

# Grasslands species diversity mapping from hyperspectral remote sensing

 $5^e$  Colloque Groupe Hyperspectral SFPT-GH

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| Context |  |  |  |
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### Outline

#### Context

#### Measure of heterogeneity

High dimensional discriminant analysis

Experimental protocol

#### Primary results

Conclusions and perspectives

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### Grasslands species diversity

- Plants diversity in semi-natural landscapes in an important biodiversity factor,
- It ensures several ecosystems services (regulation, pollination),
- Grasslands represent a significant source of biodiversity in farmed landscapes,
- Grasslands area and diversity are declining [OMa12],
- Maps over grassland diversity are required over large area extend.







### Spectral Variation Hypothesis

- It assumes that the spectral heterogeneity is correlated with spatial variations and heterogeneity of the habitat [Pal+02]
- Spectral heterogeneity can be used as a proxy for species diversity [Roc+16]
- Several index have been proposed
  - Standard deviation or coefficient of variations of NDVI
  - PCA
  - Distance to centroids
  - Clustering

### Objectives

- Project MUESLI
- Use hyperspectral images to monitor species richness at the parcel level
- Methodological contributions
  - Use of robust high dimensional clustering method
  - Extend conventional heterogeneity/diversity index

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Proposed by Rocchini et. al [Roc+16]

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- It consists in computing the mean euclidean distance to the centroid of a given plot:

$$H(p) = \frac{1}{n_p} \sum_{i \in p}^{n_p} \|\mathbf{x}_i - \boldsymbol{\mu}_p\|^2$$

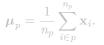
where

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Equivalently, it can be computed as the trace of the empirical covariance matrix of the plot:

$$H(p) = \mathsf{Trace}\big(\boldsymbol{\Sigma}_p\big).$$

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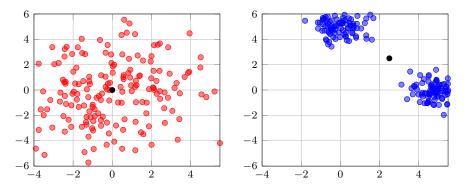
$$H(p) = \mathsf{Trace}(\boldsymbol{\Sigma}_p).$$

■ Variant: first reduce the dimensionality (PCA, ...)

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# Why MDC may not work

The following configurations have the same MDC



### Species richness

Proposed by Feret et. al [FA14]

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- Estimated by the Shannon entropy of a given plot

$$E_p = -\sum_{s=1}^{S} p_s \log(p_s)$$

where p is the considered plot, S the total number of species/classes/clusters and  $p_s$  is the relative proportion.

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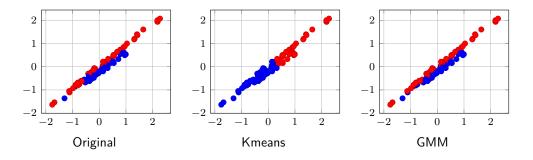
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where p is the considered plot, S the total number of species/classes/clusters and  $p_s$  is the relative proportion.

Clusters estimated through the *PCA+Kmeans* pipeline applied on the whole image.

### Why Kmeans may not work

Measure of heterogeneity



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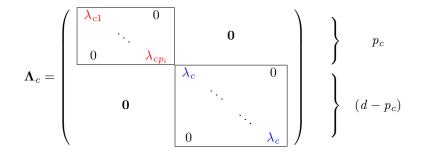
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#### Statistical model

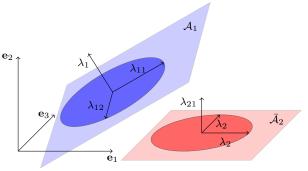
- Mixture model  $p(\mathbf{x}) = \sum_{c=1}^{C} \pi_c p(\mathbf{x}|c)$ ,
- $\blacksquare$  Under Gaussian assumption  $p(\mathbf{x}|c)$  is a d-dimensional Gaussian distribution

$$p(\mathbf{x}|c) = \frac{1}{(2\pi)^{d/2} |\mathbf{\Sigma}_c|^{1/2}} \exp\left(-\frac{1}{2} (\mathbf{x} - \boldsymbol{\mu}_c)^\top \mathbf{\Sigma}_c^{-1} (\mathbf{x} - \boldsymbol{\mu}_c)\right)$$

• Curse of dimensionality: special structure for the covariance matrix  $\mathbf{\Sigma}_c = \mathbf{Q}_c \mathbf{\Lambda}_c \mathbf{Q}_c^ op$ 



# High dimensional GMM [BGS07]



Under the HDDA model

$$\begin{split} \boldsymbol{\Sigma}_{i} &= \tilde{\mathbf{Q}}_{i} \tilde{\boldsymbol{\Lambda}}_{i} \tilde{\mathbf{Q}}_{i}^{\top} + \lambda_{i} \mathbf{I}_{d} \\ \boldsymbol{\Sigma}_{i}^{-1} &= \tilde{\mathbf{Q}}_{i} \tilde{\mathbf{V}}_{i} \tilde{\mathbf{Q}}_{i}^{\top} + \lambda_{i}^{-1} \mathbf{I}_{d} \end{split}$$

with  $\tilde{\mathbf{Q}}_i = \begin{bmatrix} \mathbf{q}_{i1}, \dots, \mathbf{q}_{ip_i} \end{bmatrix}$ ,  $\tilde{\mathbf{\Lambda}}_i = \operatorname{diag} \begin{bmatrix} \lambda_{i1} - \lambda_i, \dots, \lambda_{ip_i} - \lambda_i \end{bmatrix}$ ,  $\tilde{\mathbf{V}}_i = \operatorname{diag} \begin{bmatrix} \frac{1}{\lambda_{i1}} - \frac{1}{\lambda_i}, \dots, \frac{1}{\lambda_{ip_i}} - \frac{1}{\lambda_i} \end{bmatrix}$ and  $\mathbf{I}_d$  is the identity matrix of size d.

#### Spectral heterogeneity revisited 1/2

 $\blacksquare$  Samples covariance matrix for a given plot p

$$\mathbf{\Sigma}_p = \mathbf{B}_p + \mathbf{W}_p$$

where

•  $\mathbf{B}_p$  is the between class covariance matrix of plot p

$$\mathbf{B}_p = \sum_{c=1}^{C_p} \pi_{pc} (oldsymbol{\mu}_{pc} - oldsymbol{\mu}_p) (oldsymbol{\mu}_{pc} - oldsymbol{\mu}_p)^ op$$

W<sub>p</sub> is the within class covariance matrix of plot p

$$\mathbf{W}_p = \sum_{c=1}^{C_p} \pi_{pc} \mathbf{\Sigma}_{pc}$$

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# Spectral heterogeneity revisited 2/2

Trace(
$$\Sigma_p$$
) = Trace( $\mathbf{B}_p$ ) + Trace( $\mathbf{W}_p$ )  
Trace( $\mathbf{B}_p$ ) =  $\sum_{c=1}^{C_p} \pi_{pc} \|\boldsymbol{\mu}_{pc} - \boldsymbol{\mu}_p\|^2$   
Trace( $\mathbf{W}_p$ ) =  $\frac{1}{n_p} \sum_{i=1}^{C_p} \sum_{k \in c} \|\mathbf{x}_{pk} - \boldsymbol{\mu}_{pc}\|^2$ 

|        | $Trace(\boldsymbol{\Sigma}_p)$ | $Trace(\mathbf{B}_p)$ | $Trace(\mathbf{W}_p)$ |
|--------|--------------------------------|-----------------------|-----------------------|
| Plot 1 | 13.63                          | 0                     | 13.63                 |
| Plot 2 | 13.74                          | 12.71                 | 0.973                 |

#### Improved species richness

For each pixel of the plot, the vector of posterior probabilities is available

$$\left[p(C=1|\mathbf{x}),\ldots,p(C=C_p|\mathbf{x})\right]$$

The relative proportion is then computed as:

$$p_c = \frac{1}{n_p} \sum_{k \in c} p(C = c | \mathbf{x}) = \pi_c$$

It allows to let a pixel belonging to several clusters (not a crisp affectation)

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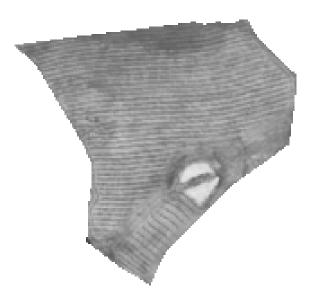
Primary results

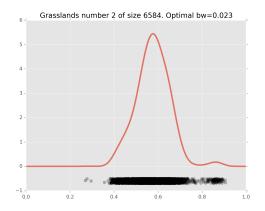
Conclusions and perspectives

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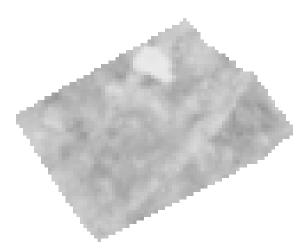
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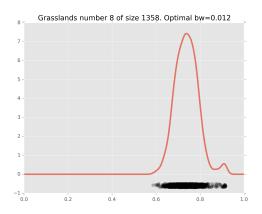
#### Data collection





#### Data collection

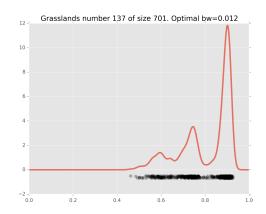




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### Data collection





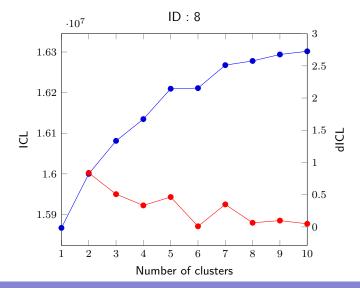
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|  | Experimental protocol |  |  |
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### Simulations

 $\blacksquare$  Select the number of classes using ICL: stop when dICL ${<}1\%$ 



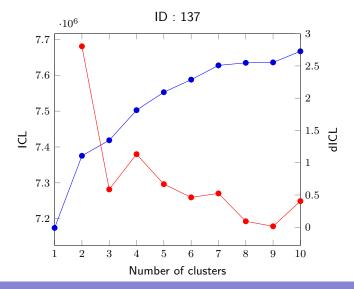
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|  | Experimental protocol |  |  |
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### Simulations

• Select the number of classes using ICL: stop when dICL < 1%



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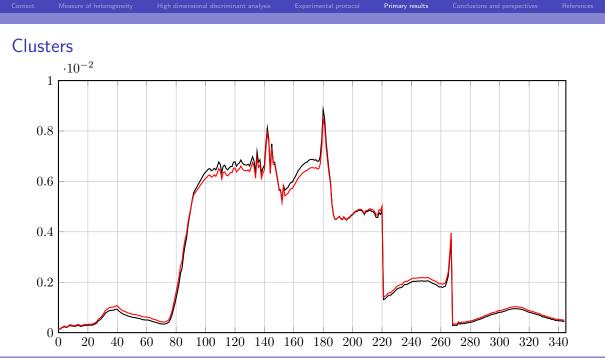
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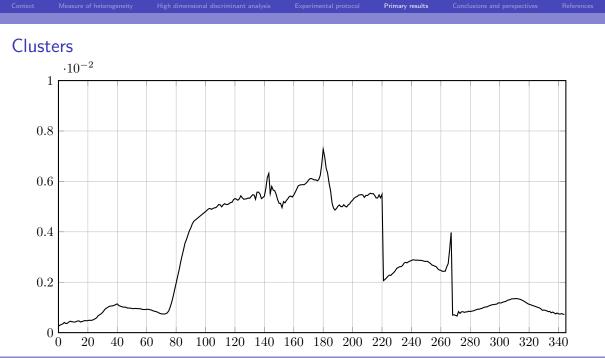
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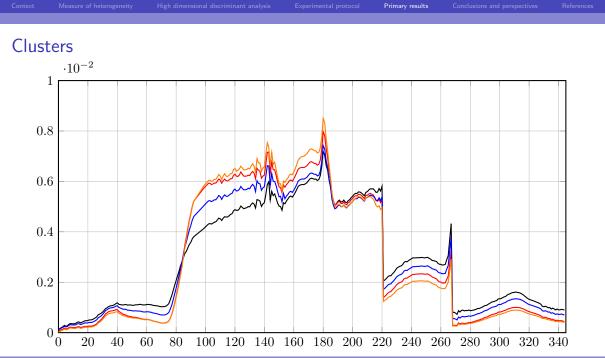
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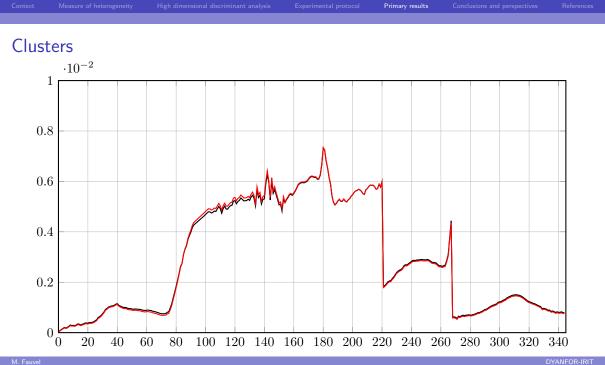


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#### M. Fauvel

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### Mesure of heterogeneity

| ID  | С | E    | В     | W     | V     | Н    | D    |
|-----|---|------|-------|-------|-------|------|------|
| 6   | 2 | 0.68 | 13.16 | 11.32 | 11.17 | 0.97 | 0.13 |
| 8   | 1 | 0.0  | inf   | 11.12 | 11.12 | 0.09 | 3.81 |
| 137 | 4 | 1.31 | 10.36 | 10.97 | 9.93  | 0.08 | 3.97 |
| 143 | 2 | 0.68 | 15.02 | 11.57 | 11.54 | 0.04 | 5.06 |

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Species diversity in semi-natural grasslands

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#### Conclusions and perspectives

- Species diversity in semi-natural grasslands
- Extension of heterogeneity measures with high dimensional clustering techniques

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- Species diversity in semi-natural grasslands
- Extension of heterogeneity measures with high dimensional clustering techniques
- Estimated diversity does not correlated (yet!) with field work

### Bibliography I

Bouveyron, Charles, Stephane Girard, and Cordelia Schmid. "High-Dimensional Data Clustering". In: Computational Statistics and Data Analysis 52.1 (Sept. 2007), pp. 502–519. DOI: 10.1016/j.csda.2007.02.009. URL: https://hal.archives-ouvertes.fr/hal-00022183. Féret, Jean-Baptiste and Gregory P Asner. "Mapping tropical forest canopy diversity using high-fidelity imaging spectroscopy". In: Ecological Applications 24.6 (2014), pp. 1289–1296. O'Mara, F. P. "The role of grasslands in food security and climate change". In: Annals of Botany 110.6 (2012), p. 1263. DOI: 10.1093/aob/mcs209. eprint: /oup/backfile/Content public/Journal/aob/110/6/10.1093/aob/mcs209/2/mcs209.pdf. URL: +%20http://dx.doi.org/10.1093/aob/mcs209. Palmer, Michael W. et al. "Quantitative tools for perfecting species lists". In: Environmetrics 13.2 (2002), pp. 121-137. ISSN: 1099-095X. DOI: 10.1002/env.516. URL: http://dx.doi.org/10.1002/env.516. Rocchini, Duccio et al. "Satellite remote sensing to monitor species diversity: potential and pitfalls". In: Remote Sensing in Ecology and Conservation 2.1 (2016), pp. 25–36. ISSN: 2056-3485. DOI:

10.1002/rse2.9. URL: http://dx.doi.org/10.1002/rse2.9.

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