

# Multivariate Data Analysis in Microbial Ecology

## New Skin for the old Ceremony

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# Headlines

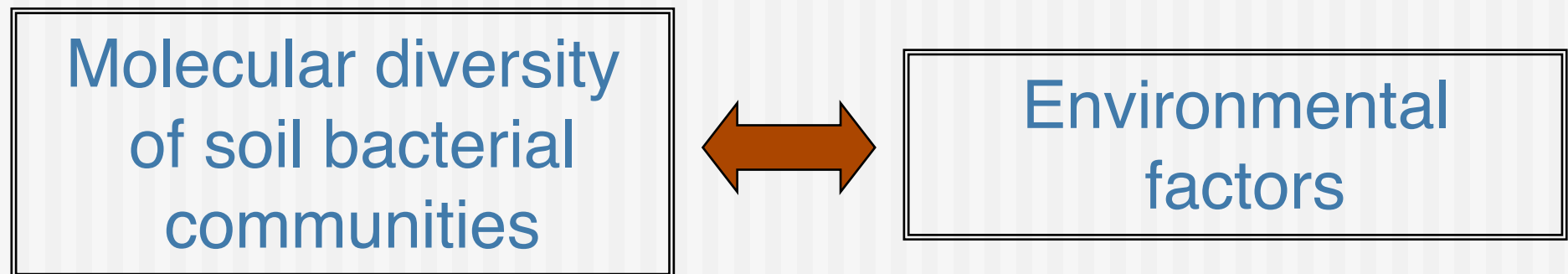
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- Topic: Environmetrics and Ecology
  - ✓ descriptive exploratory multivariate data analysis ("Geometric Data Analysis")
  - ✓ ade4 and ade4TkGUI packages
  - ✓ case studies
- The EcoMic – RMQS project
- Mycorrhizal symbiosis in tropical soils

# The EcoMic – RMQS project

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- Analyse the relationships between soil microbial molecular diversity and environmental factors at the regional and national scales in France.



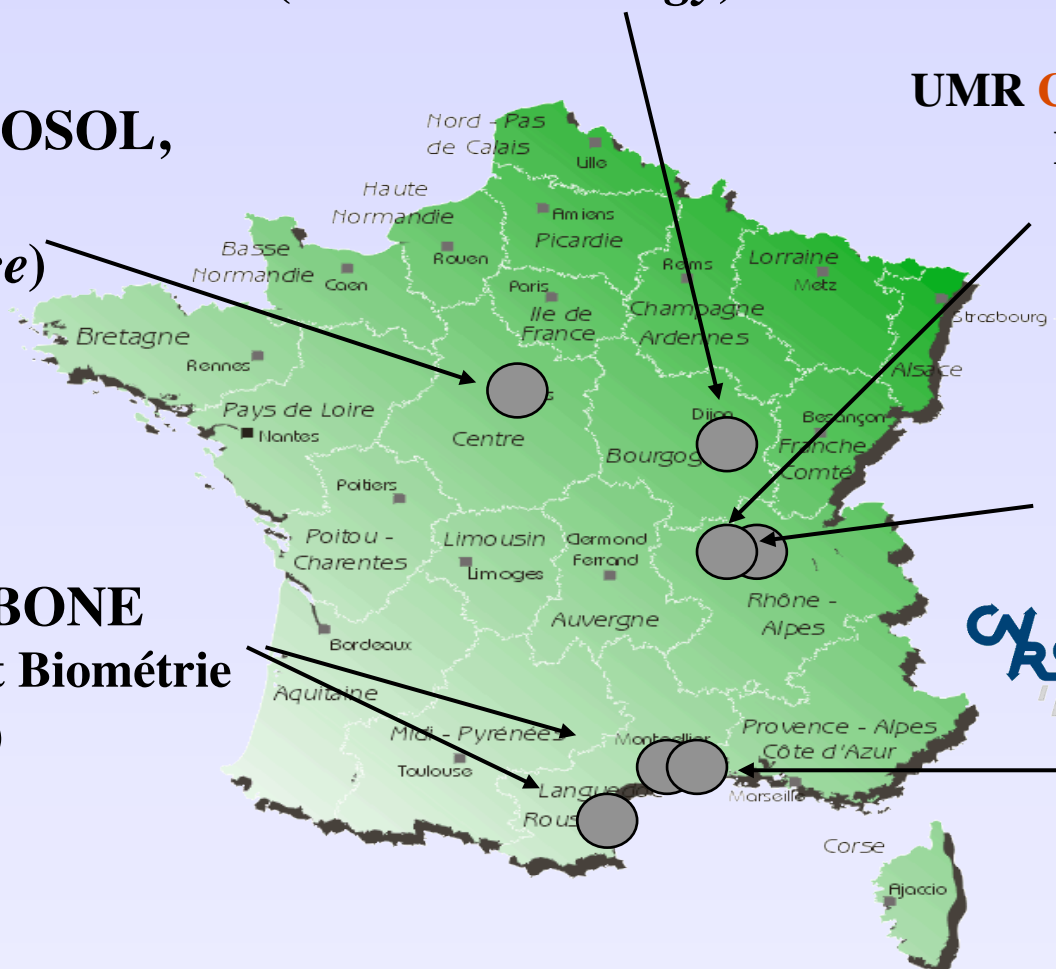
**Coordinator : L Ranjard, UMR INRA/ U-Bourgogne**  
**Microbiologie et Géochimie des Sols, Dijon**  
*(Microbial Ecology)*



**Unité INRA INFOSOL,**  
**Orléans**  
*(Soil Science)*



**LBE INRA-NARBONE**  
**Analyse des Systèmes et Biométrie**  
*(Modelling)*



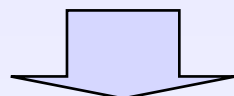
**UMR CNRS Génomique Microbienne**  
**Environnementale, Lyon**  
*(Microbial Ecology)*



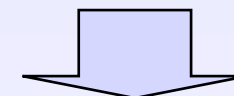
**UMR CNRS/UCBL Biométrie**  
**Biologie Evolutive, Lyon**  
*(Data analysis)*



**DREAM Unit,**  
**CEFE-CNRS**  
**Montpellier**  
*(Soil Science)*



**Multidisciplinary**  
*(Soil science, Microbial ecology,  
Modelling, Data analysis)*



**Multi-institutionnal**  
*(INRA, CNRS, Universities)*

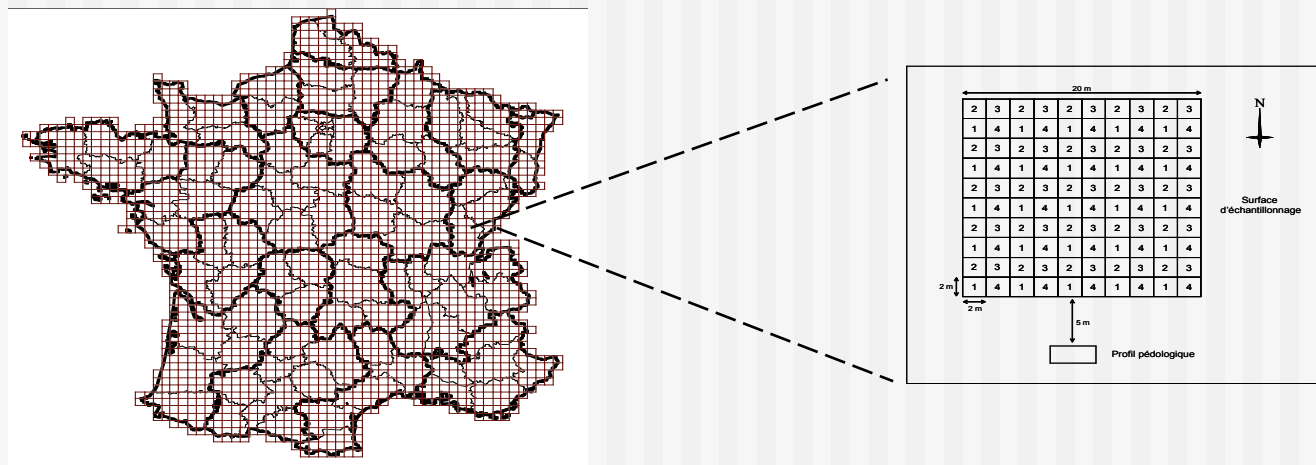
# The EcoMic – RMQS project

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- Large (2M€) ANR project on Microbial Ecology of French soils
- Microbial diversity in soil
  - ✓ Evaluate beta diversity
  - ✓ Processes generating and maintaining this diversity
  - ✓ Large spatial scale (France)
  - ✓ Molecular tools (PCR, DNA fingerprints, DNA  $\mu$ arrays)
- Based on the **RMQS soil library**

# The RMQS

- Soil Quality Measure Network
- Started in 2002 by Infosol - INRA Orleans
- Square sampling grid over all France 16 x 16 km
- 2200 sampling points, finished in 2009
- Renewed every 10 years.



# The RMQS

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Many parameters are measured:

- Physico-chemical parameters (pedology)
  - ✓ granulometry, pH
  - ✓ C, N, Ca, Na, heavy metals, etc.
- Vegetation cover, lanscape, agricultural practices, etc.
- Molecular data (DNA extraction from raw soil samples)

# Six regions

- Based on vegetation, landscape, climate, pedology, and *available samples (578)*

Region 1: North, intermediate

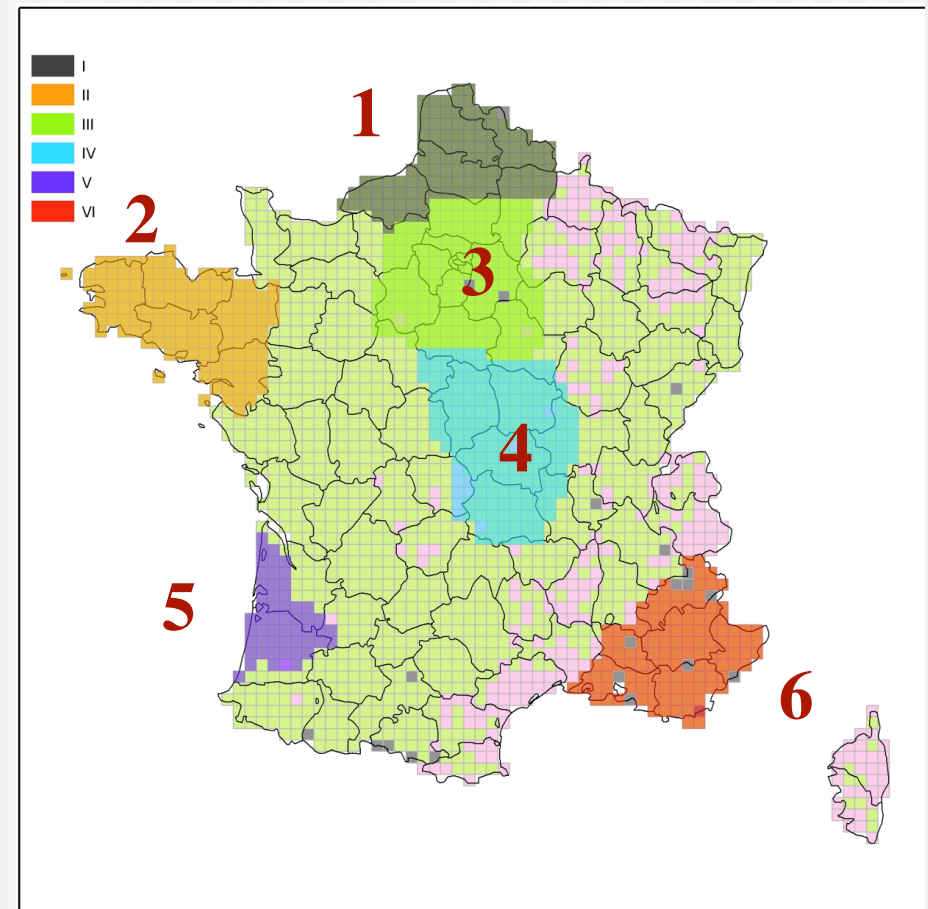
Region 2: Brittany, low diversity

Region 3: grand Paris, highly urbanized

Region 4: Center, intermediate

Region 5: Landes, very low diversity,  
sand dunes and pine forests


Region 6: South Alps, highest diversity,  
mountains, contrasted climate





# Molecular data

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- RISA: Ribosomal Intergene Spacer Analysis
  - ✓ length polymorphism of the intergene sequence between the large and small ribosomal subunit genes
  - ✓ no information on taxonomic level (OTU: Operational Taxonomical Unit)
  - ✓ data already available for almost 1000 sites
- Sequencer data must be processed before analysis
  -  ✓ prepRISA package: rectangular data tables (sites x OTU)
  - ✓ hundreds of OTU
  - ✓ typical data table size  $\approx 2200 \times 500$

# Molecular data

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- DNA  $\mu$ arrays
  - ✓ probes can be specific of particular taxonomic levels
  - ✓ data not yet available
  - ✓ thousands of probes
  - ✓ typical data table size  $\approx 2200 \times 10\ 000$

# Microbiogeography questions

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- "Everything is everywhere, *but*, the environment selects." Baas Becking, 1934.
- "Are microbial communities a black box with no spatial structure or, like macroorganisms do they exhibit a particular distribution with predictable aggregates patterns from local to regional scales ? " Horner-Devine et al., *Nature*, 2004.
- "Identify the environmental factors (edaphic, climatic, anthropogenic...) which exert the strongest influences on microbial communities in nature." Martiny et al., *Nature Reviews*, 2006.

# Biological objectives

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- Inventory of bacterial diversity in French soils
- ***Spatial components*** of this diversity and ecological models to explain it (***species-area relationship***)
- Mechanisms determining this diversity (pedology, climate, vegetation, etc.)
- Quantify the impact of human activities (agriculture, industrial sites, wastes)
- Microbiological markers of soil evolution in various ecological situations

# Species - area relationship

- S = number of species, A = area under study

$$S = CA^z$$

- When using RISA, OTU  $\neq$  species

- ✓ OTU<sub>A</sub> and OTU<sub>a</sub> number of OTU in areas A and a

$$OTU_a = OTU_A \left( \frac{a}{A} \right)^z$$

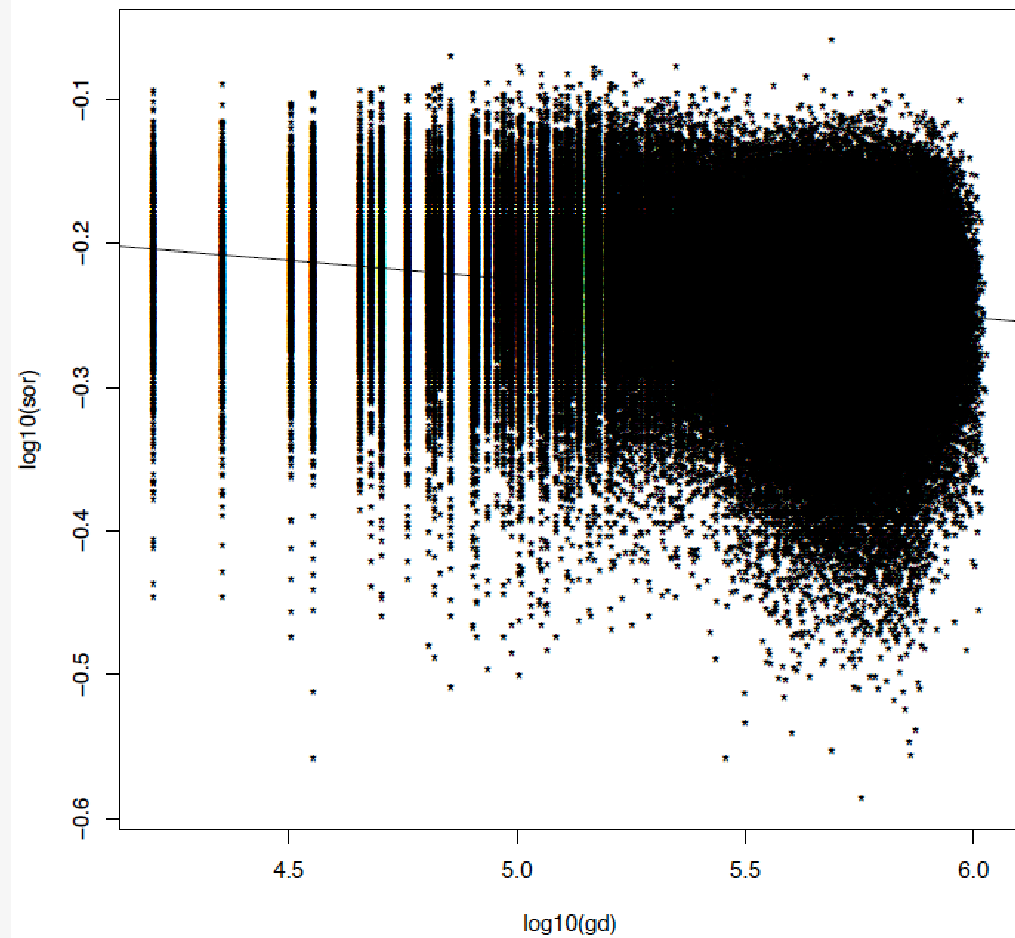
- ✓ Sørensen index for 2 samples at distances D and d

$$\chi_d = \chi_D \left( \frac{d}{D} \right)^{-2z}$$

- ✓ Green *et al.* 2004, *Nature*, **432**, 747-750

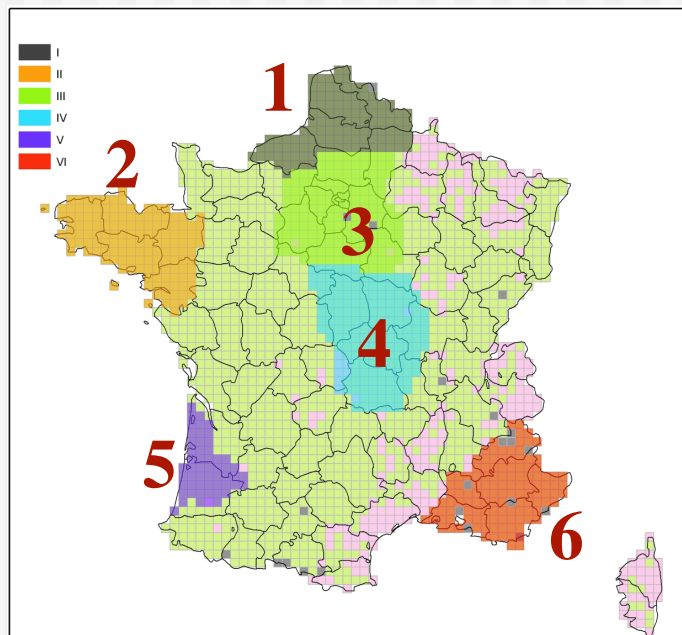
# Species - area relationship

- Computations:  (packages: vegan, labdsv)



# Species - area relationship

<b>Region 1</b>	Slope = -0.00590	p = 0.031
<b>Region 2</b>	Slope = -0.00022	p = 0.002
<b>Region 3</b>	Slope = +0.00494	p = 0.018
<b>Region 4</b>	Slope = -0.00683	p = 0.008
<b>Region 5</b>	Slope = -0.00416	p = 0.690
<b>Region 6</b>	Slope = -0.01280	p = 0.000
<b>Total</b>	Slope = -0.02657	p = 0.000



Slopes are negative: **diversity increases**

Region 5: very homogeneous (p-value NS)

Region 3: slope is positive (urbanized)

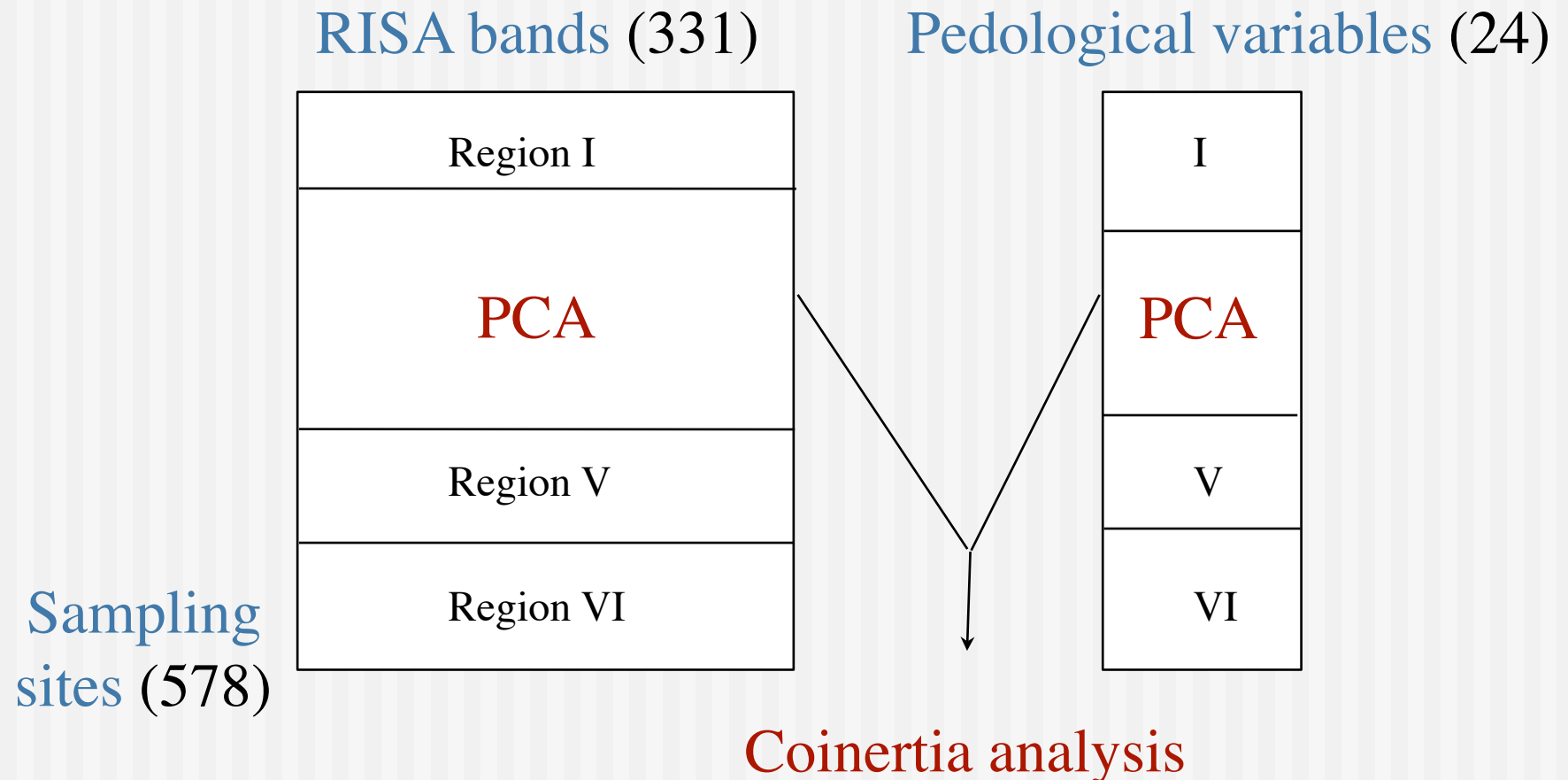
Region 6: high landscape diversity

Region 2: low diversity

Regions 1 and 4: intermediate

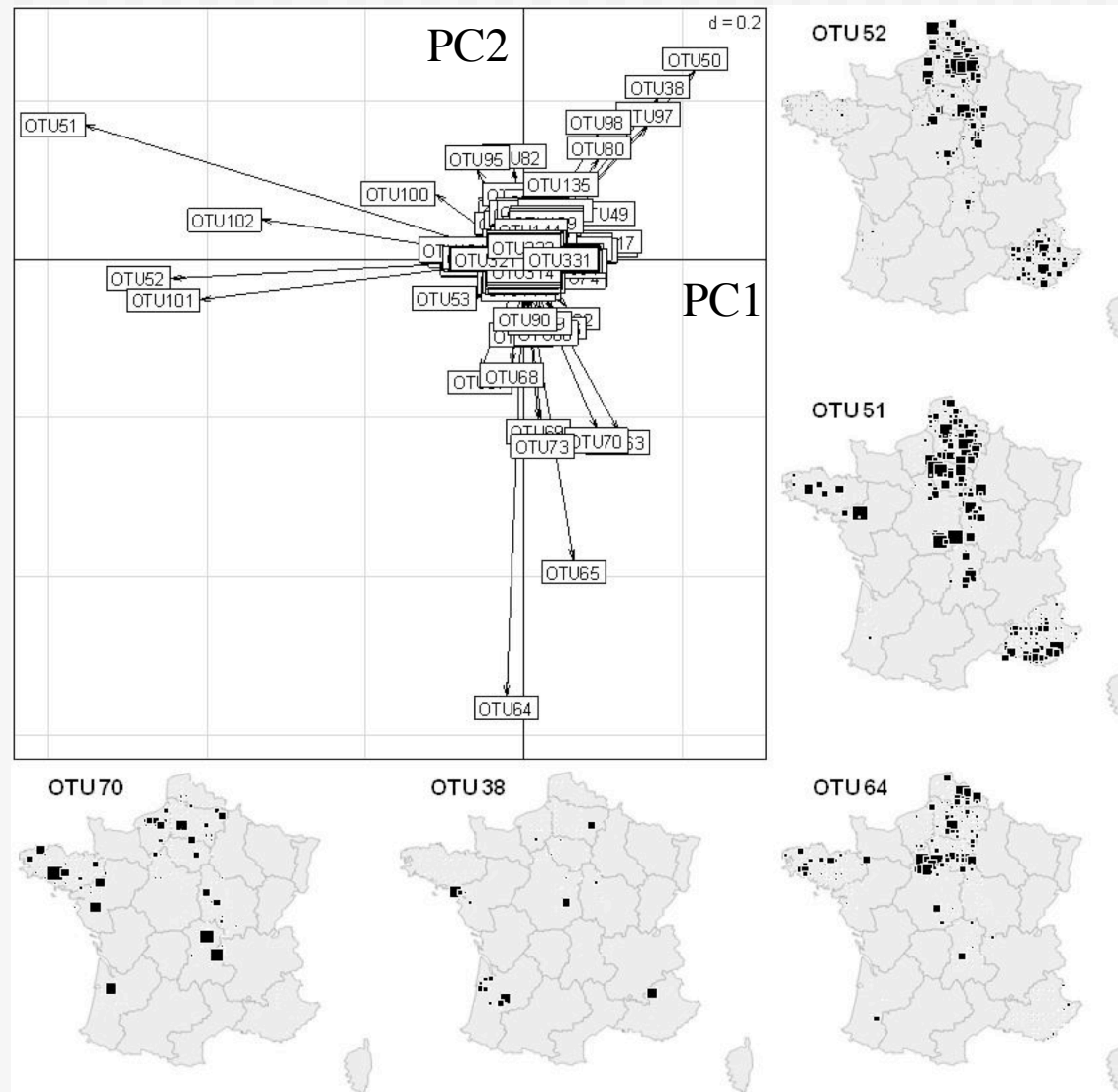
# Multivariate analysis: data sets

- Computations:  (prepRISA, ade4 + ade4TkGUI)

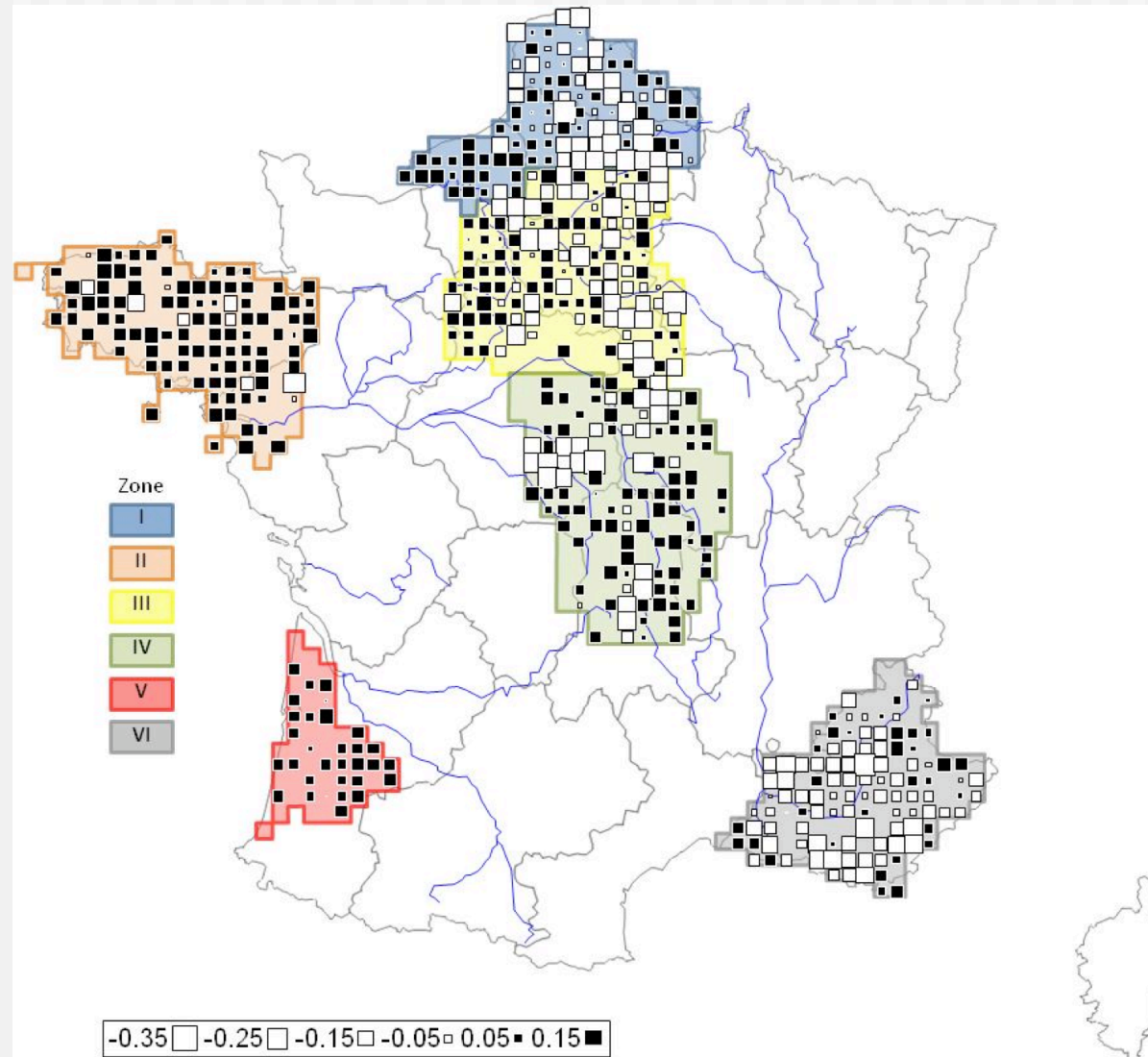




# PCA of RISA data: OTU distrib.

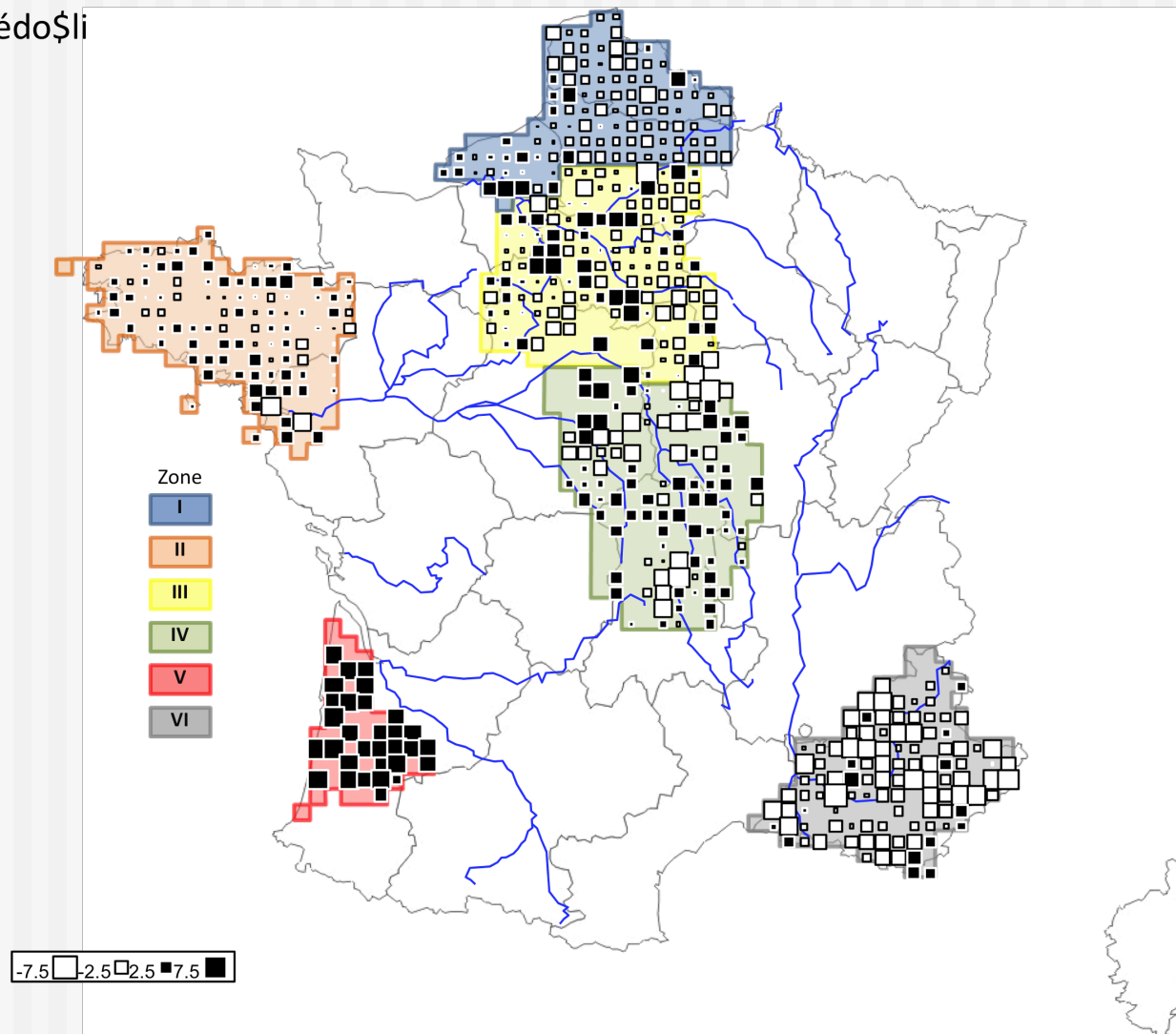


# PCA of RISA data (PC1)



# PCA of pedological data (PC1)

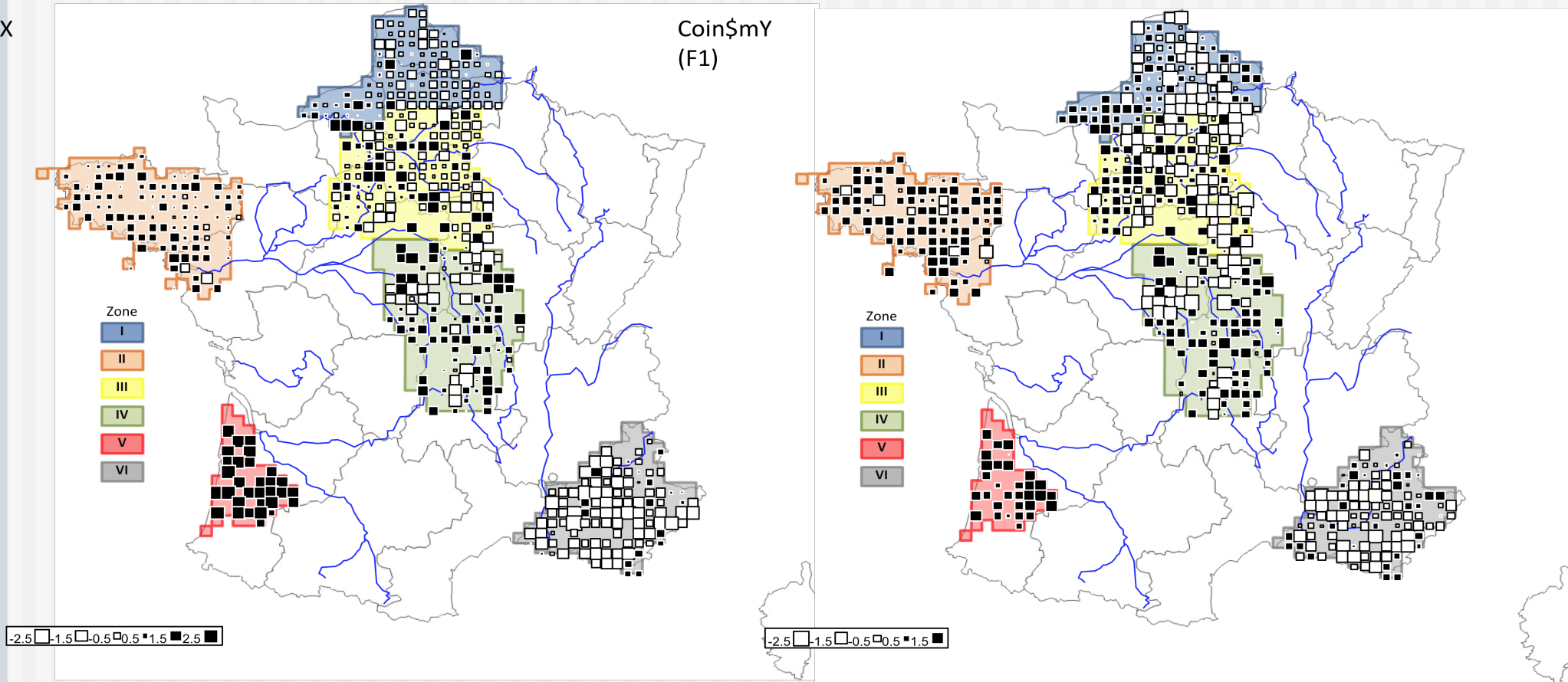
PCA\_pédošli  
(F1)



# Coinertia analysis (pedo/RISA)

Coin\$mX  
(F1)

Coin\$mY  
(F1)

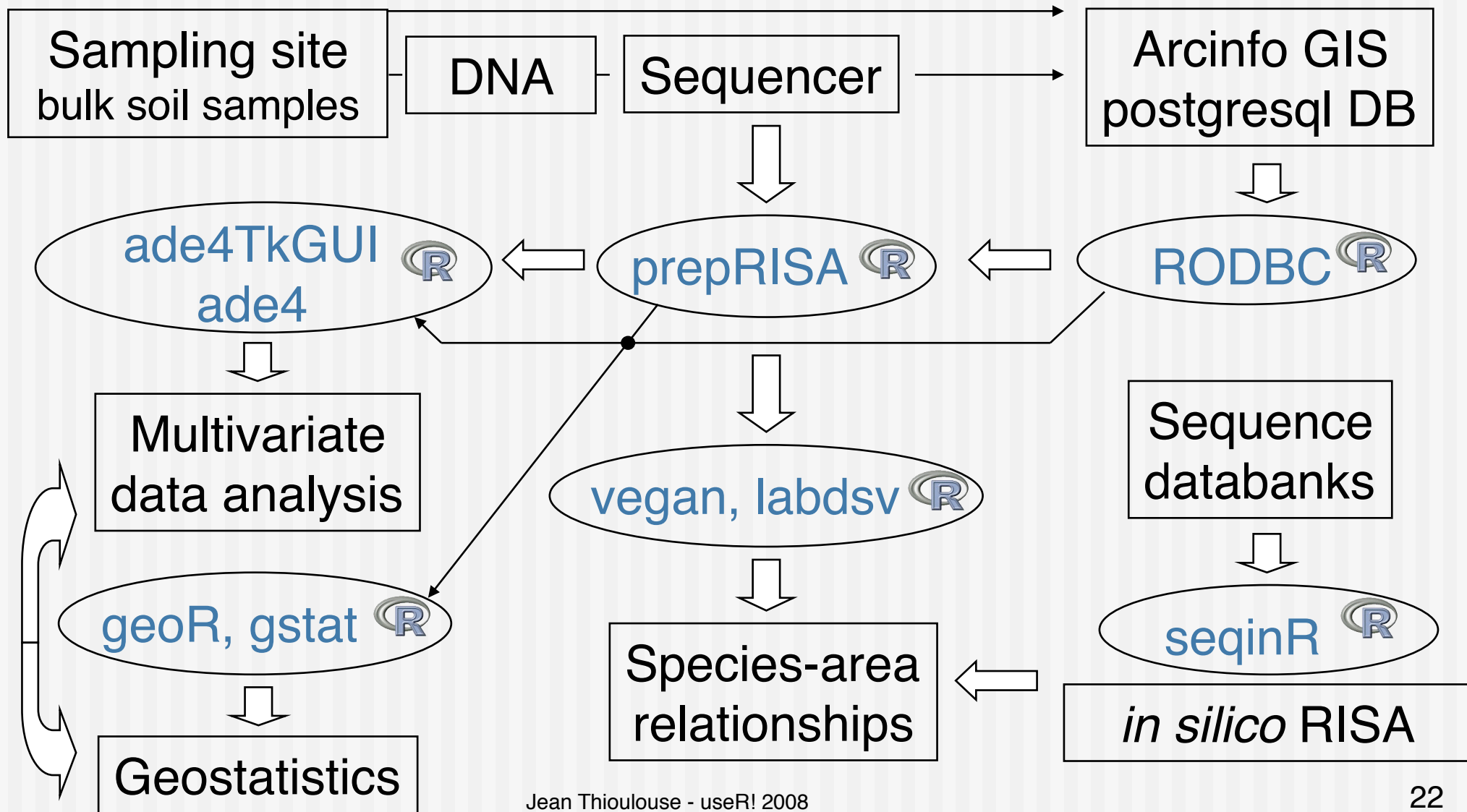


# Biological interpretations

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- The spatial structures of physico-chemical pedological variables and RISA data are very similar, and this similarity exists at both regional and national scales (within and between regions)
- Ecological processes responsible of spatial structures in animals and plants (differentiation, extinction, endemism) **either** do not exist for bacterias, **or** may be masked by bacteria characteristics, such as dispersion capacities, stress resistance, or short generation time.
- "everything is everywhere, but, the environment selects"
- These results are for RISA OTU, which are mostly unknown. But (hopefully) more to come with DNA  $\mu$ arrays...

# RISA methodological flow chart



# Mycorrhizal symbiosis in tropical soils

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- Soil is a very complex environment, with many interactions between plants, mycorrhizal fungi, soil bacterial communities, and abiotic factors
- Research project started in 2000 in collaboration with several IRD research labs in Africa:
  - ✓ Dakar (Senegal)
  - ✓ Ouagadougou (Burkina Faso)
  - ✓ Marrakech (Morocco)
  - ✓ Antananarivo (Madagascar)

# Mycorrhizal symbiosis in tropical soils

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- Relationships between plants, mycorrhizal symbiosis, and the soil bacterial microflora
- Review of 15 papers published since 2005 on this topic in microbial ecology journals
  - ✓ Effects of mycorrhizal symbiosis
  - ✓ Nurse plants
  - ✓ Termite mound powder amendment




# Mycorrhizal symbiosis in tropical soils

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- Data used to study the diversity of soil bacteria
  - ✓ RISA and DNA  $\mu$ arrays are too complex to be used
  - ✓ Catabolic profiles / SIR (substrate induced response) profile = measure of CO<sub>2</sub> production for  $\approx$  30 substrates  
functional diversity vs. taxonomic diversity
  - ✓ DNA fingerprint: DGGE

# Mycorrhizal symbiosis in tropical soils

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- Statistical data analysis methods (ade4 )
  - ✓ BGA (between group analysis): robust alternative to discriminant analysis to separate groups. PCA on group means, with projection of original data
  - ✓ Coinertia analysis: analyse the relationships between two data tables. Robust alternative to Canonical Analysis or Canonical Correspondence Analysis
  - ✓ both methods allow the use of low numbers of samples as compared to the number of variables
  - ✓ permutation test

# Mycorrhizal symbiosis in tropical soils

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- Statistical data analysis methods
  - ✓ Cluster analysis on DGGE fingerprints (hclust<sup>®</sup>)
  - ✓ Linear model for various hypothesis test (lm, nlme<sup>®</sup>)

# Results

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- Effects of mycorrhizal symbiosis
  - ✓ improves plant growth (*Cupressus atlantica*, *Acacia holosericea*, *Acacia seyal*, *Uapaca bojeri*)
  - ✓ improves P solubilization and assimilation
  - ✓ improves seedling survival (*C.a.*) in degraded soils
  - ✓ improves the functional diversity of soil microflora
  - ✓ counterbalance the negative effect of an exotic plant species on the structure and functioning of soil bacterial communities

# Results

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- Nurse plant effects
  - ✓ *Lavandula* species (*L. stoechas*, *L. dentata*, *L. multifida*) act as nurse plants for *C. Atlantica*
  - ✓ improve plant growth
  - ✓ improve mycorrhizal soil infectivity
  - ✓ interactions with the functional diversity of soil bacteria
  - ✓ *Thymus satureioides* also improves plant growth and functional diversity

# Results

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- Termite mound powder amendment effect
  - ✓ improves mycorrhizal symbiosis and plant growth of *A. holosericea* and *A. seyal* (MHB: mycorrhiza helper bacteria)
  - ✓ improves nutrient supplies (effect on soil microflora)
  - ✓ can be used for biological control of phytoparasite *Striga hermontica* (effect on soil microflora)
  - ✓ decreases Cd toxicity and improves its accumulation in plants (sorghum)

# Result examples: BGA on SIR

Graphical display (PC2 biplot) of BGA on catabolic profiles.

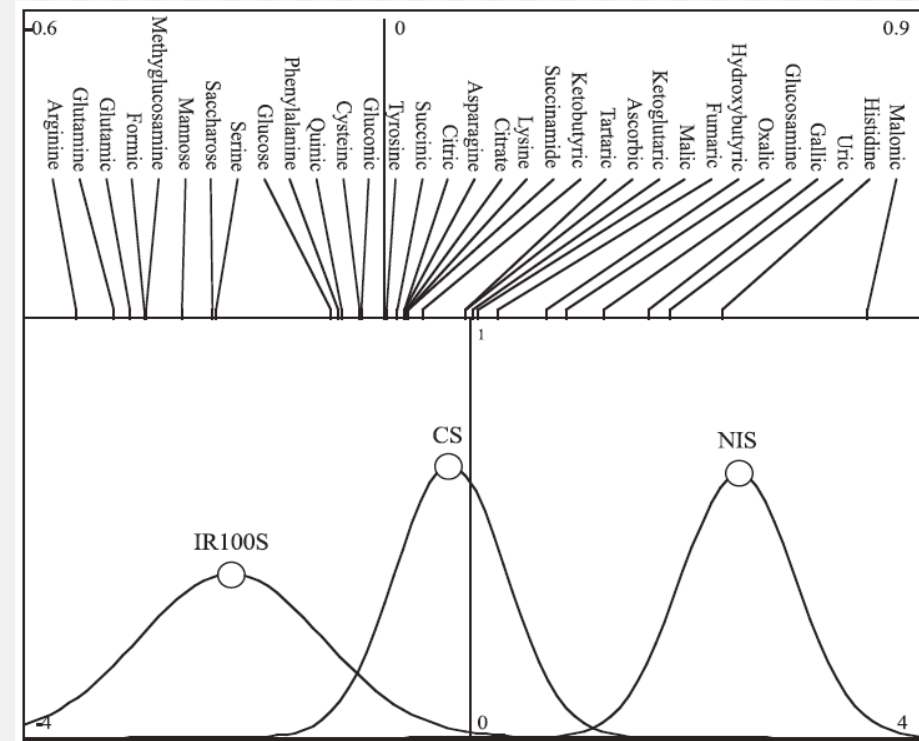
Up: scores of the 33 substrates.

Down: the three Gauss curves represent the mean and variance of the scores of soil samples (three treatments).

CS: crop soil

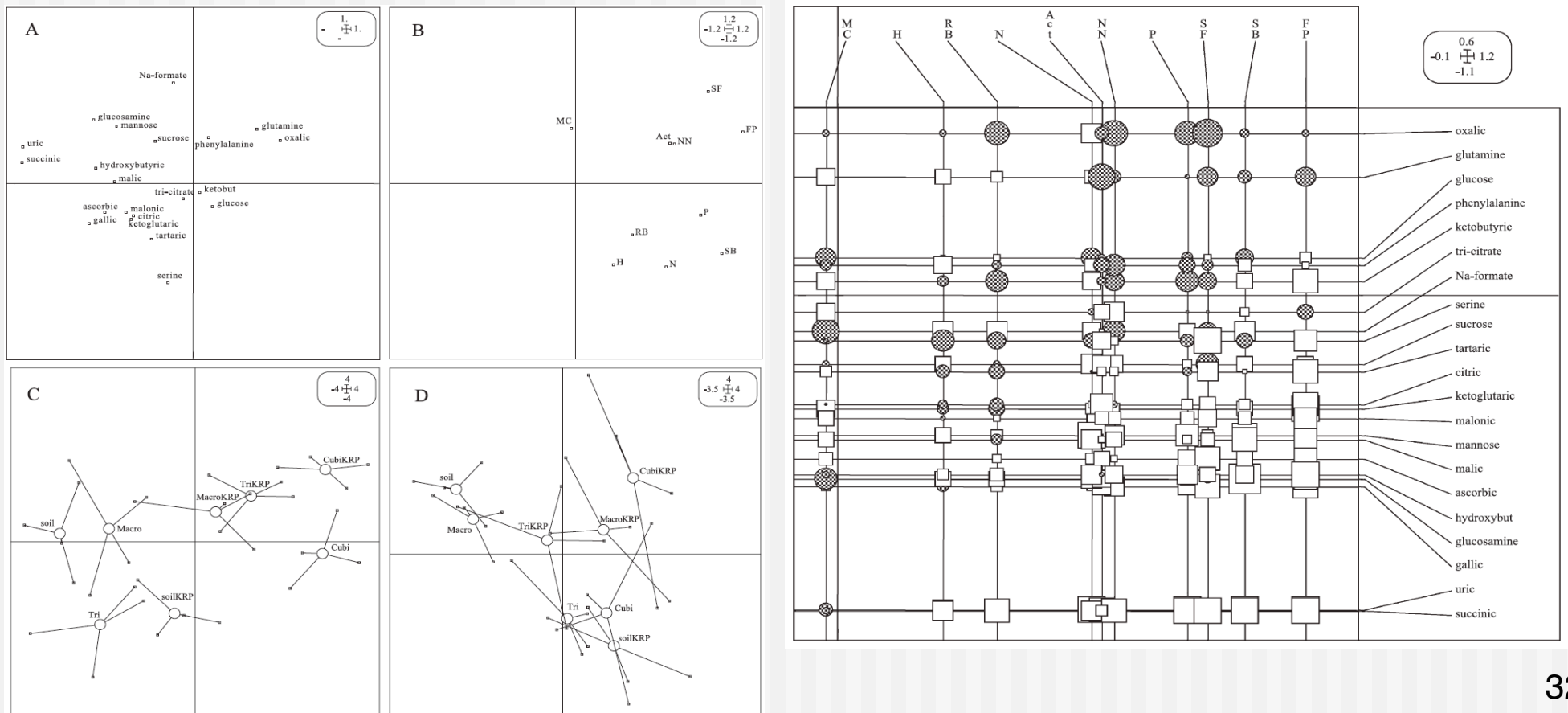
NIS: soil from uninoculated trees

IR100S: soil from *P. albus* IR100 fungi inoculated trees



# Result examples: Coinertia on SIR


Graphical display of Coinertia analysis between catabolic profiles and plant growth parameters. Left: F1xF2 factor maps. Right: cross-covariances





# Conclusion

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-  in the Biometry lab
  - ✓ Has become an indispensable tool in just a few years
  - ✓ Teaching (all levels)
  - ✓ 2 mailing lists: « rpackdev » and « rpourlesnuls »
  - ✓ 6 packages (on CRAN): ade4 and spin-off packages
  - ✓ ade4TkGUI, adehabitat, adegenet
  - ✓ seqinR, nlstools

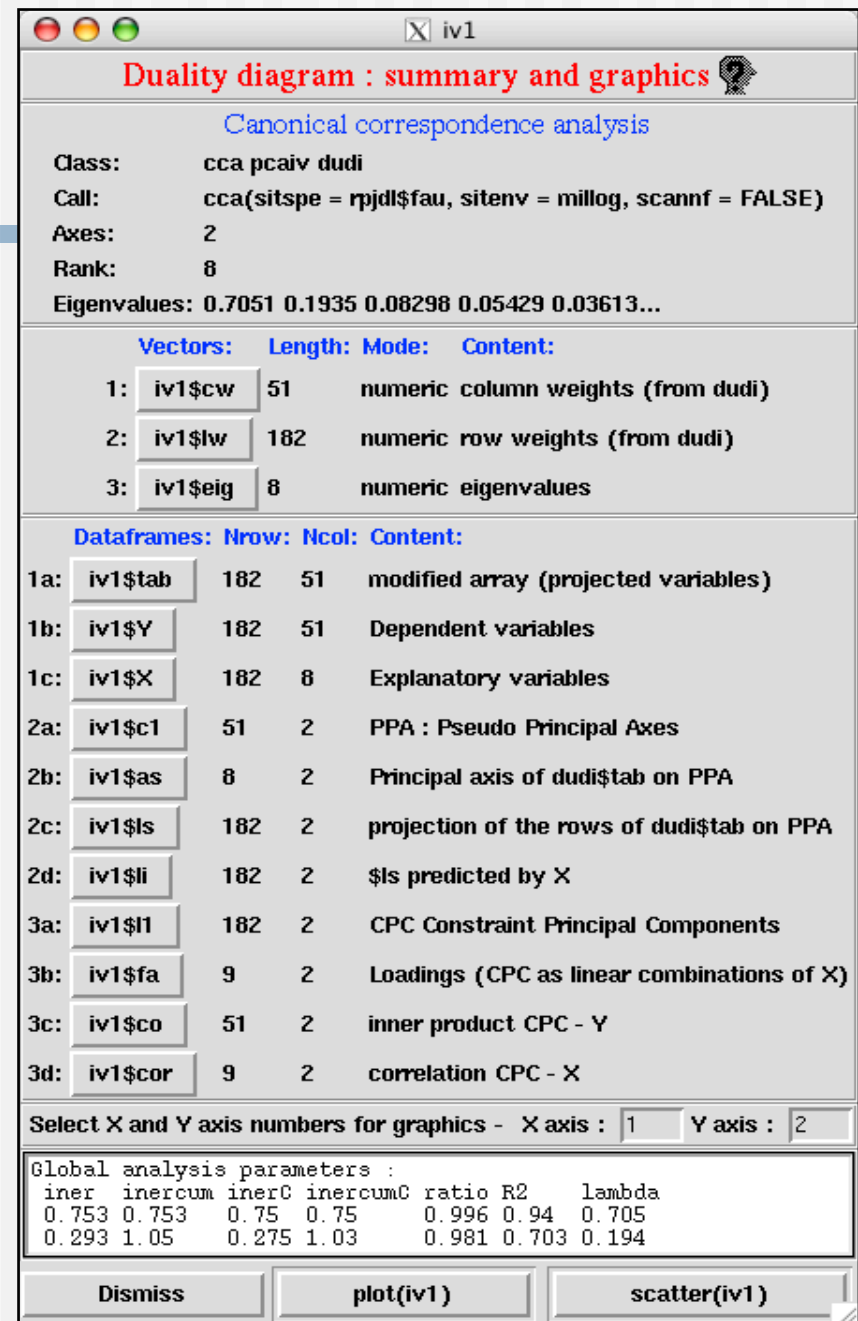
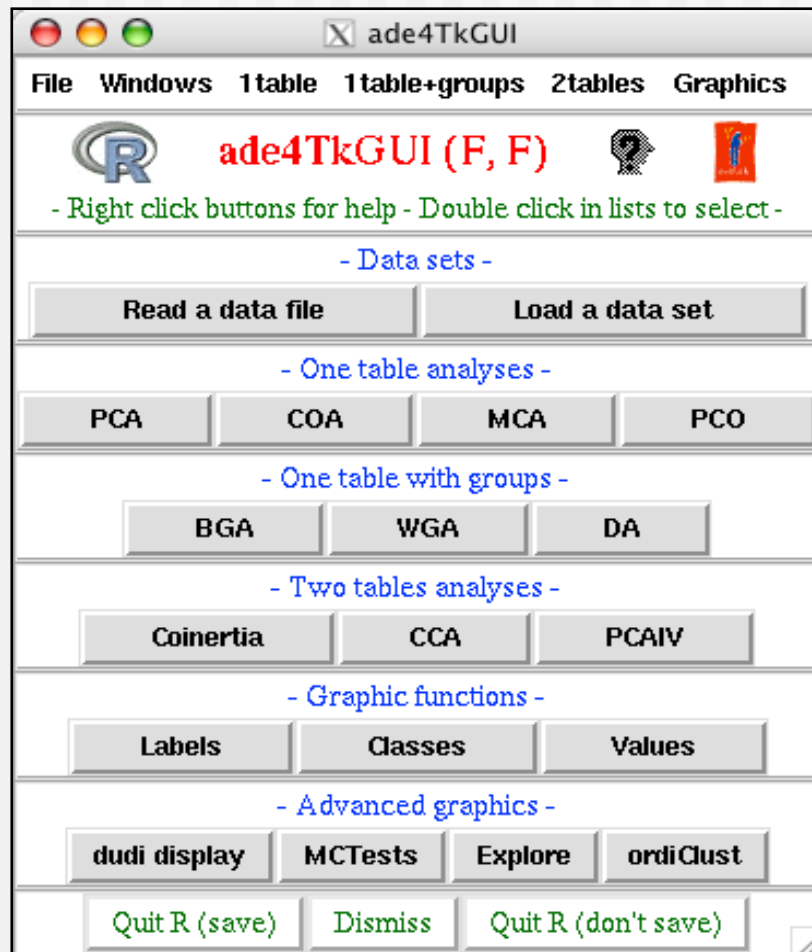
# Conclusion

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- Need for GUIs
  - ✓ For teaching
  - ✓ For biologists
  - ✓ ade4TkGUI screenshots

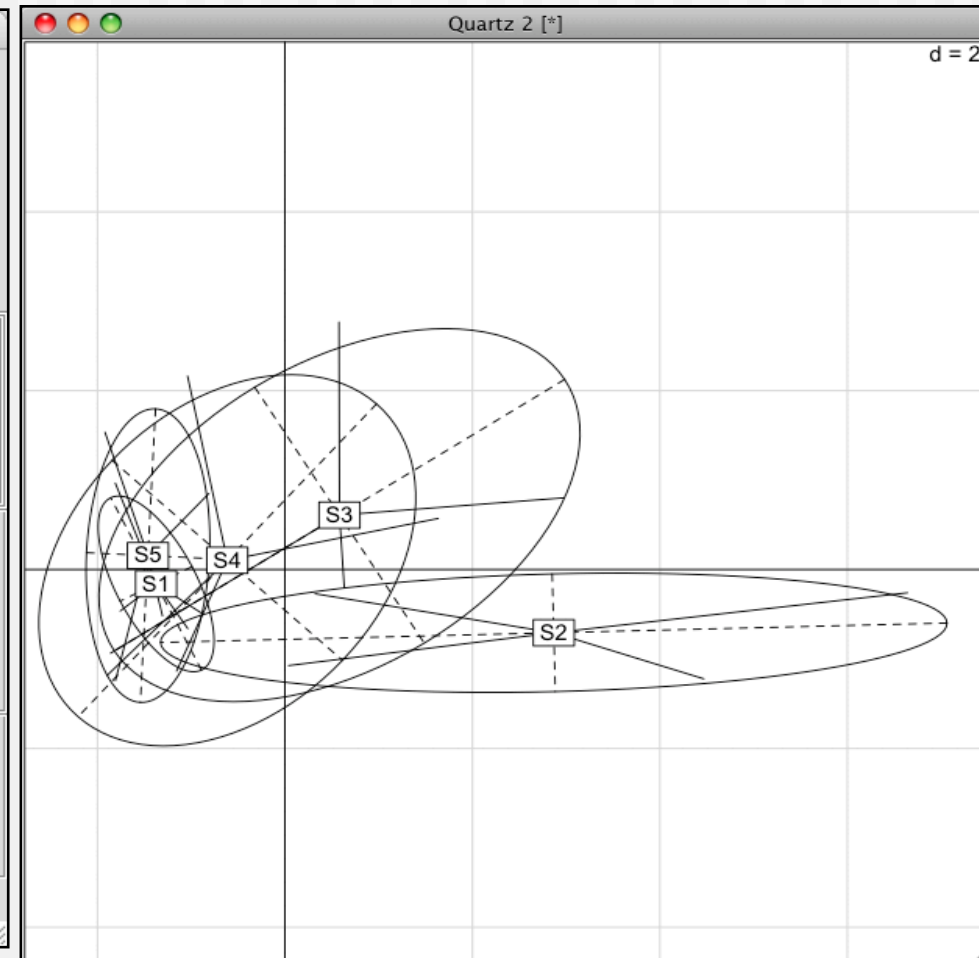
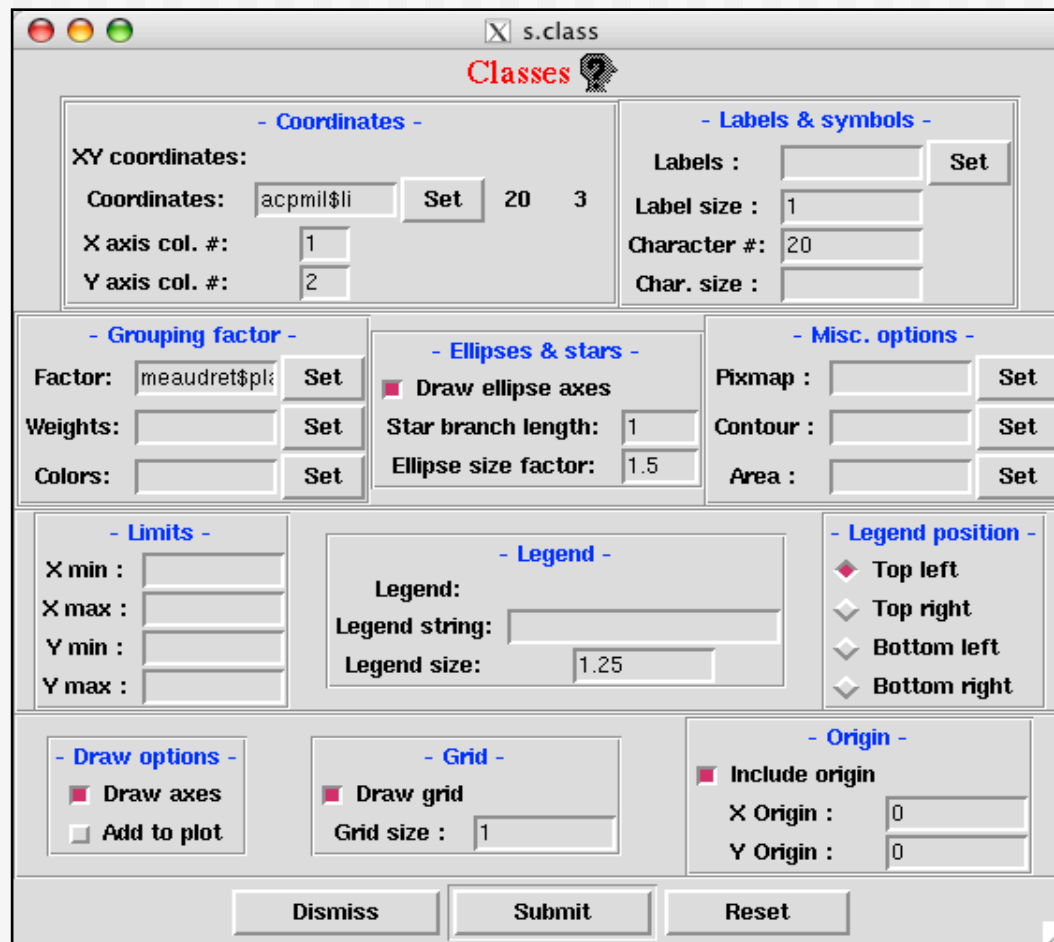
# Conclusion

## Synthetic display



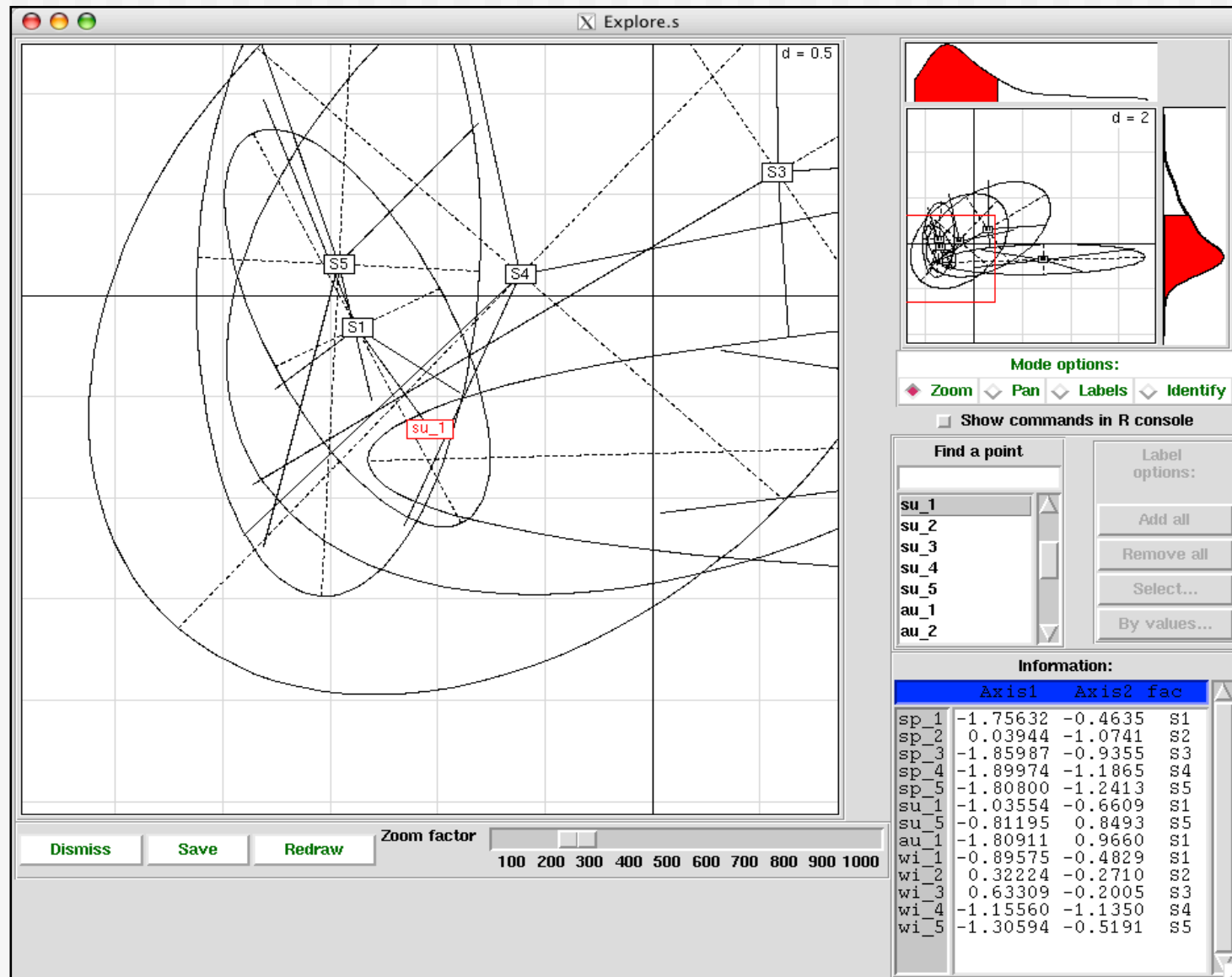
# Conclusion

## Complex graphs



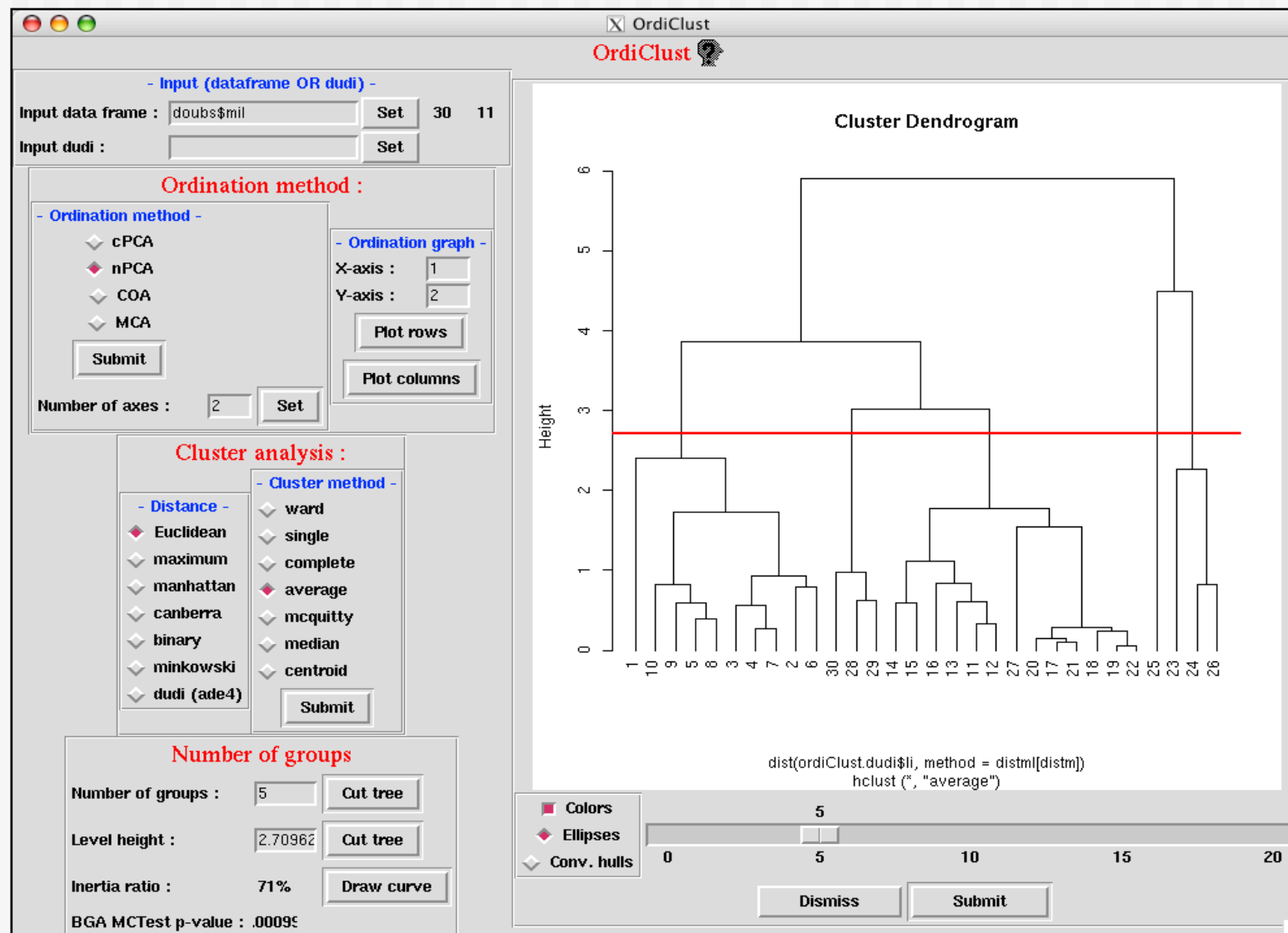
# Conclusion

## Interactive factor map



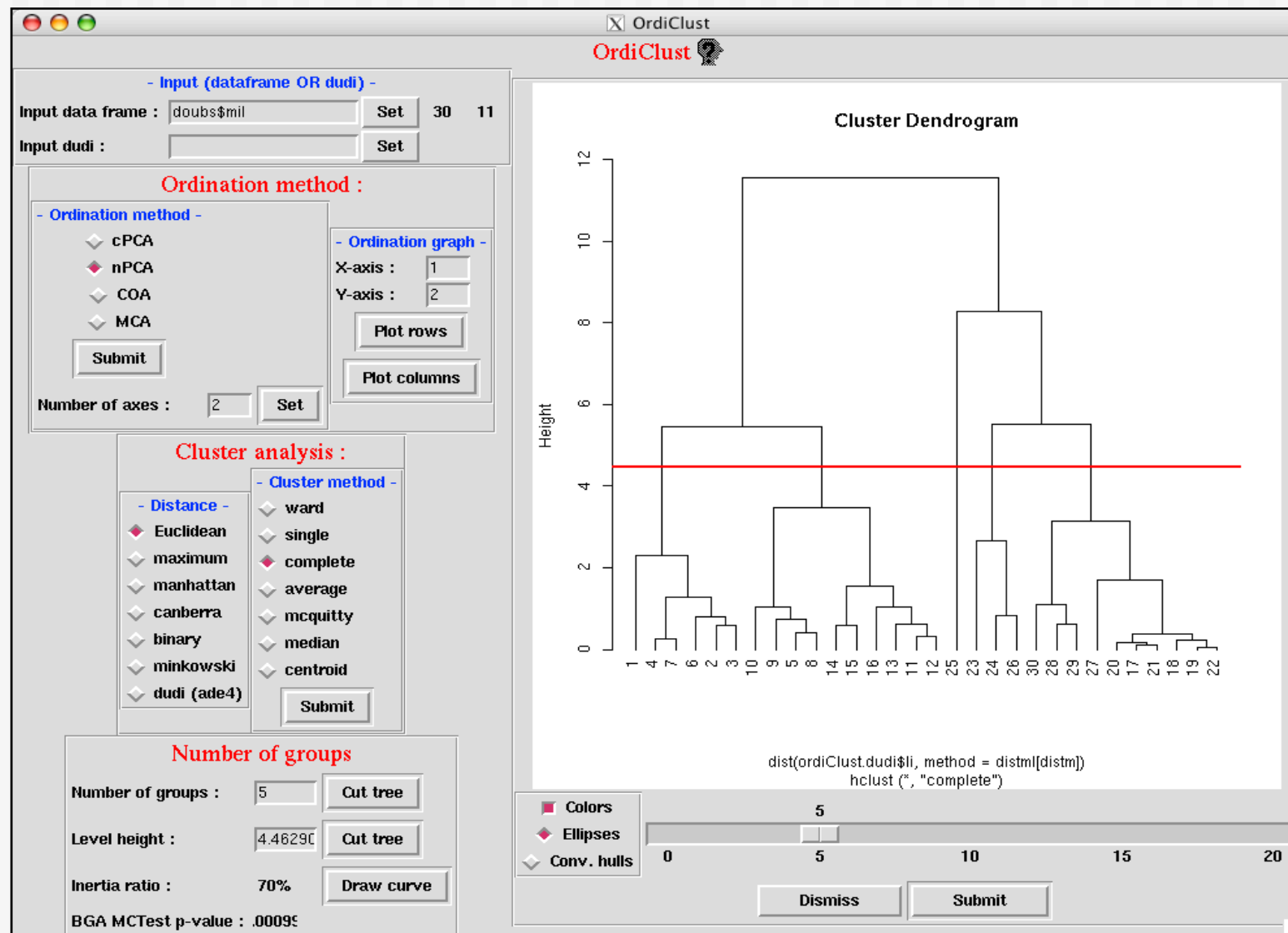
# Conclusion

## Interactive data analysis



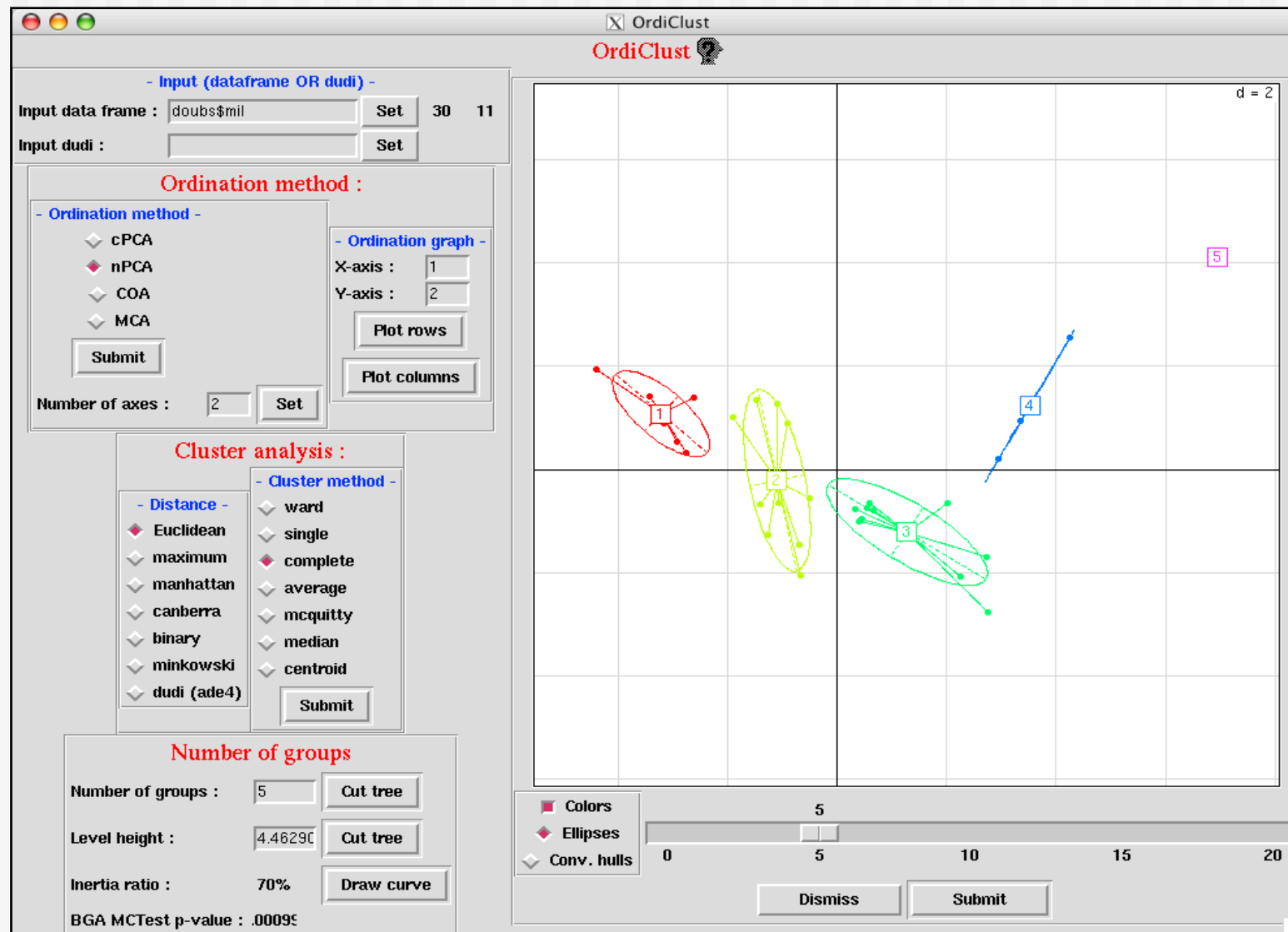
# Conclusion

## Interactive data analysis



# Conclusion

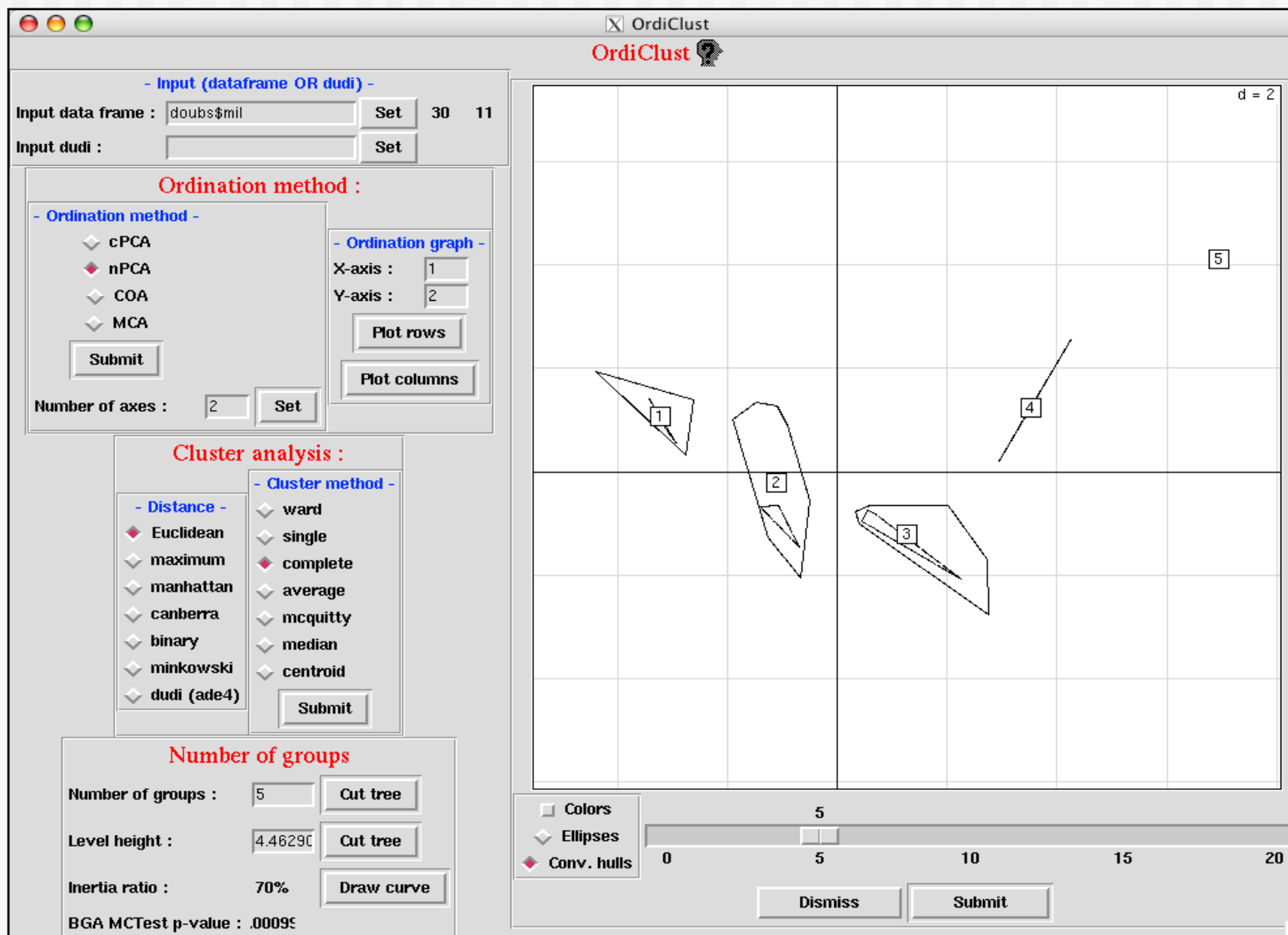
## Interactive data analysis





# Conclusion

## Interactive data analysis

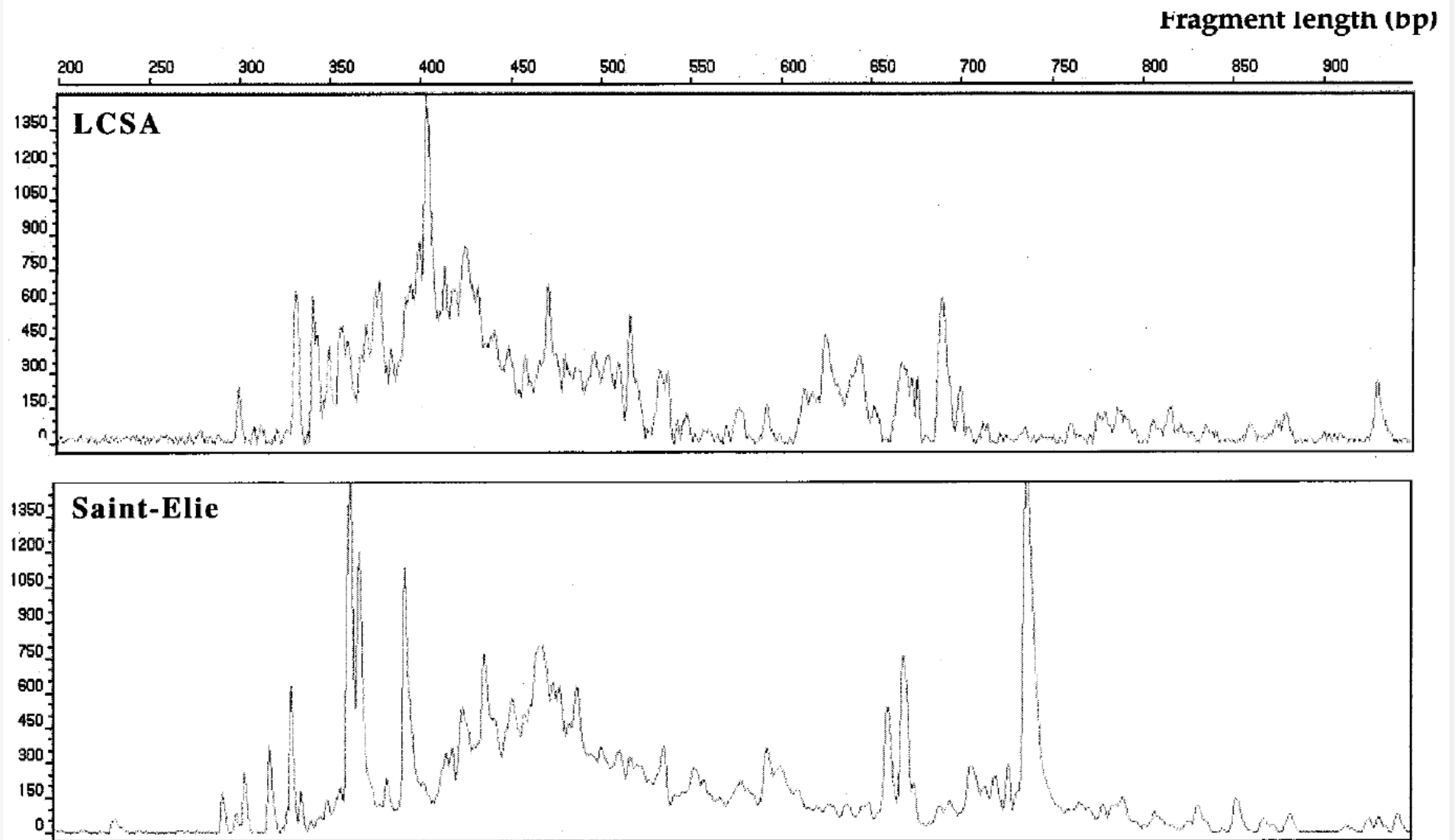


# Acknowledgments

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- EcoMic - RMQS
  - ✓ Lionel Ranjard, Samuel Dequiedt - INRA Lab in Dijon
  - ✓ Bruno Saby, Manuel Martin - INRA Lab in Orleans
- Mycorrhizal symbiosis
  - ✓ Robin Duponnois - IRD Lab in Dakar & Ouagadougou
- ade4 package
  - ✓ Stéphane Dray, Anne-Béatrice Dufour - Biometry Lab in Lyon

# RISA profiles



- Remigi P., Faye A., Kane A., Deruaz M., Thioulouse J., Cissoko M., Prin Y., Galiana A., Dreyfus B., & Duponnois R. (2008). *Applied and Environmental Microbiology* 74, 5, 1485-1493.
- Andrianjaka Z., Bally R., Lepage M., Thioulouse J., Comte G., & Duponnois, R. (2007). *Applied Soil Ecology* 37, 175-183.
- Kisa M., Sanon A., Thioulouse J., Assigbetse K., Sylla S., Dieng L., Berthelin J., Prin Y., Galiana A., Lepage M. & Duponnois R. (2007). *FEMS Microbiology Ecology*, 62, 32-44.
- Ouahmane L., Hafidi M., Thioulouse J., Ducouso M., Kisa M., Prin Y., Galiana A., Boumezzough A., & Duponnois R. (2007). *Journal of Applied Microbiology* 103, 683-690.
- Ouahmane L., Thioulouse J., Hafidi M., Prin Y., Galiana A., Plenchette C., Kisa M., & Duponnois R. (2007). *Forest Ecology and Management* 241, 200-208.
- Ramanankierana N., Ducouso M., Rakotoarimanga N., Prin Y., Thioulouse J., Randrianjohany E., Ramaroson L., Kisa M., Galiana A. & Duponnois, R. (2007). *Mycorrhiza*, 17, 3, 195-208.
- Duponnois R., Assigbetse K., Ramanankierana H., Kisa M., Thioulouse, J. & Lepage, M. (2006). *FEMS Microbiology Ecology*, 56, 292-303.
- Duponnois R., Kisa M., Assigbetse K., Prin Y., Thioulouse J., Issartel M., Moulin P., & Lepage M. (2006). *Science of the Total Environment*, 370, 391-400.
- Ouahmane L., Hafidi M., Plenchette C., Kisa M., Boumezouch A., Thioulouse J. & Duponnois R. (2006). *Applied Soil Ecology*, 34, 190-199.
- Ouahmane L., Duponnois R., Hafidi M., Kisa M., Boumezouch A., Thioulouse J. & Plenchette C. (2006). *Plant Ecology*, 185, 123-134.
- Ramanankierana N., Rakotoarimanga N., Thioulouse J., Kisa M., Randrianjohany E., Ramaroson L. & Duponnois R. (2006). *International Journal of Soil Science*, 1, 8-19.
- Sanon A., Martin P., Thioulouse J., Plenchette C., Spichiger R., Lepage M. & Duponnois R. (2006). *Mycorrhiza*, 16, 125-132.
- Assigbetse K., Gueye M., Thioulouse, J. & Duponnois R. (2005). *Microbial Ecology*, 50, 350-359.
- Duponnois, R., Colombet, A., Hien, V., & Thioulouse, J. (2005). *Soil Biology and Biochemistry*, 37, 1460-1468.
- Duponnois, R., Paugy, M., Thioulouse J., Masse, D. & Lepage, M. (2005). *Geoderma*, 124, 349-361.