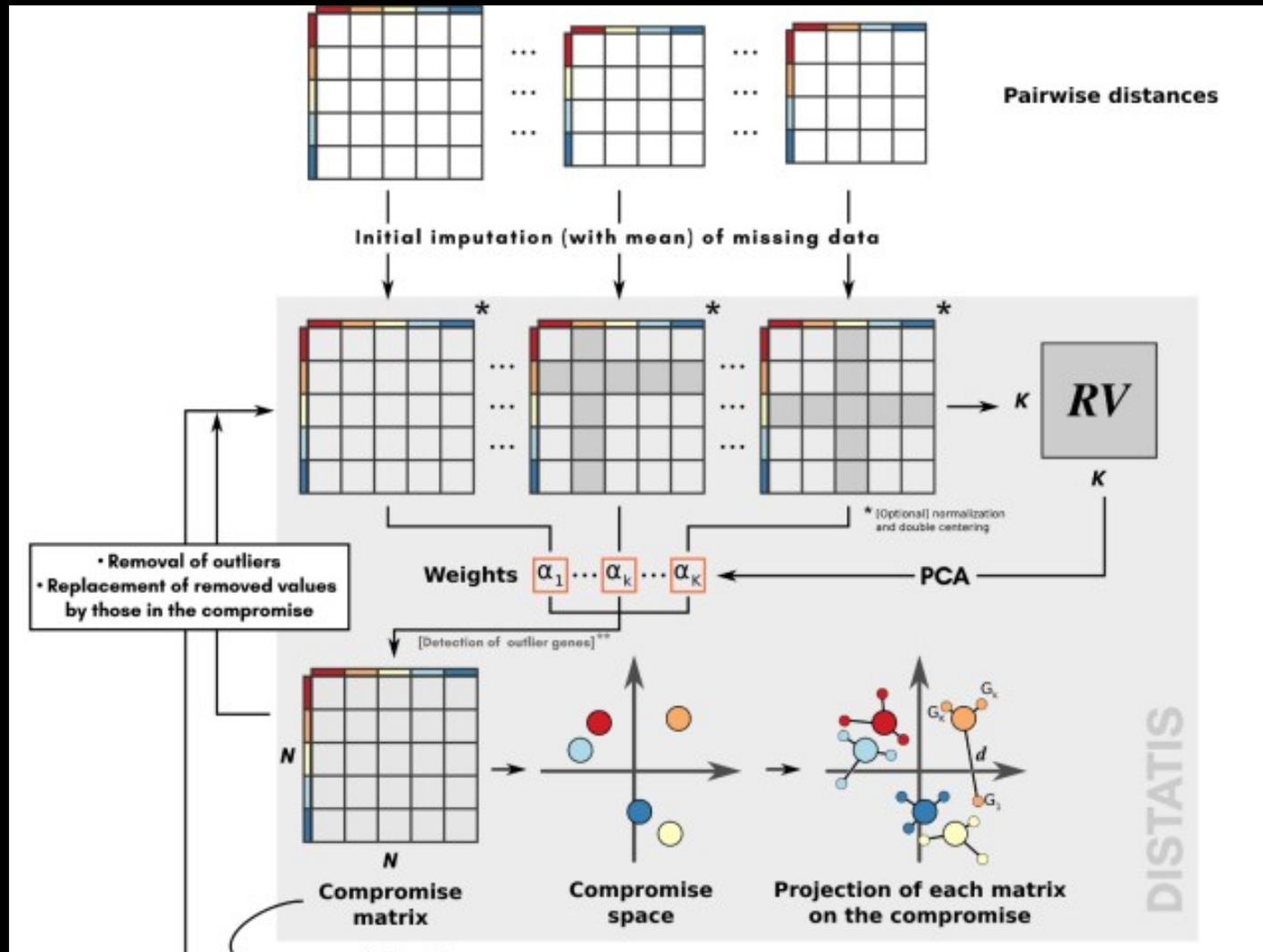


- Est-ce que tous les gènes racontent la même histoire évolutive ?
- Quels gènes et/ou espèces représentant une « anomalie » ?

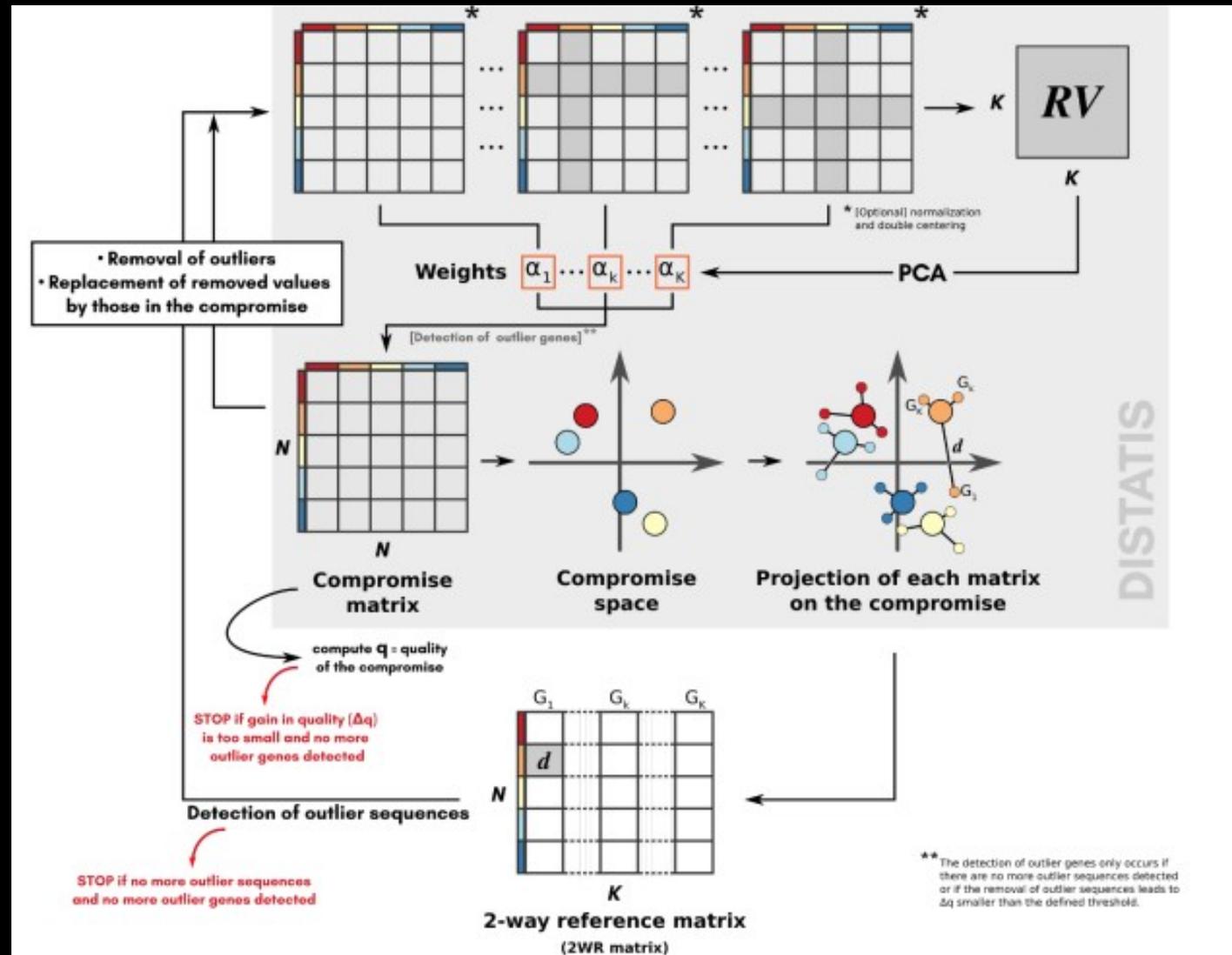
Congruence d'arbres de gènes



Congruence d'arbres de gènes



Congruence d'arbres de gènes



Analyses multivariées et génomique

The community ecology perspective of omics data



Stephanie D. Jurgburg^{1,2,3*}, François Buscot^{2,4}, Antonis Chatzinotas^{1,2,3}, Narendrakumar M. Chaudhari^{2,5}, Adam T. Clark⁶, Magda Garbowski^{2,7}, Matthias Grenié^{2,3}, Erik F. Y. Hom^{2,8}, Canan Karakoç^{1,2,9}, Susanne Marr^{2,10,11}, Steffen Neumann^{2,11}, Mika Tarkka^{2,4}, Nicole M. van Anna Heintz-Buschart¹³

A multivariate approach to the integration of multi-omics datasets

Chen Meng¹, Bernhard Kuster^{1,2}, Aedín C Culhane^{3,4*} and Amin Moghaddas Gholami^{1*}

phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data

Paul J. McMurdie, Susan Holmes*

Dimension reduction techniques for the integrative analysis of multi-omics data

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Statistical analysis of metagenomics data

M. Luz Calle*

Integration of omics data to unravel root microbiome recruitment[☆]

Anouk Zancarini^{1,2}, Johan A Westerhuis², Age K Smilde² and Harro J Bouwmeester¹

MiBiOmics: an interactive web application for multi-omics data exploration and integration

Johanna Zoppi¹, Jean-François Guillaume², Michel Neunlist¹ and Samuel Chaffron^{3,4*}

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Merci
Et bonne retraite Denis