Introduction	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions	Conclusion	References
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Beyond the search of ideal typical sequences Analyzing, interpreting and visualizing relationships between sequences and explanatory factors using discrepancy analysis

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Lausanne Conference on Sequence Analysis (LaCOSA), Lausanne, 6<sup>th</sup> of June 2012

Introduction	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions	Conclusion	References
00	00000000	00000	00000	0	00	

# Outline

#### Introduction

- Objectives
- Example problematic
- 2 Cluster-based strategy
  - Clustering
  - Testing differences between groups of trajectories
- Oiscrepancy analysis
  - Introduction
- Interpreting the differences
  - Interpreting differences
  - Implicative Statistics
  - Residual gains
- 5 Extensions
  - Regression trees
- 6 Conclusion
  - Conclusion



Introduction ●○	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Object	tives					

- Studying the relationships between trajectories and explanatory factors.
  - Sex and academic carrier.
  - Cohort and familial trajectory.
  - Social origin and sequence of school to work transitions.
- Multifactor approach.
  - Sex, horizontal segregation and academic carrier.

Objectives of the presentation:

- The usual cluster-based strategy.
- The discrepancy analysis framework.
- Present new tools to interpret the results.

Introduction ●○	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Object	tives					

- Studying the relationships between trajectories and explanatory factors.
  - Sex and academic carrier.
  - Cohort and familial trajectory.
  - Social origin and sequence of school to work transitions.

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- Multifactor approach.
  - Sex, horizontal segregation and academic carrier.

Objectives of the presentation:

- The usual cluster-based strategy.
- The discrepancy analysis framework.
- Present new tools to interpret the results.

Introduction ○●	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Examp	ole problema	atic				

- Study of sequences of school-to-work transitions in North Irland by McVicar and Anyadike-Danes (2002).
- Focus on father unemployment: do we observe some kind of joblessness transmission?
- Sequences begin at the end of compulsory school.
- Length: 70 months.
- Alphabet (states): EM (Employment), FE (Further Education), HE (Higher Education), JL (Joblessness), SC (School), TR (Training).

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Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
<b>•</b> ••						

# Outline

#### Introduction

- Objectives
- Example problematic
- 2 Cluster-based strategy
  - Clustering
  - Testing differences between groups of trajectories
- Oiscrepancy analysis
  - Introduction
- Interpreting the differences
  - Interpreting differences
  - Implicative Statistics
  - Residual gains
- 5 Extensions
  - Regression trees
- 6 Conclusion
  - Conclusion





- Start by building a typology of the sequences using cluster analysis.
- Keep three groups (best Average Silhouette Width=0.41).



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Comparing groups of sequences: father unemployment

• To test if the trajectories differ according to father unemployment status...



We test this:



• Chi-square p-value:  $1.939 \times 10^{-6}$ , Cramer's v: 0.192





### No relationships with the test factor ?

- To test if the trajectories differ according to the test factor...
- The test factor was artificially built using an MDS.



• We test this:



• Chi-square p-value: 0.999, Cramer's v: 0.002



Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
What'	s the proble	em?				

- The clustering is a simplification of the sequences.
- By using the typology in the chi-square test, implicit assumptions are made:
  - The typology carries enough information to describe all the differences between sequences.
  - I.e. The sequences in each groups are all equals.
  - The groups are equally different.
- But the "test" covariate explains the differences of sequences inside each groups.

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• In this case, the simplification is abusive.

Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References		
Clustering and test factor								

- Clustering and test factor
  - Example: difference inside cluster "Higher Education" according to test factor.
  - All sequences are not equals in this cluster!
  - The same applies to the other clusters.



Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
What'	s the proble	em?				

- These assumptions may be correct if:
  - If the clusters are very homogeneous.
  - And if the clusters are clearly separated from each other.
- Otherwise, this simplification may hide or create an association with a covariate.



Introduction 00	Cluster-based strategy ○○○○○●○○	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Sociol	ogical assur	nptions				

- We assign to each individual sequence an ideal-type of sequences.
- The difference between the individual sequence and the ideal-type is ignored.
- Justification:
  - The sequence are realization of well defined ideal-types (common patterns) of sequences (Abbott and Forrest, 1986).
  - I.e. The sequence were generated following a well defined model (common pattern) of trajectories.
  - The small differences between individual sequence and common pattern can be ignored because:
  - These common patterns (models) were correctly identified by the cluster analysis.
  - Intra-cluster variability is a kind of uninformative error term.

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• These are rather strong assumptions!

Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References	
Sociological assumptions							

Link to complexity of sequential models (Abbott, 1992).

- Natural histories.
  - Sequences are strongly structured.
  - Example: sequence of compulsory schooling.
  - Cluster based strategy may be ok.
  - But what if small accidents (repeating a grade) only happen to those from a peculiar social origin?

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- More complexes trajectories.
  - Lot of different trajectories.
  - Some sequences are often between two ideal-types.
  - These assumptions are too strong.

Introduction 00	Cluster-based strategy ○○○○○○○●	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
Why ι	ising cluster	r analysis?				

- Cluster analysis is a *descriptive* method.
  - Find some common patterns that may results from social, legal or economical constraints on trajectories.
  - Identify the main common patterns that may act as models of trajectories (Abbott and Hrycak, 1990).
  - Common patterns may highlight dependencies between different moment in the trajectories.
- These kind of interpretations are powerful and can be done using cluster analysis.
- The problematic assumptions are made when the typology is used in an explanatory analysis.

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Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Outlin	e					

#### Introduction

- Objectives
- Example problematic
- 2 Cluster-based strategy
  - Clustering
  - Testing differences between groups of trajectories

#### Oiscrepancy analysis

- Introduction
- Interpreting the differences
  - Interpreting differences
  - Implicative Statistics
  - Residual gains

## 5 Extensions

Regression trees

### 6 Conclusion

Conclusion





• Aim: study the relationships between states sequences and explanatory variables without prior clustering.



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Introduction 00	Cluster-based strategy	Discrepancy analysis 0000	Interpreting the differences	Extensions 0	Conclusion 00	References
Genera	al principles					

• Define a measure of the discrepancy of the sequences based on the distance matrix.

$$s^{2} = \frac{1}{n^{2}} \sum_{i=1}^{n} \sum_{j=i+1}^{n} (y_{i} - y_{j})^{2} = \frac{1}{n^{2}} \sum_{i=1}^{n} \sum_{j=i+1}^{n} d_{ij}$$

- Measure the strength of the relationship using the share of the total discrepancy that is explained by this covariate.
- Attest the significance of the relationship using permutation tests.
- This method is a generalization of the ANOVA.
- The method can be extended to
  - Include several covariates at the same time (control for the effect of other covariates).

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Build regression trees.

Introduction	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions	Conclusion	References
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### Discrepancy Analysis Results

	F	$R^2$	<i>p</i> -value
test	71.56	0.092	0.000
funemp	9.51	0.013	0.000

With discrepancy analysis, we can measure:

- The strength of the relationship with the  $R^2$ .
- The statistical significance using permutation tests.

Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Under						

- Main sequence analysis are preserved because of the use of distance.
- Holistic view (Abbott, 1992)
  - Highlight the endogenous dynamic (logic) of trajectories (enchainment).
  - Analyze the order of sequences (order).
- Relationships between sequences and exploratory factors.
  - Effect of exogenous condition on endogenous logic.
  - Trajectories are shaped by social and/or historic context (Elder, 1999).
- Focus on discrepancy:
  - Preserve the notion of inter-individual variability of the individual within these context.
  - Inside that context individual are able to make choices (Elder, 1999).

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Introduction	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions	Conclusion	References
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## When use discrepancy analysis?

- If there is an interest in the effect of exogenous factors.
- More complex sequential models.
- For instance, we may think that:
  - Some contexts influence the beginning of the trajectories.
  - Others influence the end.
  - People are inserted in many different contexts that influence, each on its own way, the trajectories.

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- This leads to a large amount of individual trajectories.
- Using discrepancy analysis, less assumptions are made!

Introduction	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions	Conclusion	References
00	00000000	00000	00000	0	00	

# Outline

#### Introduction

- Objectives
- Example problematic
- 2 Cluster-based strategy
  - Clustering
  - Testing differences between groups of trajectories
- Oiscrepancy analysis
  - Introduction

### Interpreting the differences

- Interpreting differences
- Implicative Statistics
- Residual gains

### 5 Extensions

Regression trees

### 6 Conclusion

Conclusion



Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
Interpreting differences						

- The sequences are significantly different according to father unemployment.
  - What does this mean?
  - What are the differences?

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Introdu 00	ction	Cluster-b	ased stra	tegy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
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### Implicative Statistic

- Aim: Measure the relevance of the rule "*C* implies  $A_t$ " (Gras, 1979).
- Let C be one of the category of the explanatory variable.
- Let  $A_t$  denote being in state A at time t
- In each plot *C*, we represent the evolution of the relevance of the rule "*C* implies *A<sub>t</sub>*".



Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
Implic	ative Statis	tic				

- This plot makes the interpretation easier.
- Highlights the most important differences in occupied states.
- Similar to distribution plot (chronogram), it is a sequence of transversal characteristics.
- We loose all longitudinal information!
- Are there patterns that differ according to father unemployment?



Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Residual gain						

- Residual gain: Gain for each sequences to take an explanatory factor into account.
- Residual gain are computed from discrepancy analysis.
- Plot of the sequences sorted according to residual gains.
- Sequences at the bottom are the most typical of each profile (highest gain).



Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
Residu	ial gain					

- Interpretation: tendencies to follow the kind of sequences that have the highest gains.
- Possible extensions:
  - Multifactor analysis: regression like interpretation of the effect (proper effect).

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- Tree structured analysis.
- Residual gain allows to visualize the relationships between explanatory factors and sequences.

Introduction	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions	Conclusion	References
00	00000000	00000	00000	0	00	

# Outline

#### Introduction

- Objectives
- Example problematic
- 2 Cluster-based strategy
  - Clustering
  - Testing differences between groups of trajectories
- Oiscrepancy analysis
  - Introduction
- Interpreting the differences
  - Interpreting differences
  - Implicative Statistics
  - Residual gains

## 5 Extensions

Regression trees

### 6 Conclusion

Conclusion



Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions •	Conclusion 00	References	
Pograssian tracs							







Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion	References

# Outline

#### Introduction

- Objectives
- Example problematic
- 2 Cluster-based strategy
  - Clustering
  - Testing differences between groups of trajectories
- Oiscrepancy analysis
  - Introduction
- Interpreting the differences
  - Interpreting differences
  - Implicative Statistics
  - Residual gains
- 5 Extensions
  - Regression trees
- 6 Conclusion
  - Conclusion

Introductio 00	n Cluster-based strategy 00000000	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion ••	References	
Conc	lusion I						

- Cluster analysis.
  - Descriptive analysis.
  - Problematic assumptions in explanatory analysis.
- With discrepancy analysis, we can estimate:
  - The strength of the relationship with the  $R^2$ .
  - The statistical significance using permutation tests.
- The test are much more powerful than the one computed using clusters.
- Analyze directly the links between the trajectories and the covariates.
- Brings an explanatory framework in sequences analysis.
- Preserve the inter-individual variability of the trajectories while studying the relationships between the trajectories and their contexts.

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Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion ••	References
Conclu	usion II					

- Tools to interpret the relationship.
  - Implicative statistic plots.
  - Residual gain plots.



Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
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Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
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A D M A

Introduction 00	Cluster-based strategy	Discrepancy analysis 00000	Interpreting the differences	Extensions 0	Conclusion 00	References
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Introduction 00	Cluster-based strategy	Discrepancy analysis	Interpreting the differences	Extensions 0	Conclusion 00	References
Refere	nces IV					

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## Mathematical developments

- Using MANOVA, we can write (McArdle and Anderson, 2001).
- $tr(\mathbf{Y'Y}) = tr(\widehat{\mathbf{Y}'}\widehat{\mathbf{Y}}) + tr(\mathbf{R'R})$
- Which can be rewritten (McArdle and Anderson, 2001):
- $tr(\mathbf{Y}\mathbf{Y}') = tr(\mathbf{H}\mathbf{Y}\mathbf{Y}') + tr[(\mathbf{I} \mathbf{H})\mathbf{Y}\mathbf{Y}']$
- Let **Y**, a  $n \times q$  matrix of q centered variables.
- **YY**' = **G** (Gower, 1966, 1982).
- $G = -\frac{1}{2}(I \frac{1}{n}\mathbf{11'})D^2(I \frac{1}{n}\mathbf{11'})$
- By replacing **D**<sup>2</sup> by another distance measure, we get the discrepancy analysis framework.

## Mathematical developments

- Using MANOVA, we can write (McArdle and Anderson, 2001).
- $tr(\mathbf{Y'Y}) = tr(\widehat{\mathbf{Y}'}\widehat{\mathbf{Y}}) + tr(\mathbf{R'R})$
- Which can be rewritten (McArdle and Anderson, 2001):
- $tr(\mathbf{Y}\mathbf{Y}') = tr(\mathbf{H}\mathbf{Y}\mathbf{Y}') + tr[(\mathbf{I} \mathbf{H})\mathbf{Y}\mathbf{Y}']$
- Let **Y**, a  $n \times q$  matrix of q centered variables.
- **YY**' = **G** (Gower, 1966, 1982).
- $\mathbf{G} = -\frac{1}{2}(\mathbf{I} \frac{1}{n}\mathbf{11'})\mathbf{D^2}(\mathbf{I} \frac{1}{n}\mathbf{11'})$
- By replacing **D**<sup>2</sup> by another distance measure, we get the discrepancy analysis framework.

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## Mathematical developments II

$SS_T = SS_B + SS_W$	(1)
With:	
$SS_T = tr(\mathbf{G})$	(2)
$SS_B = tr(\mathbf{HG})$	(3)
$SS_W = tr[(\mathbf{I} - \mathbf{H})\mathbf{G}]$	(4)
	(5)

- Diagonal element of **G** are residuals of the null model.
- Diagonal element of (I H)G are residuals of the fitted model.
- Residual interpreted as distance to the center of class.
- Diagonal of -HG are the gains in term of residual if we use a given explanatory covariate.