

Franz Manni

# Some applications of linguistic research in human population genetics and vice versa.

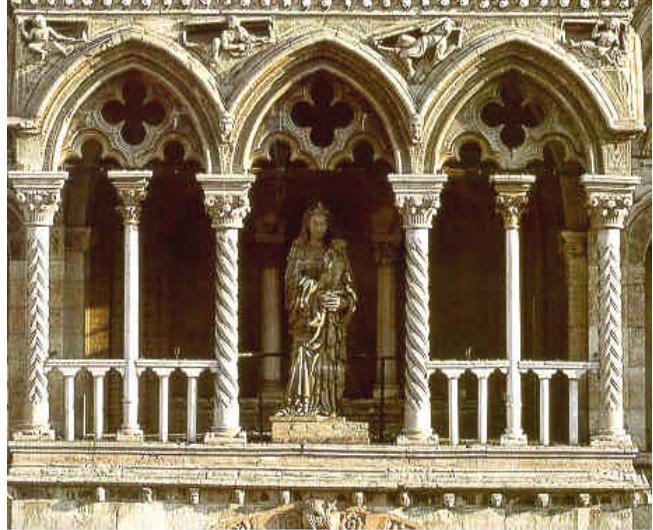
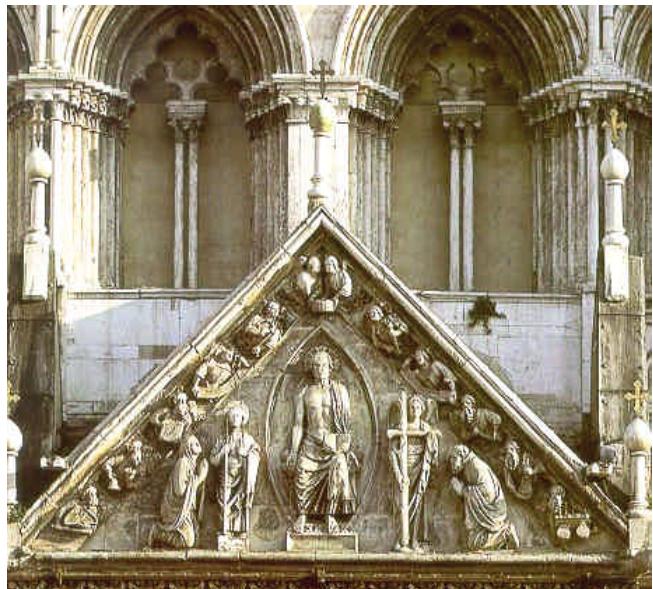
Musée de l'Homme

National Museum of Natural History, Paris, France

[manni@mnhn.fr](mailto:manni@mnhn.fr)

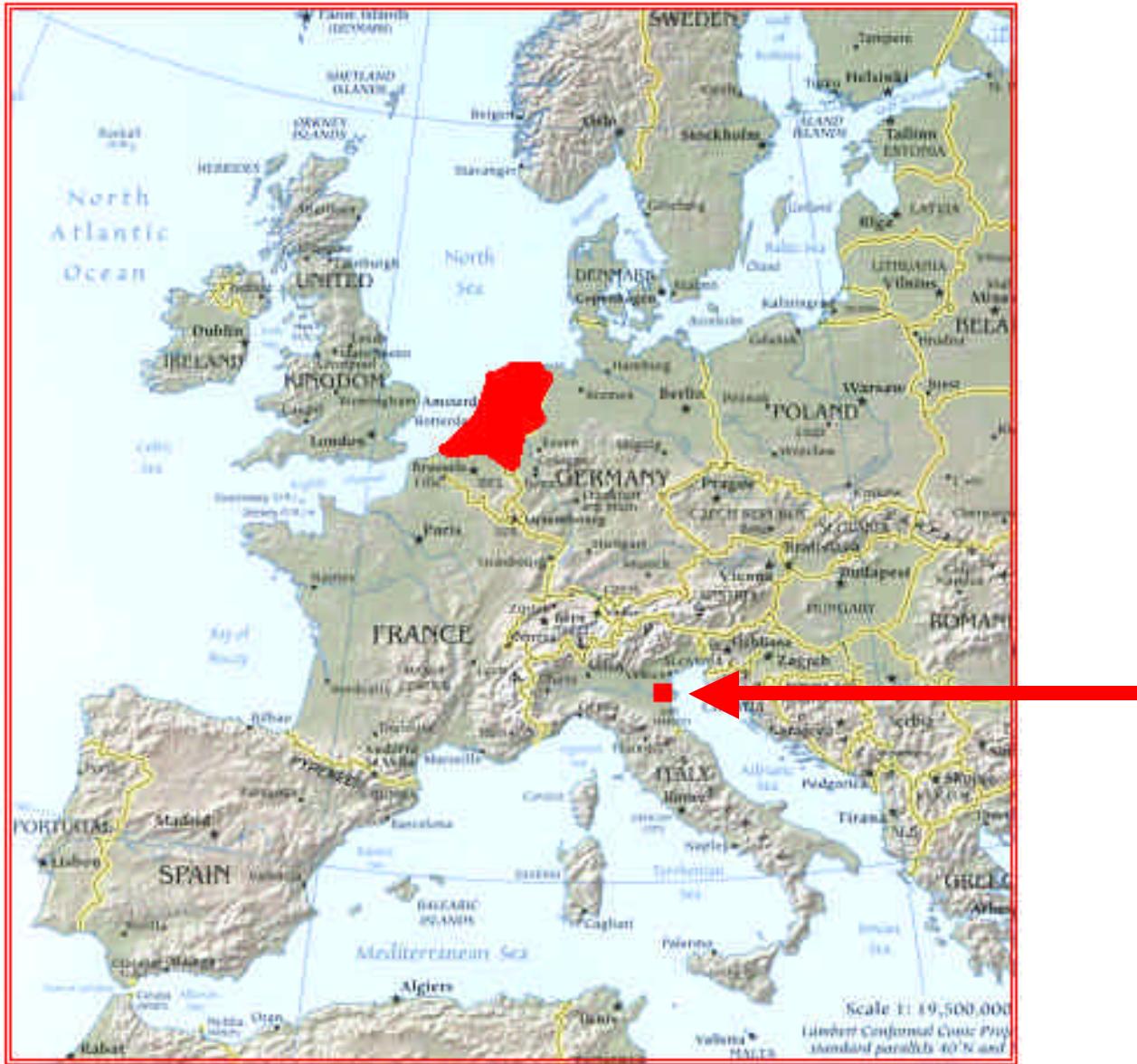


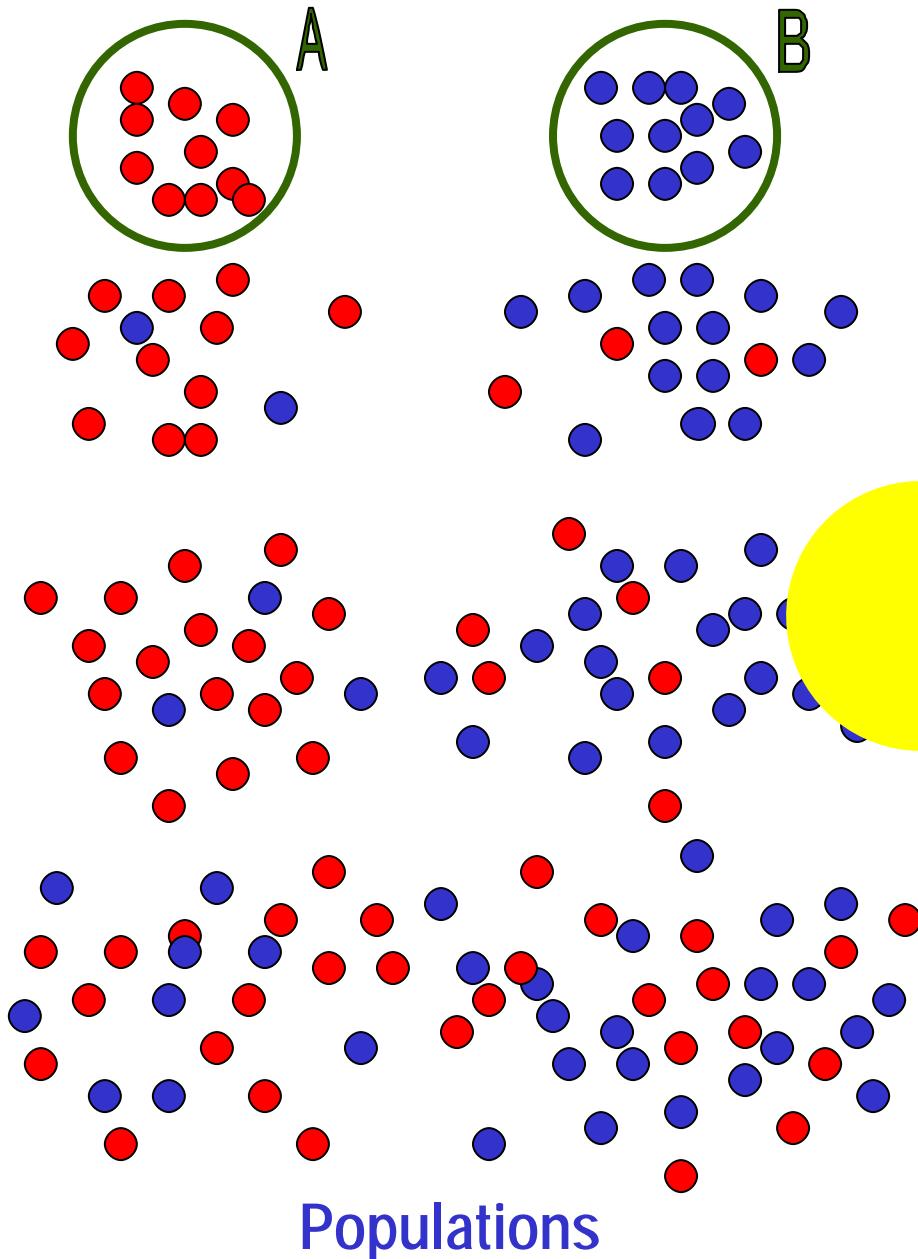
Fifth workshop of the *Netwerk Naamkunde*: family names  
*The Hague, Friday 10 October 2008*





*Cosmé Tura*





Human population genetics

Ancient times

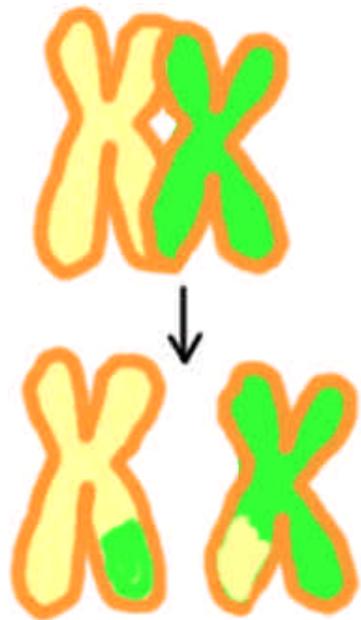
Mutation  
Selection  
Migration  
Drift

P r e s e n t

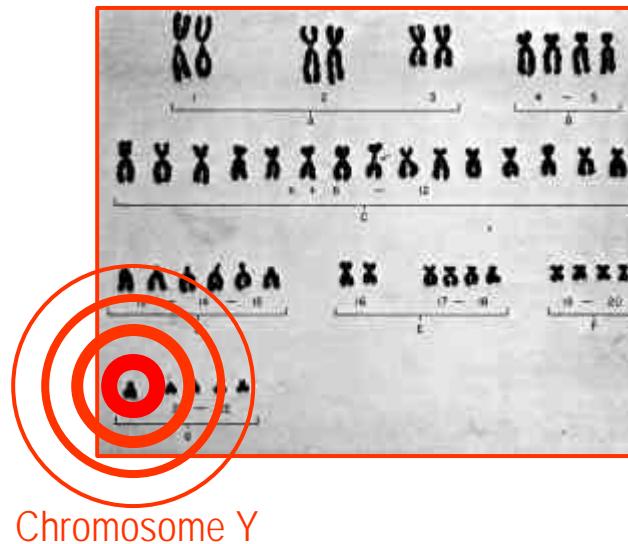
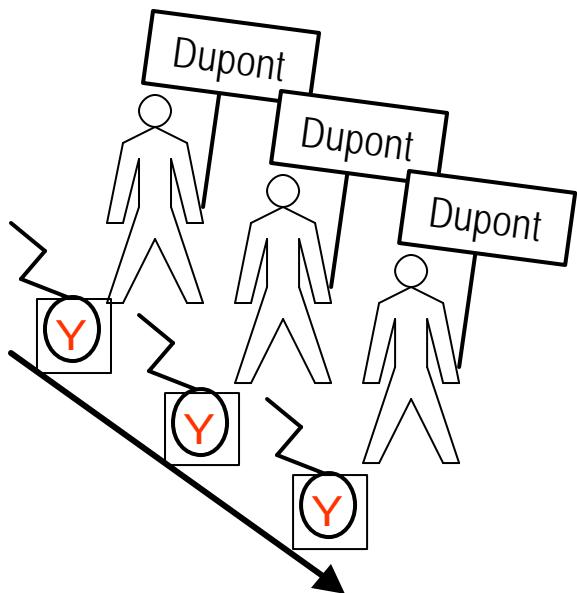
My starting point were the surnames

Surnames are a way to look at the variability of the Y-chromosome

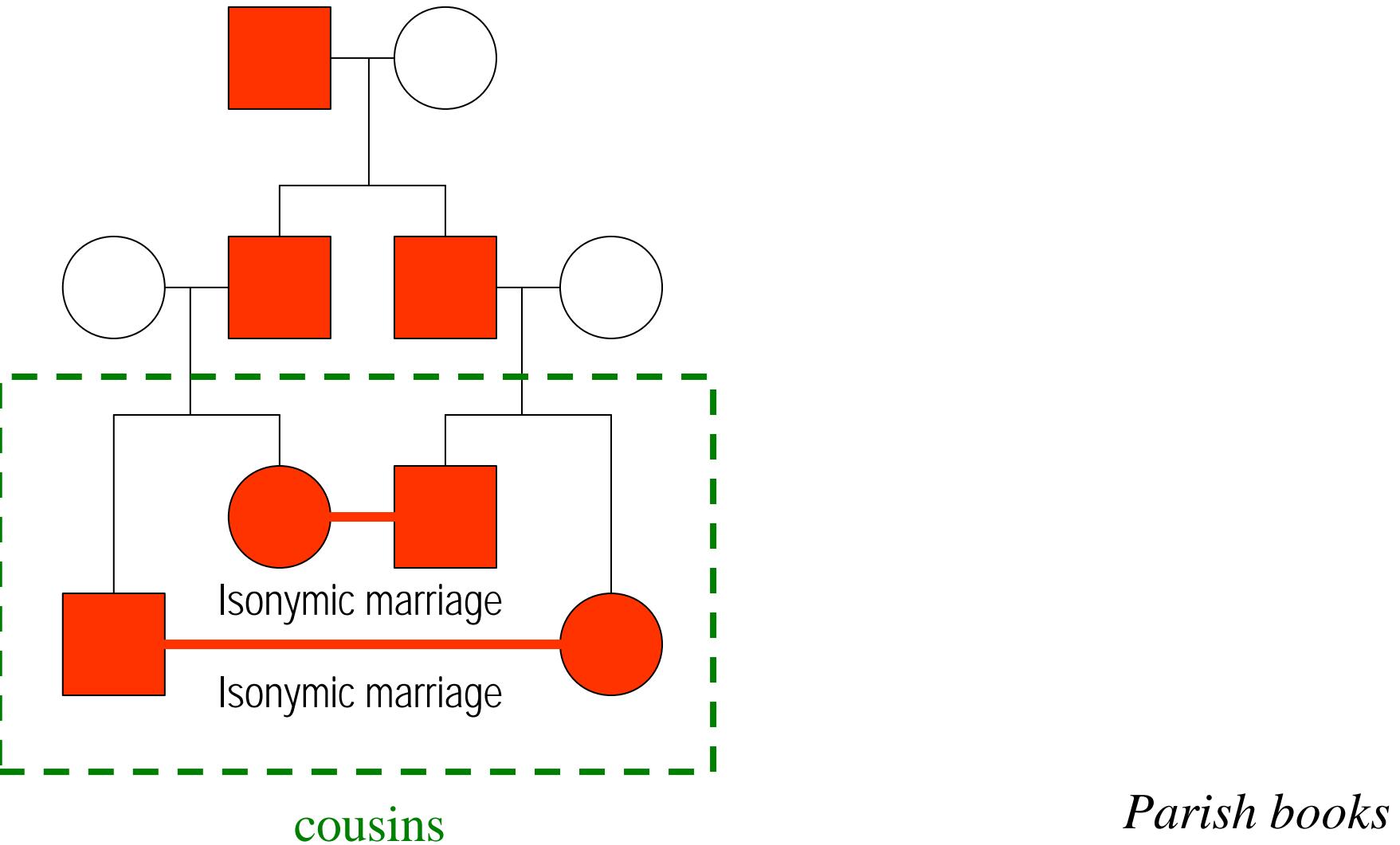
Recombinant



Non Recombinant



# From surnames to consanguinity: The definition of Isonymy



# The definition of Isonomy

The real estimation of isonymy can be computed only from real genealogies

When focusing on huge populations it is extremely difficult to have all the genealogies of the populations and, even when possible, their study requires years.

A WAY-OUT is estimate the levels of isomymy by a probabilistic model, assuming that the husband/wife is not selected according to his surname (Assumption: *I fall in love with someone whatever his/her surname*).

From the distribution of surnames we can estimate the probability of isonymic marriages:

Location A: 10 «Nerbonne» over 100 inhabitants

Location B: 25 «Nerbonne» over 100 inhabitants

$$\text{Isonomy (A)}_{\text{Nerbonne}} = 10\% \times 10\% = 0.01$$

$$\text{Isonomy (B)}_{\text{Nerbonne}} = 25\% \times 25\% = 0.0625$$

$$\text{Isonomy (AB)}_{\text{Nerbonne}} = 10\% \times 25\% = 0.025$$

*Lasker distance:*

$$S_{n_{si}} n_{sj} / 2 S_{n_{si}} S_{n_{sj}}$$

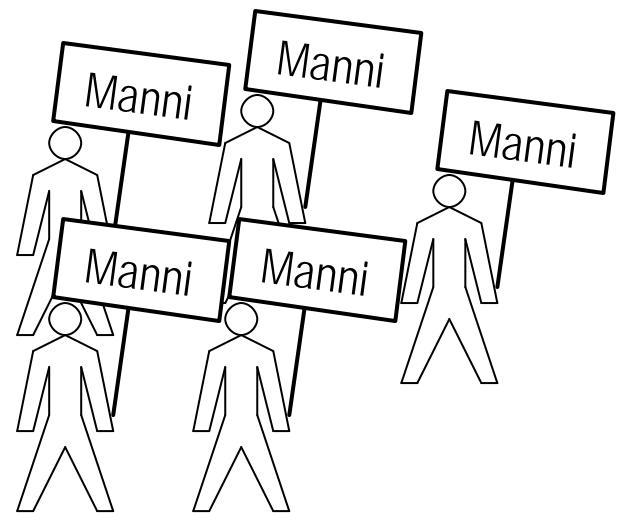
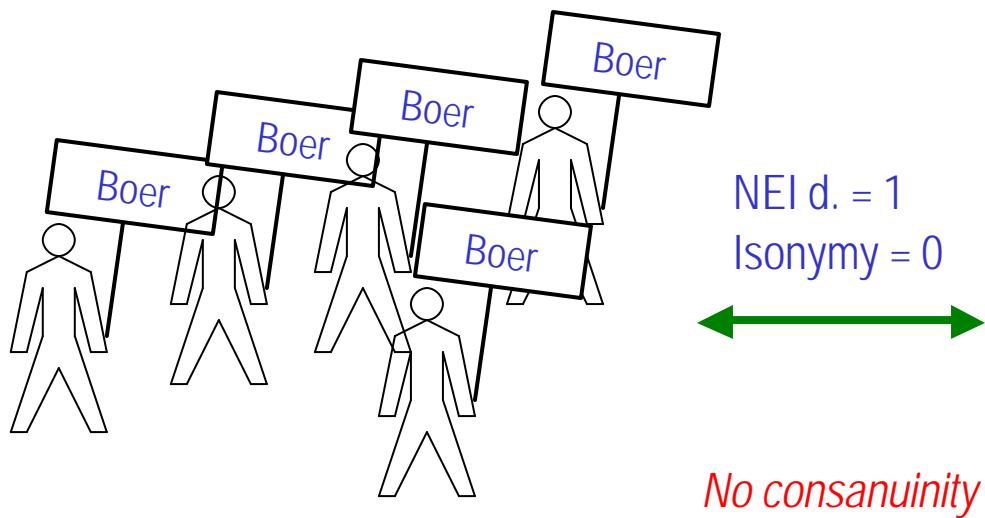
*Nei distance:*

$$S_{n_{si}} n_{sj} / (S_{n_{si}}^2 S_{n_{sj}}^2)^{\frac{1}{2}}$$

# Isonomy and the Netherlands: Nei distance

$$S\mathbf{n}_{si}n_{sj} / (S\mathbf{n}_{si}^2 S\mathbf{n}_{sj}^2)^{1/2}$$

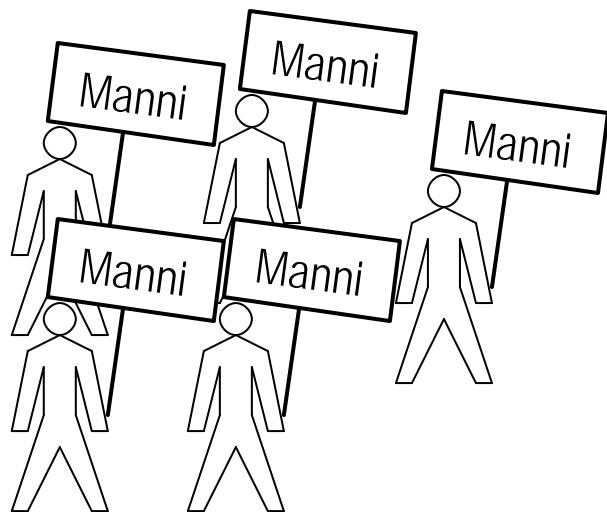
If the two locations have completely different surnames their distance will be **1**, while if they share the same set of surnames with identical relative frequencies their distance will be **null**.



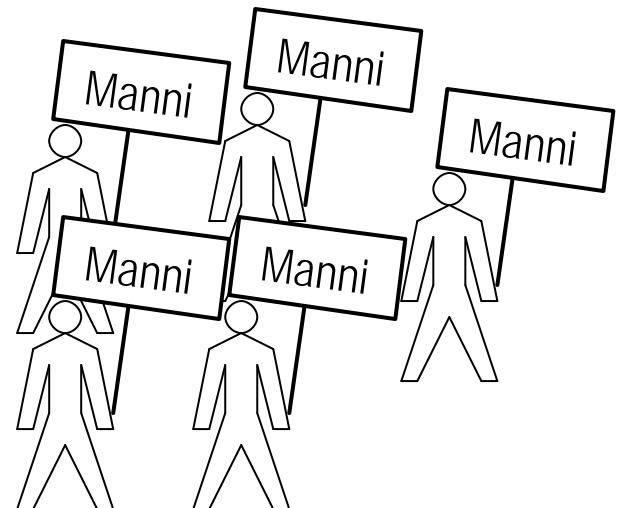
## The reverse of isonymy: Nei distance

$$S_{n_{si} n_{sj}} / (S_{n_{si}}^2 S_{n_{sj}}^2)^{1/2}$$

If the two locations have completely different surnames their distance will be **1**, while if they share the same set of surnames with identical relative frequencies their distance will be **null**.



NEI d. = 0  
Isonomy = 1  
 *HIGH consanguinity*



## Isonomy : Nei distance

Surname differentiation can be computed, according to NEI as:

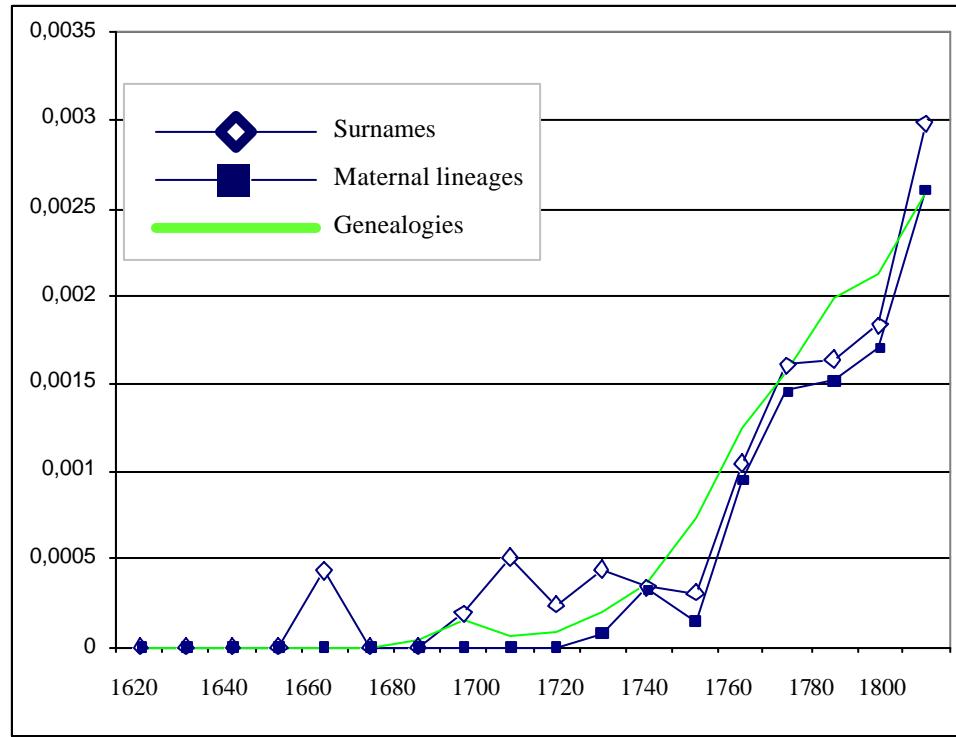
$$S\text{N}_{si} n_{sj} / (S\text{N}_{si}^2 S\text{N}_{sj}^2)^{1/2}$$

where  $n_{sj}$  denotes the frequency of a given surname  $s$  in locations  $i$  while  $n_{sj}$  denotes the frequency of the same surname in location  $j$ .

The sums are done for all surnames

By applying the formula to a surname distributions (list of surnames and their relative frequency) of all the places under study it is possible to a pairwise distance matrix accounting for the similarity of surnames in different places.

# Surnames enable the estimation of consanguinity (Isonymy)



**Alain Gagnon and Bruno Toupance (2002).**

Testing isonymy with paternal and maternal lineages in the early Québec population: the impact of polyphyletism and demographic differentials.

*Am. J. Phys. Anthropol.*

# Isonomy and the Netherlands

HOLLANDE - ILES DE MARKEN -

TYPES ET VETEMENTS

GU 0-51-2543 - 369

EV. 137.12



# The Netherlands

**Surnames** (from 1997 telephone book):

226 sample points (Manni *et al.* 2005)

2,400,000 telephone users



# The Netherlands

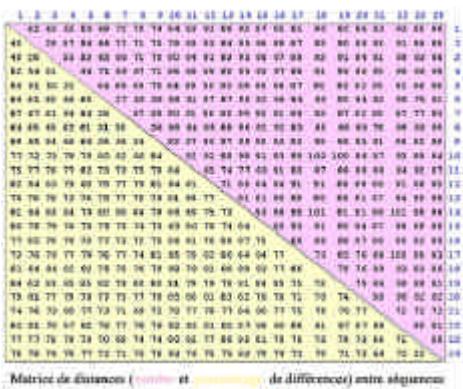
Surnames (from 1997 telephone book):

226 sample points (Manni *et al.* 2005)

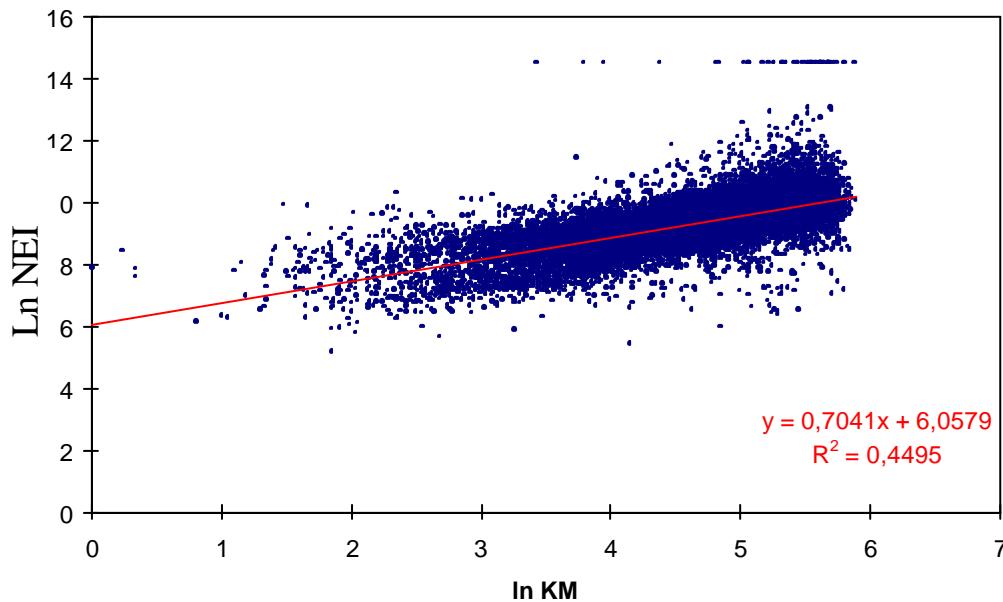
2,400,000 telephone users



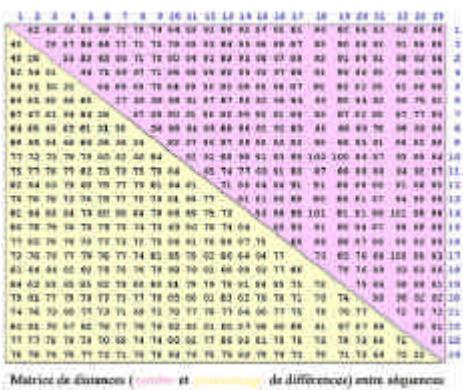
## Multidimensional plot of surname pair-wise distances: Nei



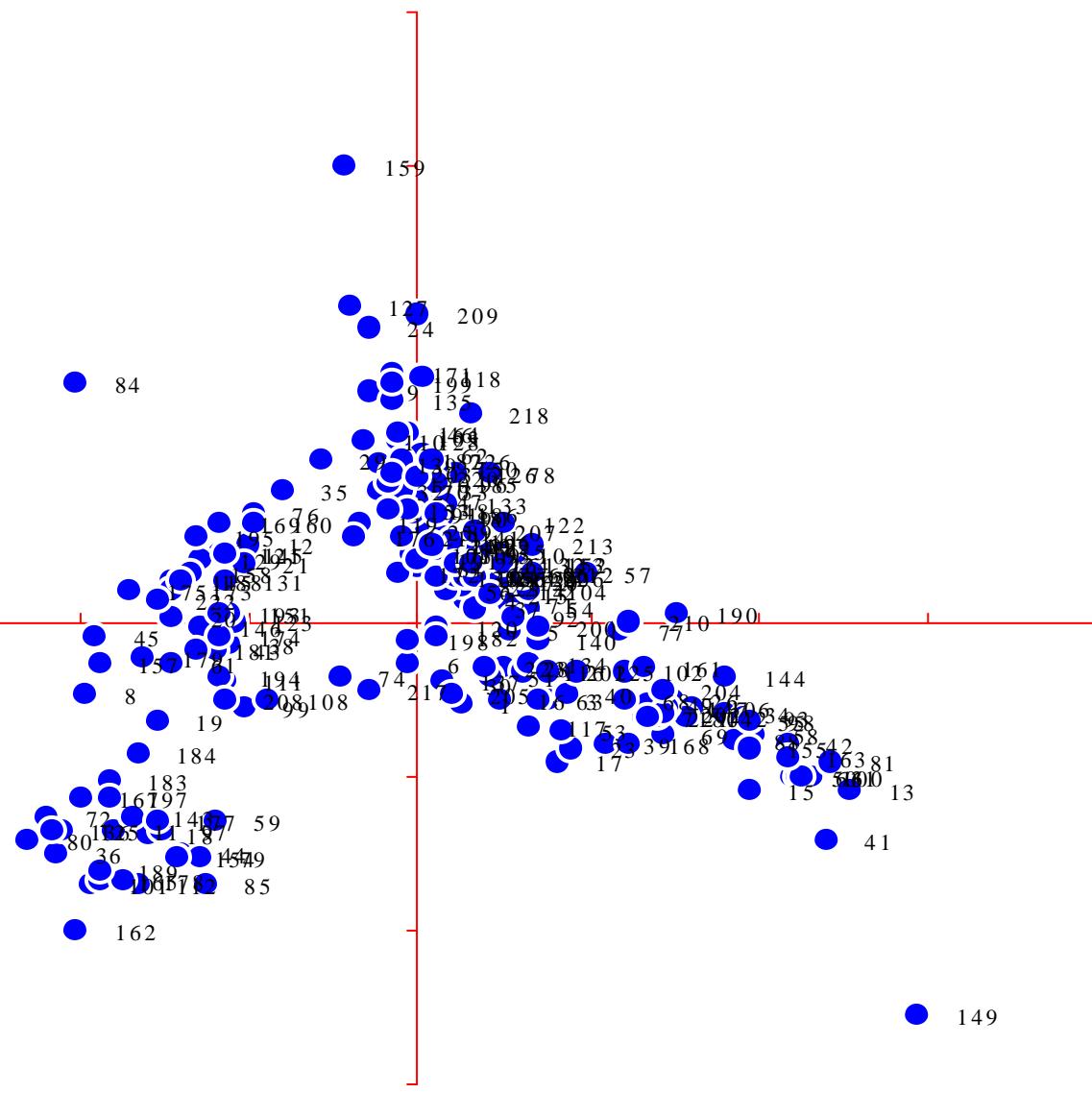
In KM vs Jasker10100 226



# Isonimy and the Netherlands: Nei distance

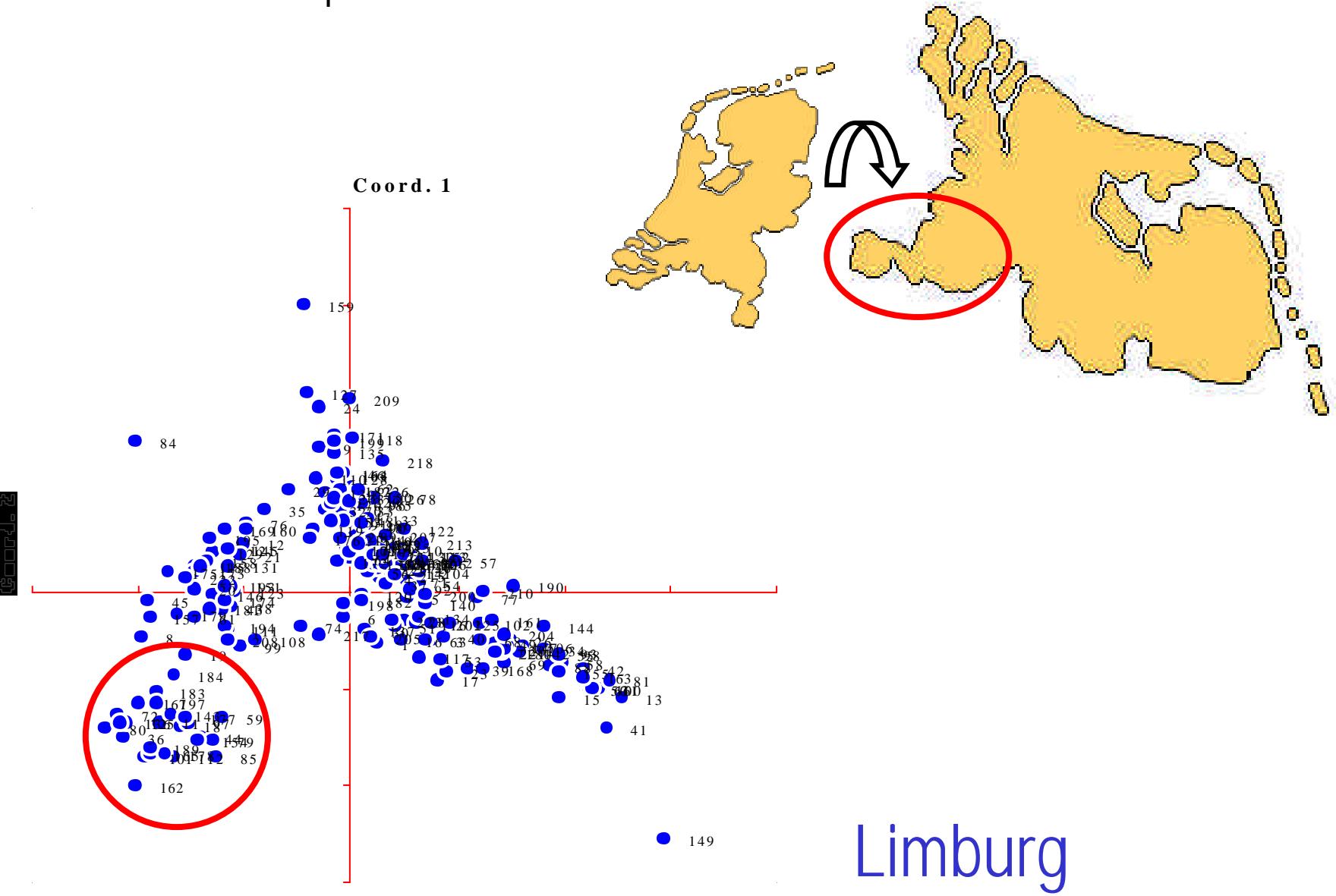


# MATRIX

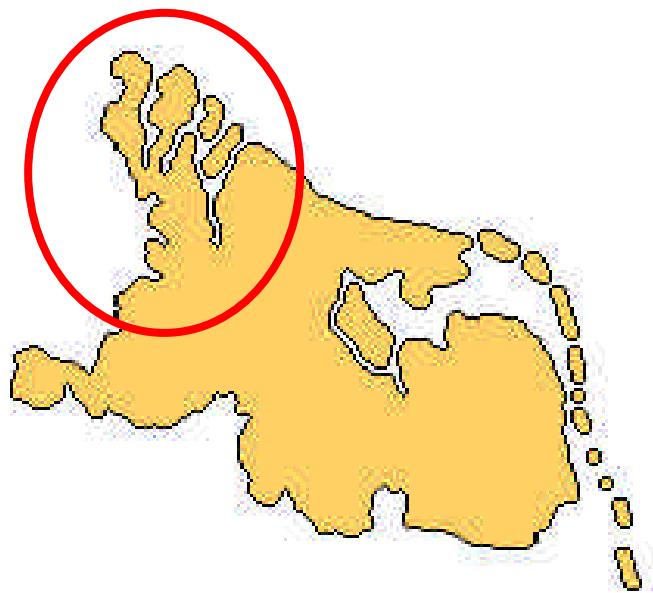
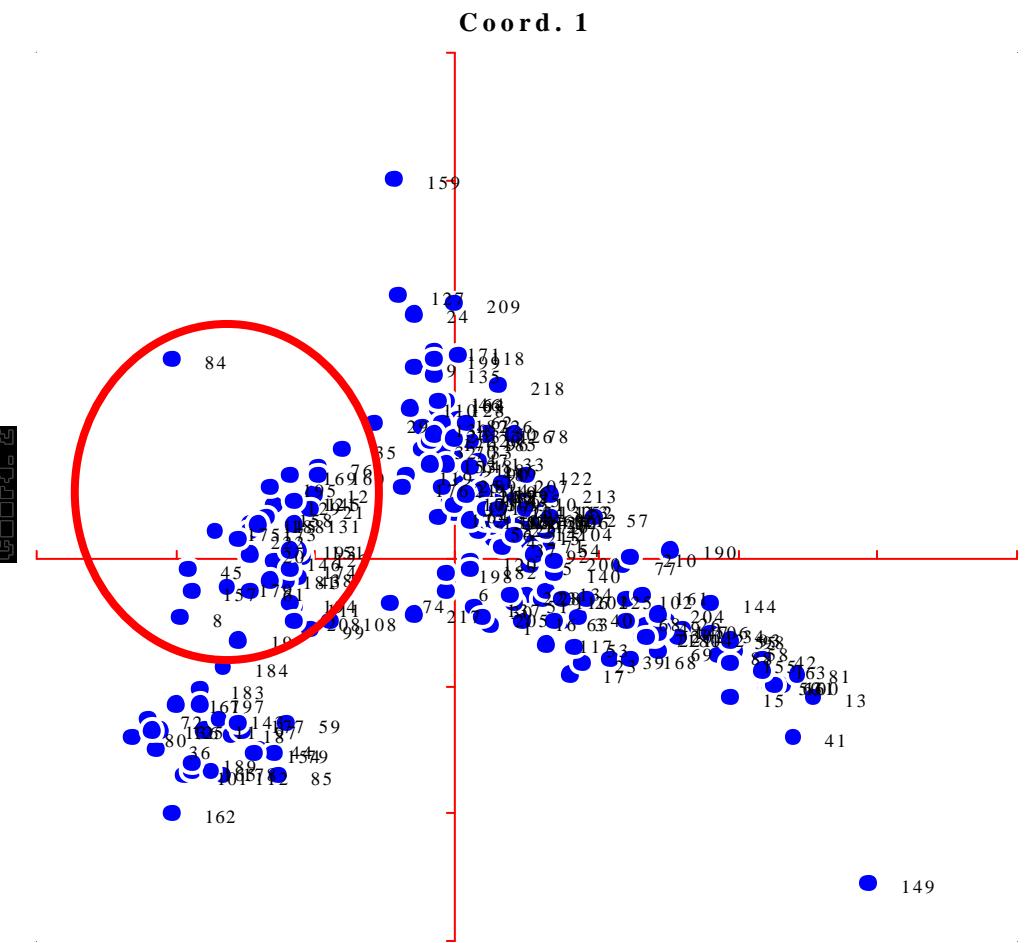


# MULTIDIMENSIONAL SCALING

# Multidimensional plot os surname distances

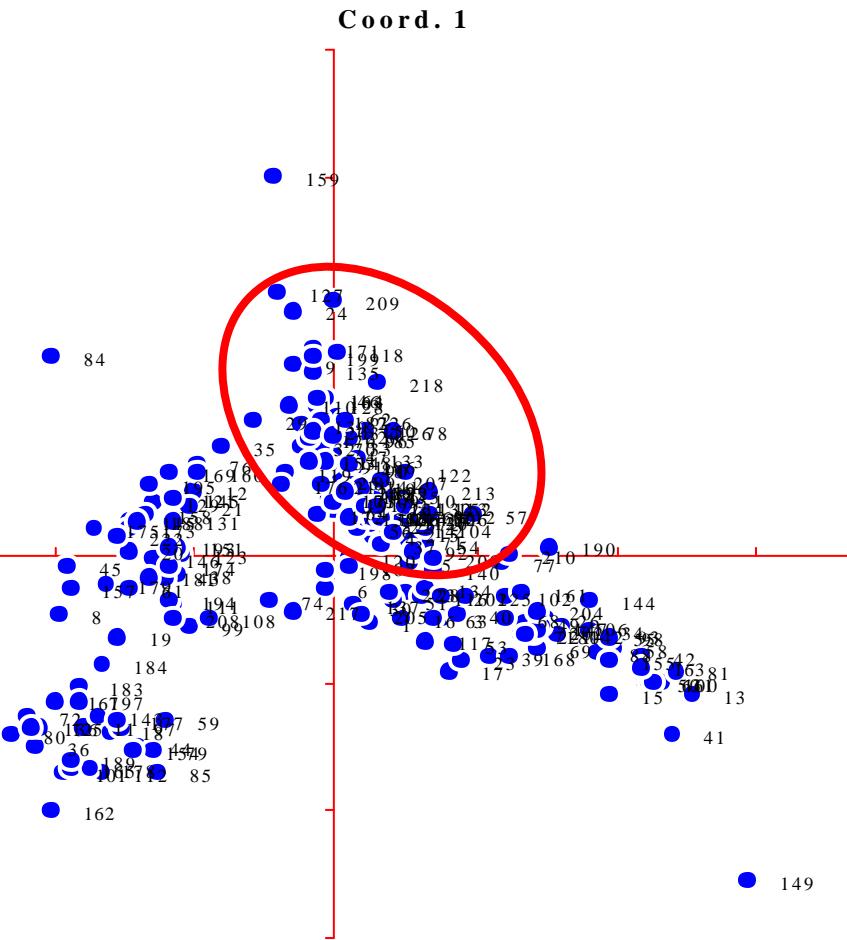


# Multidimensional plot os surname distances



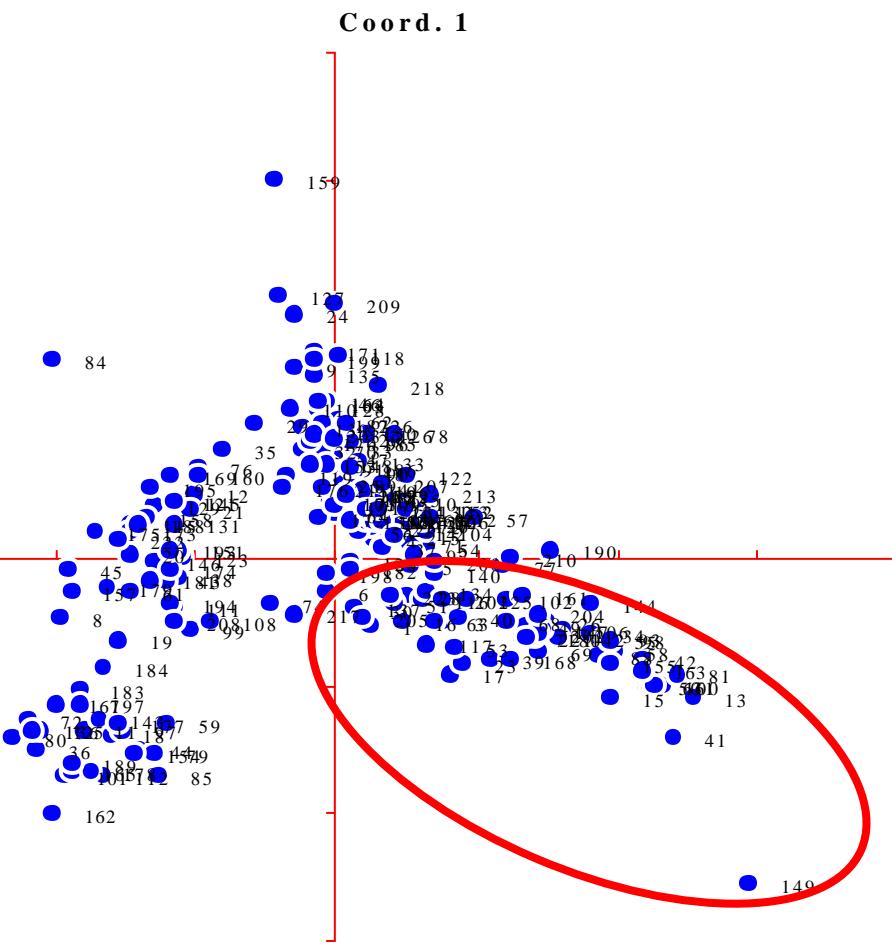
Brabant; Zeeland

# Multidimensional plot os surname distances

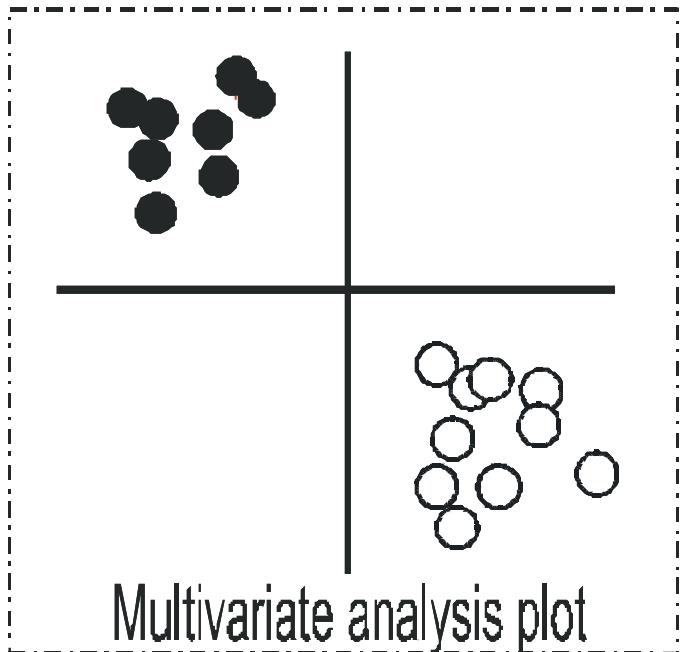


# N/S Holland

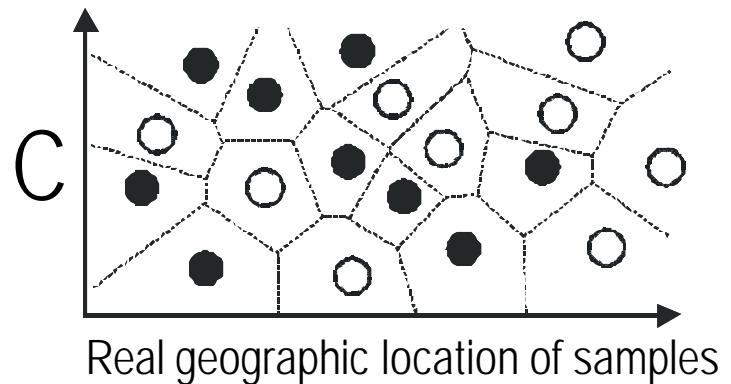
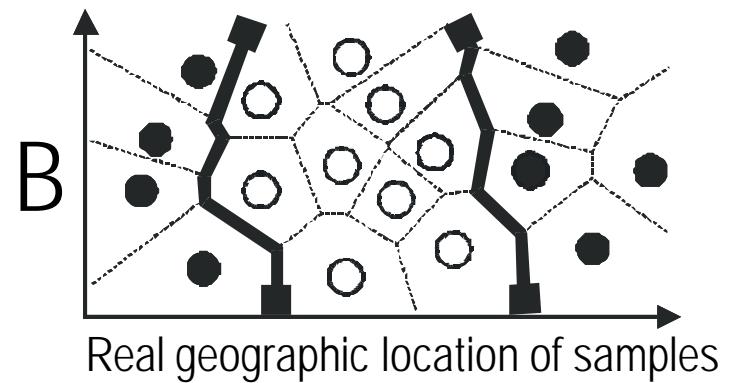
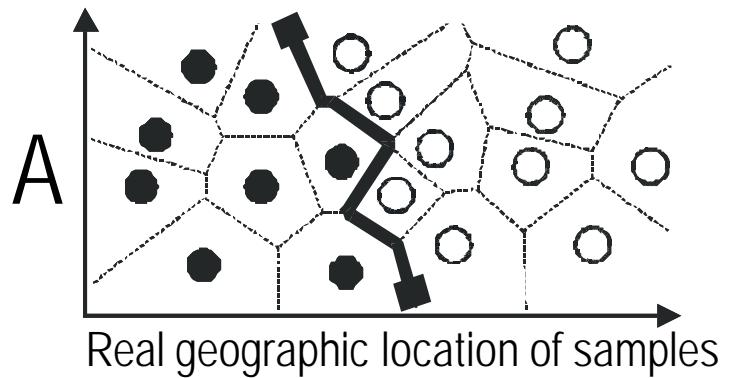
# Multidimensional plot os surname distances



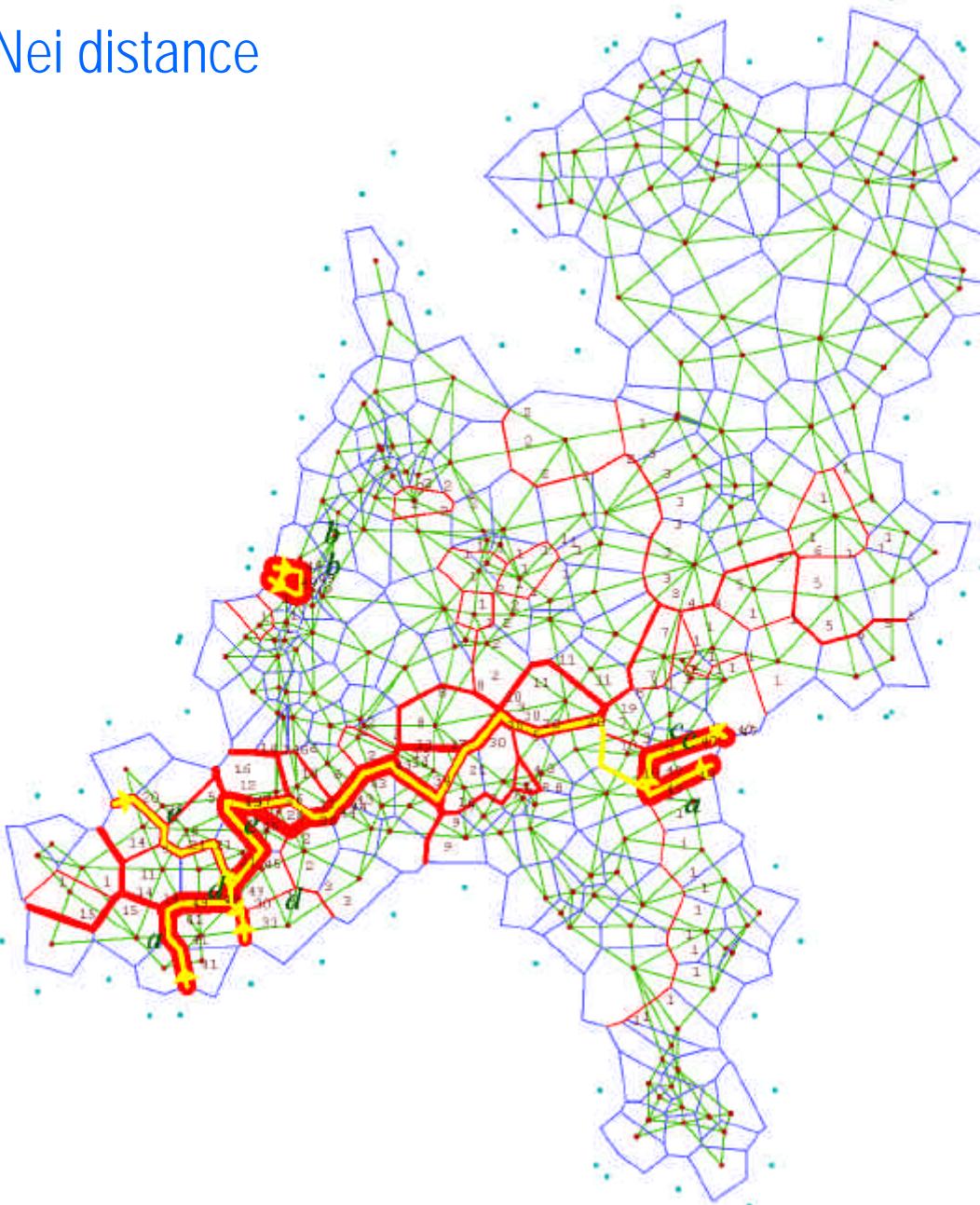
# East Netherlands



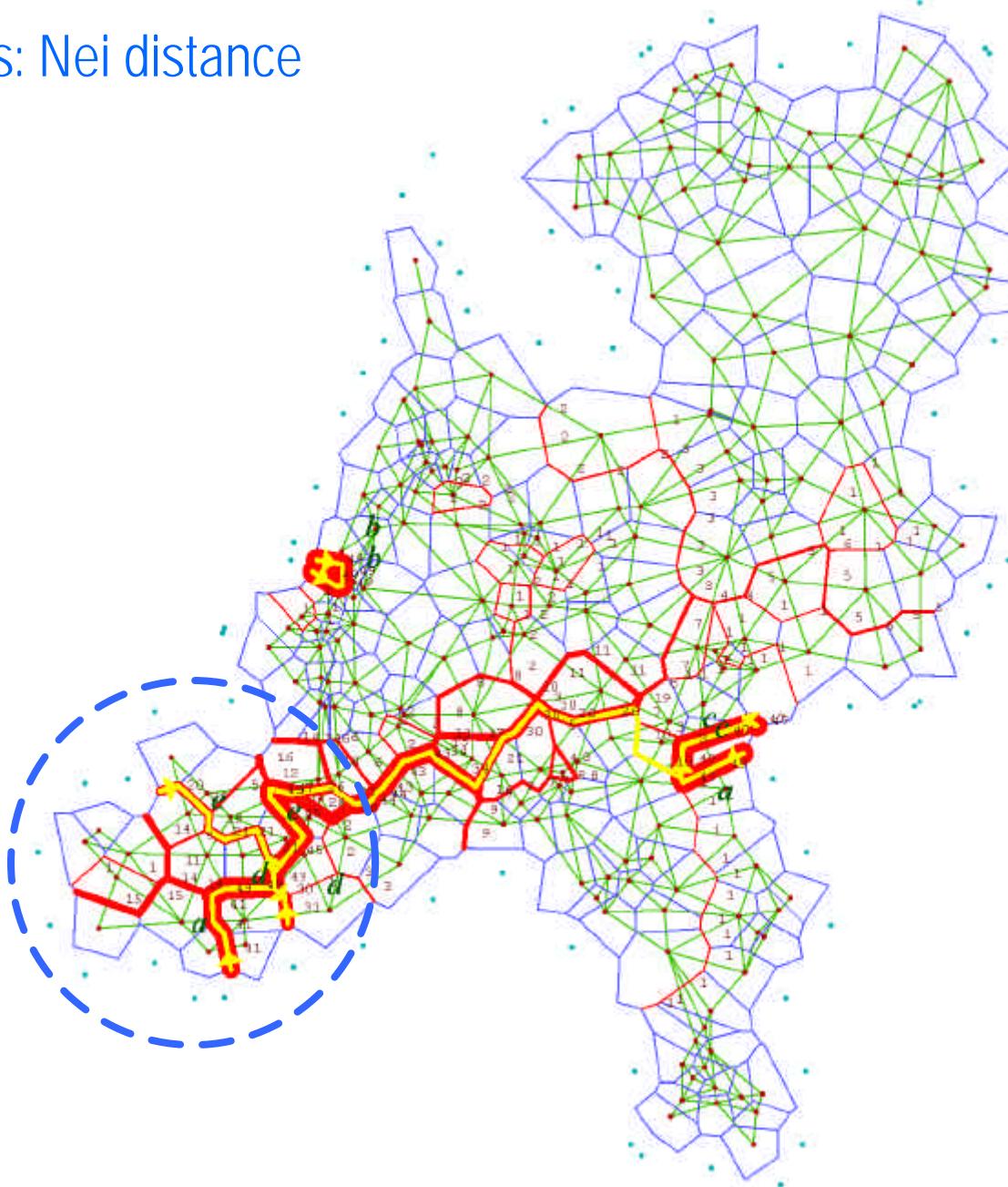
**PROBLEM !**  
Different scenarios may  
correspond to a same  
multivariate analysis  
(PCA, MDS, etc.)



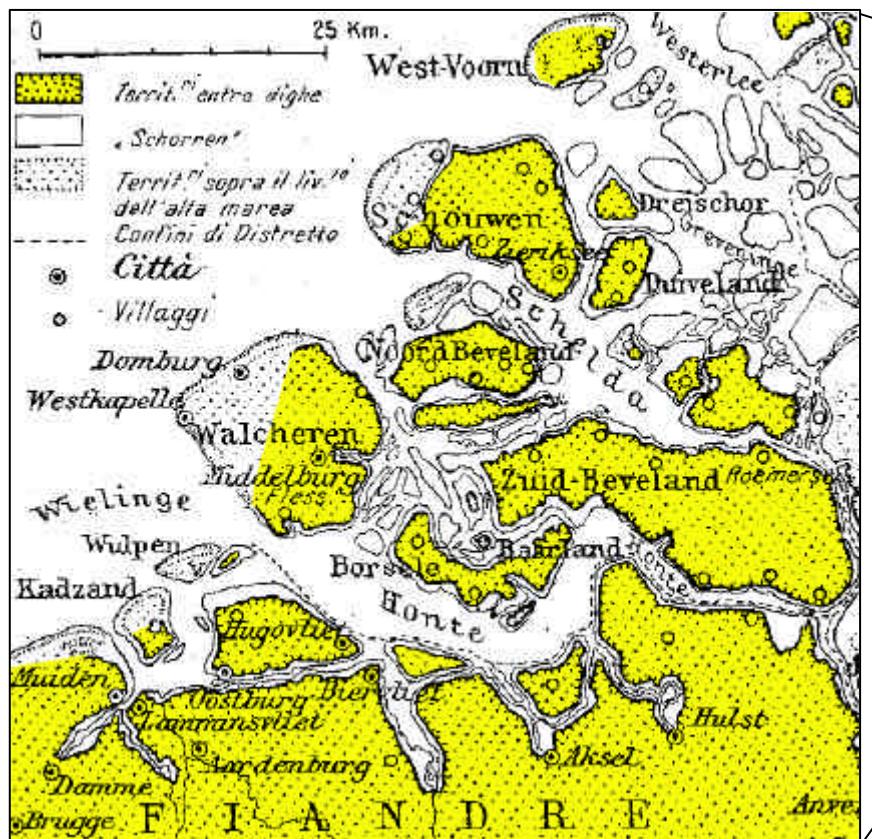
# Isonimy and the Netherlands: Nei distance

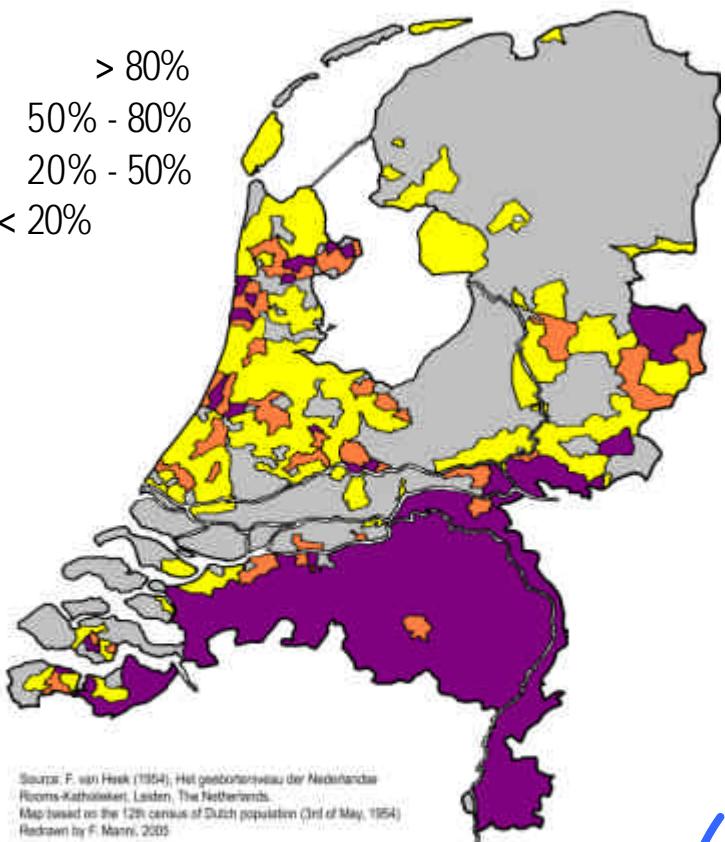
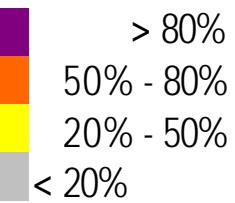


# Isonimy and the Netherlands: Nei distance

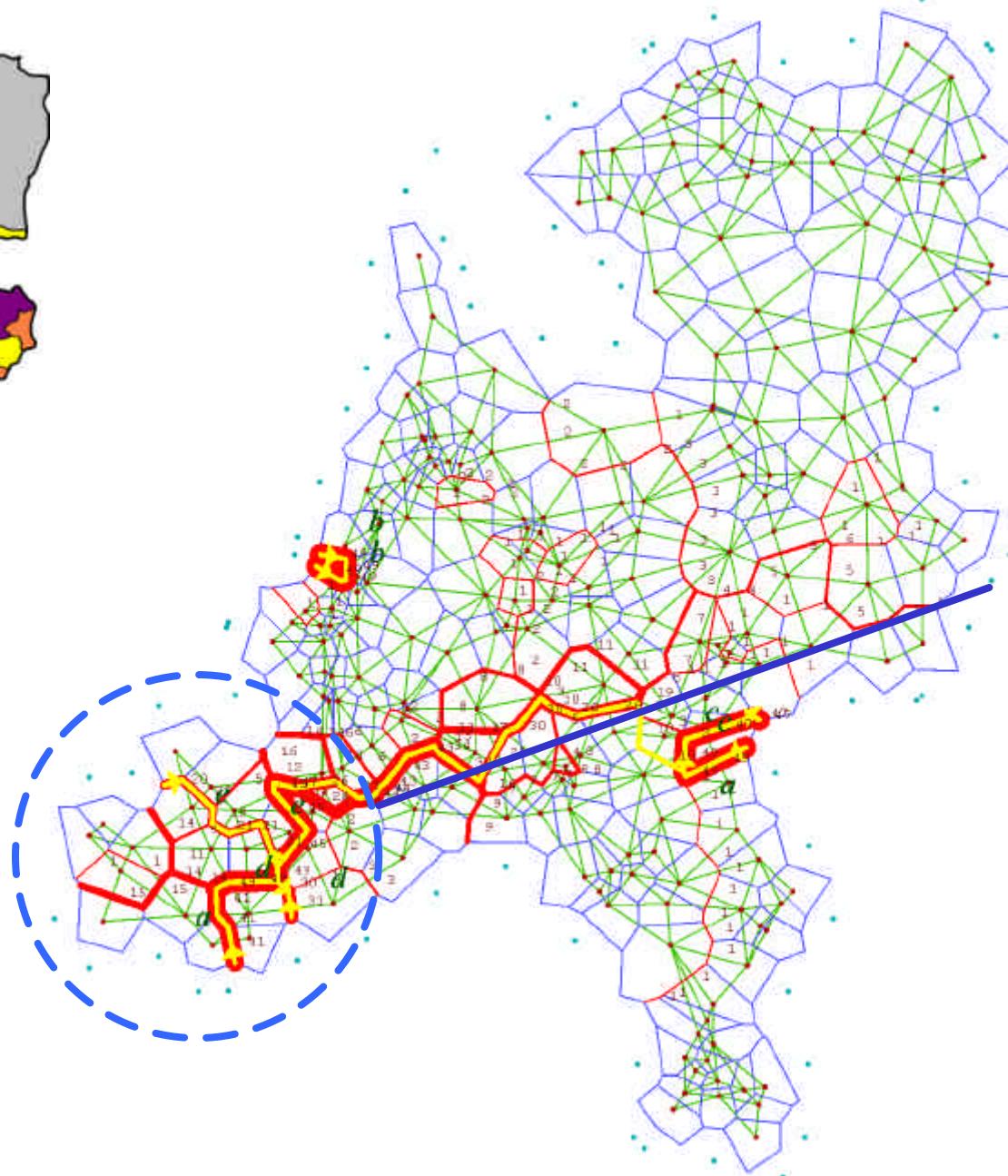


# Geographic analysis, *islands* are another explanation





Source: F. van Heek (1954); Het geboorteniveau der Nederlandse Rooms-Katholieken, Leiden, The Netherlands.  
Map based on the 12th census of Dutch population (1st of May, 1954)  
Redrawn by F. Mann, 2005



Calvin



Benedictus XVI



No intermarriages



End of first part:

« Surnames cooked with a standard sauce »

(little pause)

next:

« Surnames are also words... »

# Is there a link between cultural and genetic diversity?

## 1. Genetics

demographic history of populations,  
evolution

## 2. Linguistics

mirrors cultural differences as well as  
gastronomic traditions, basket technology,  
etc.

## 3. Surnames

They are transmitted like genetic traits  
but they are words...

Is there a link between cultural and genetic diversity?

Literary and Linguistic Computing Advance Access published September 15, 2006

# To What Extent are Surnames Words? Comparing Geographic Patterns of Surname and Dialect Variation in the Netherlands

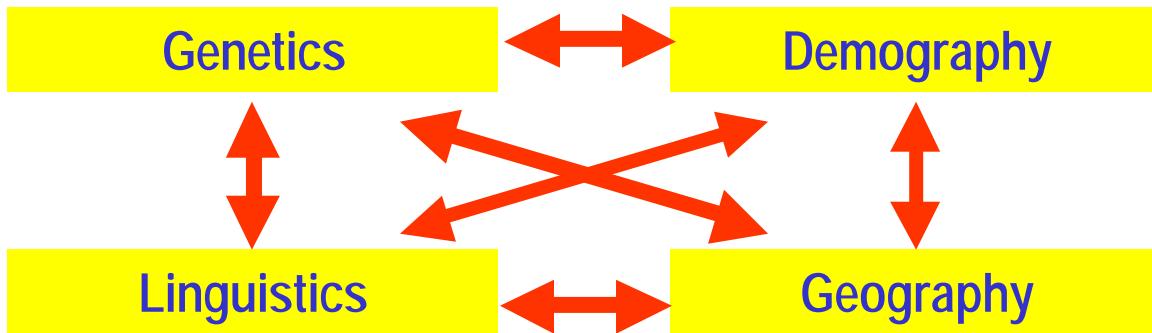
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Franz Manni

UMR 5145 CNRS, Musée de l'Homme MNHN, Paris, France

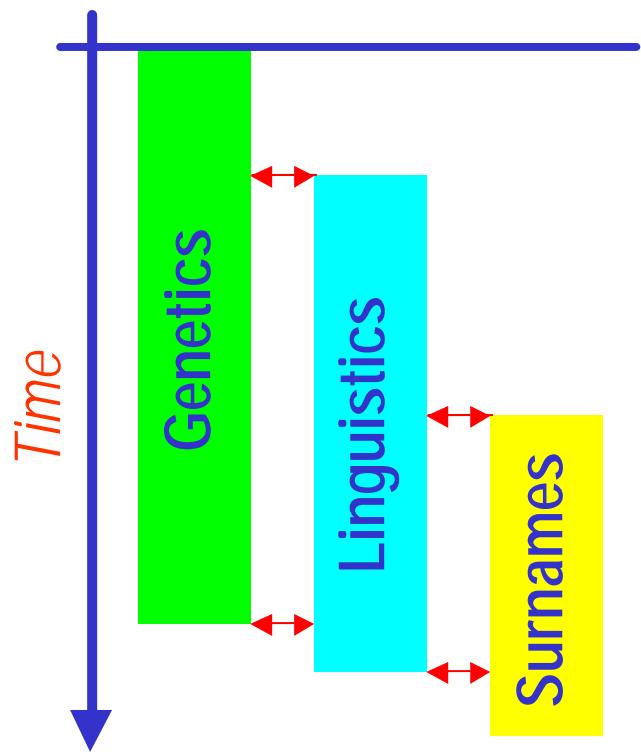
Wilbert Heeringa and John Nerbonne

Alfa-Informatica, Faculty of Arts, University of Groningen,  
The Netherlands

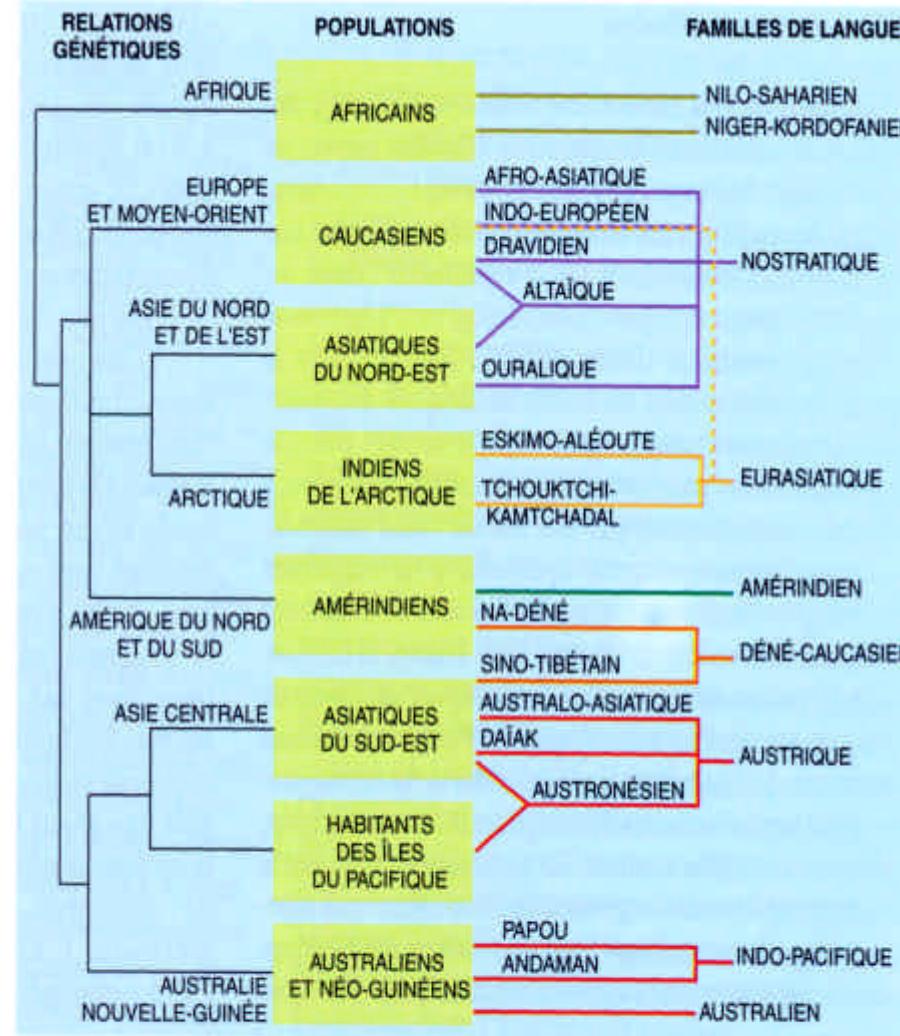


The three markers have different time depths,

Therefore each one of them represents a variability that originated over a different time frame.



# Genetics vs linguistics



Cavalli-Sforza et al. 1989

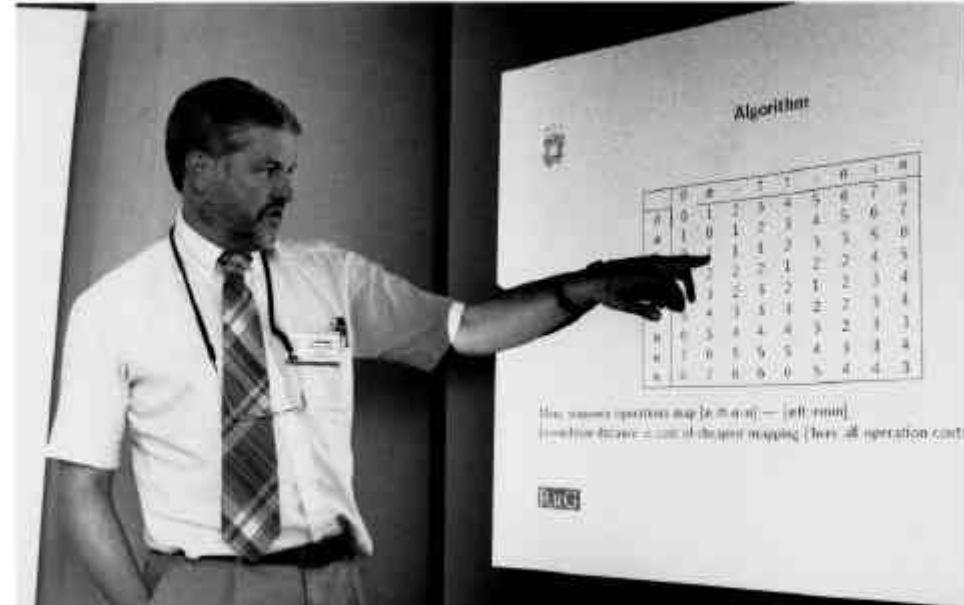
## Comparing genetic and linguistic variability

Worldwide analyses are quite controversial.

Better to focus on smaller geographic scales

Nowadays it is possible to computationally analyze dialects and similar languages. It is safer and probably more testable, to date.

# DUTCH DIALECTS: credits

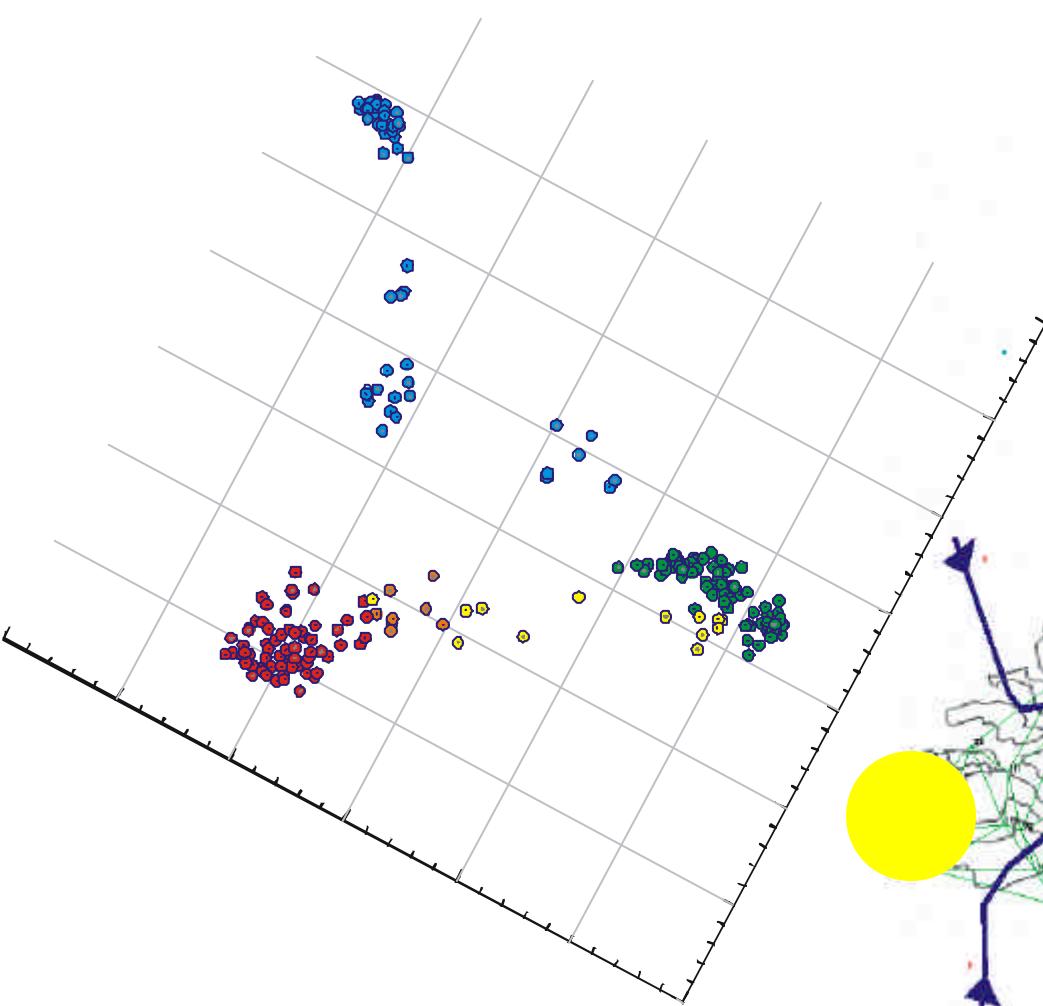


J. Nerbonne

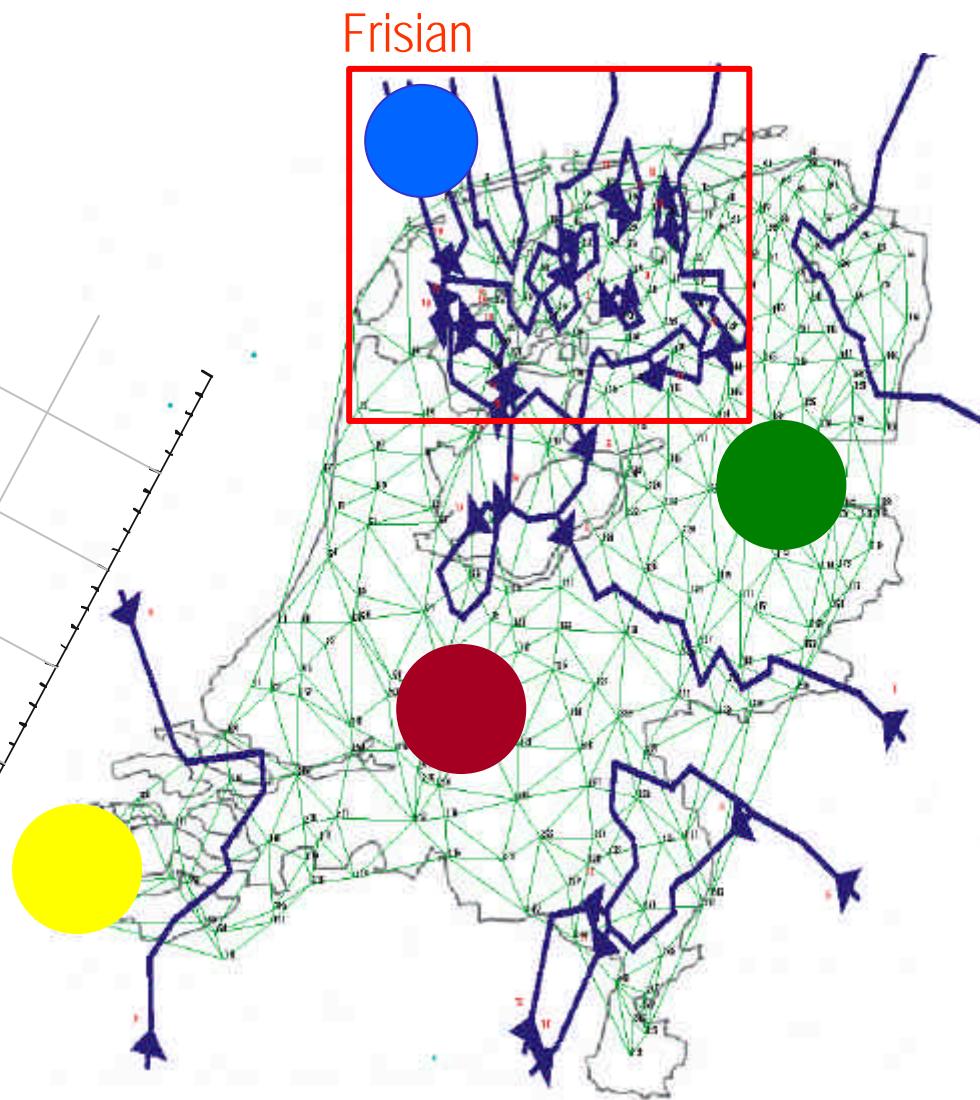


W. Heeringa

# DUTCH DIALECTS: MDS and geographic analysis with Monmonier alg.

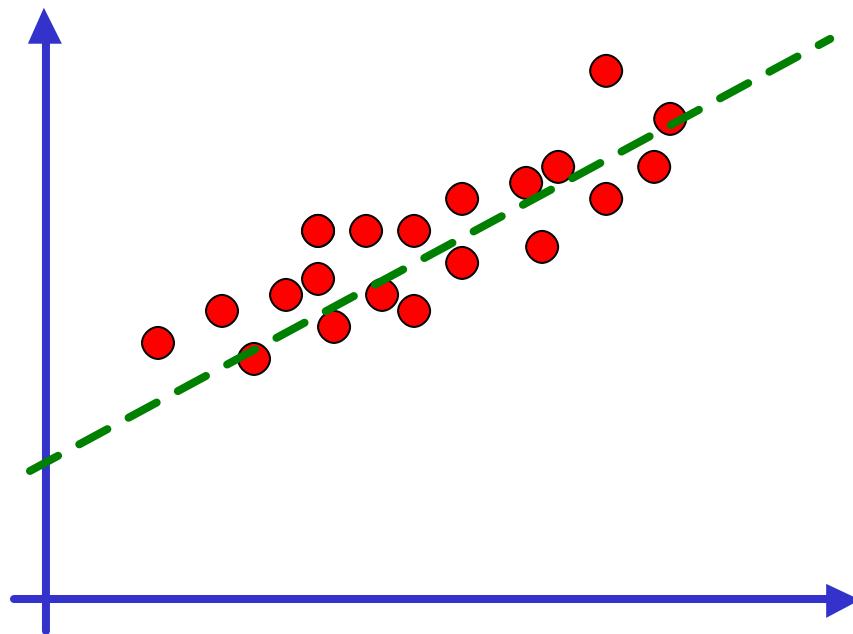


Frisian



255 samples; 20 barriers

# DUTCH DIALECTS: excellent correlation with geography

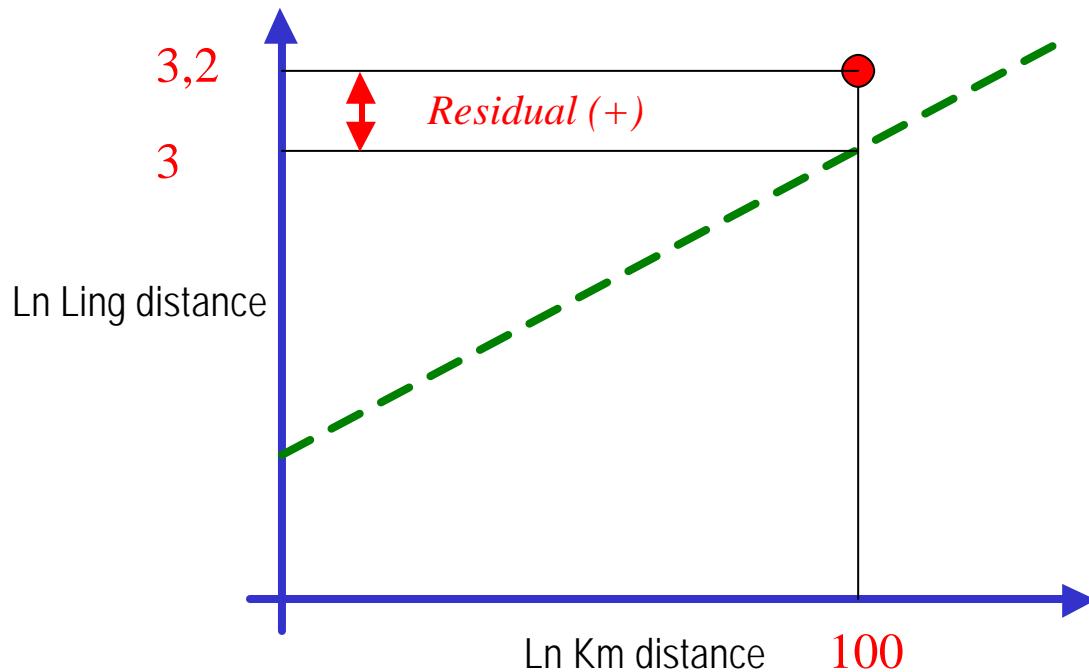


If the regression is good it means that there are some rules

We can accept the model and use it to make inferences of **EXPECTED** values of difference.

The difference between the **EXPECTED** value and the **OBSERVED** value is the **RESIDUAL**

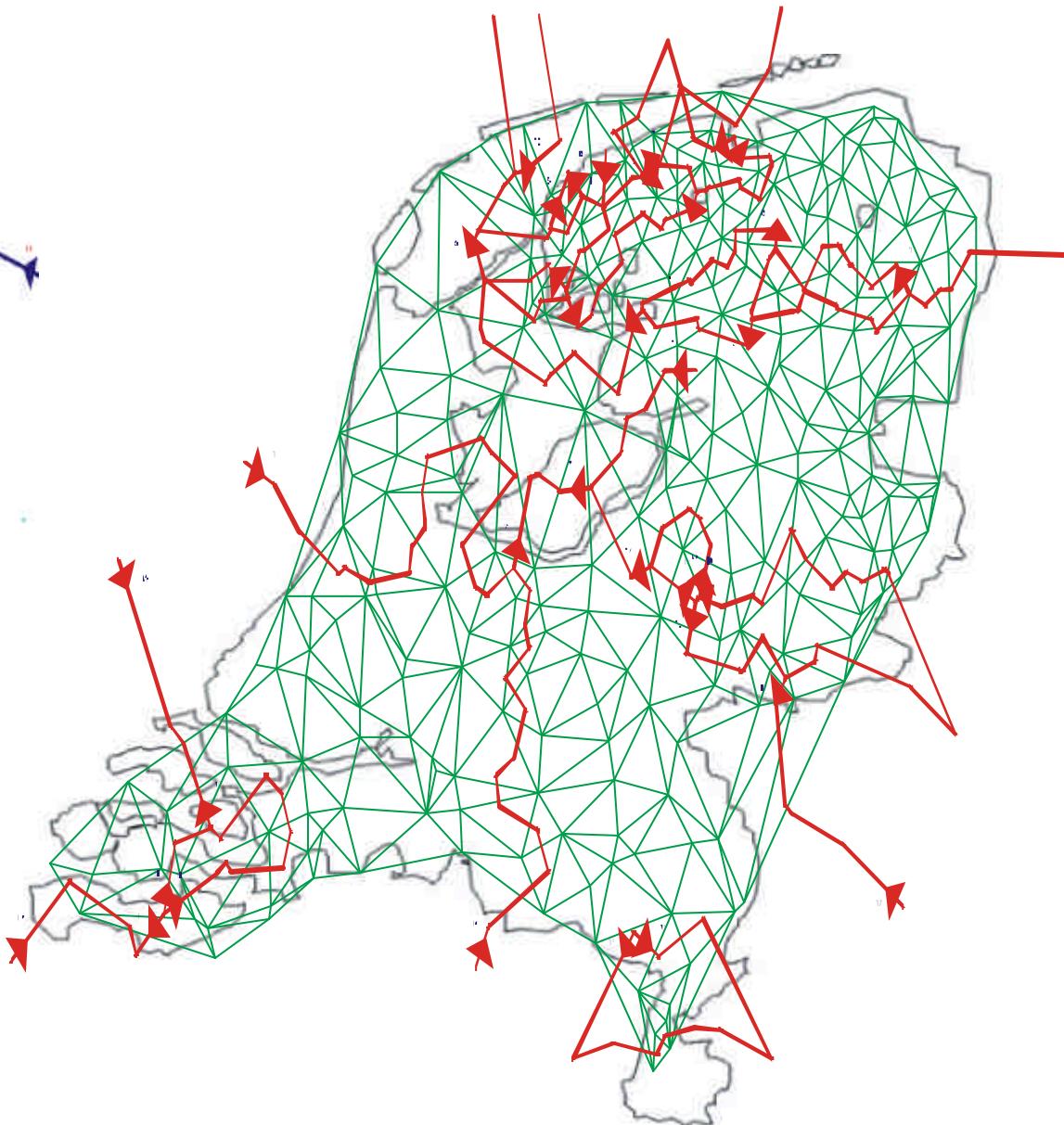
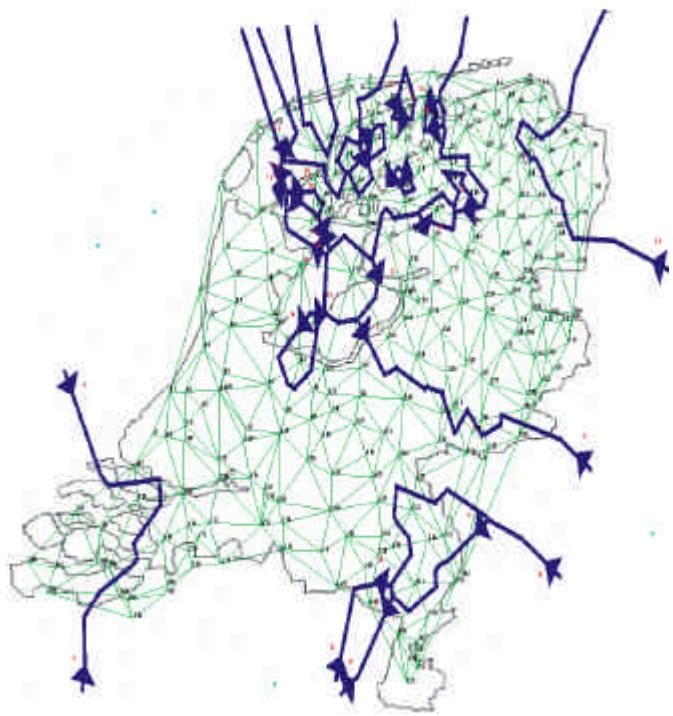
# DUTCH DIALECTS: excellent correlation with geography



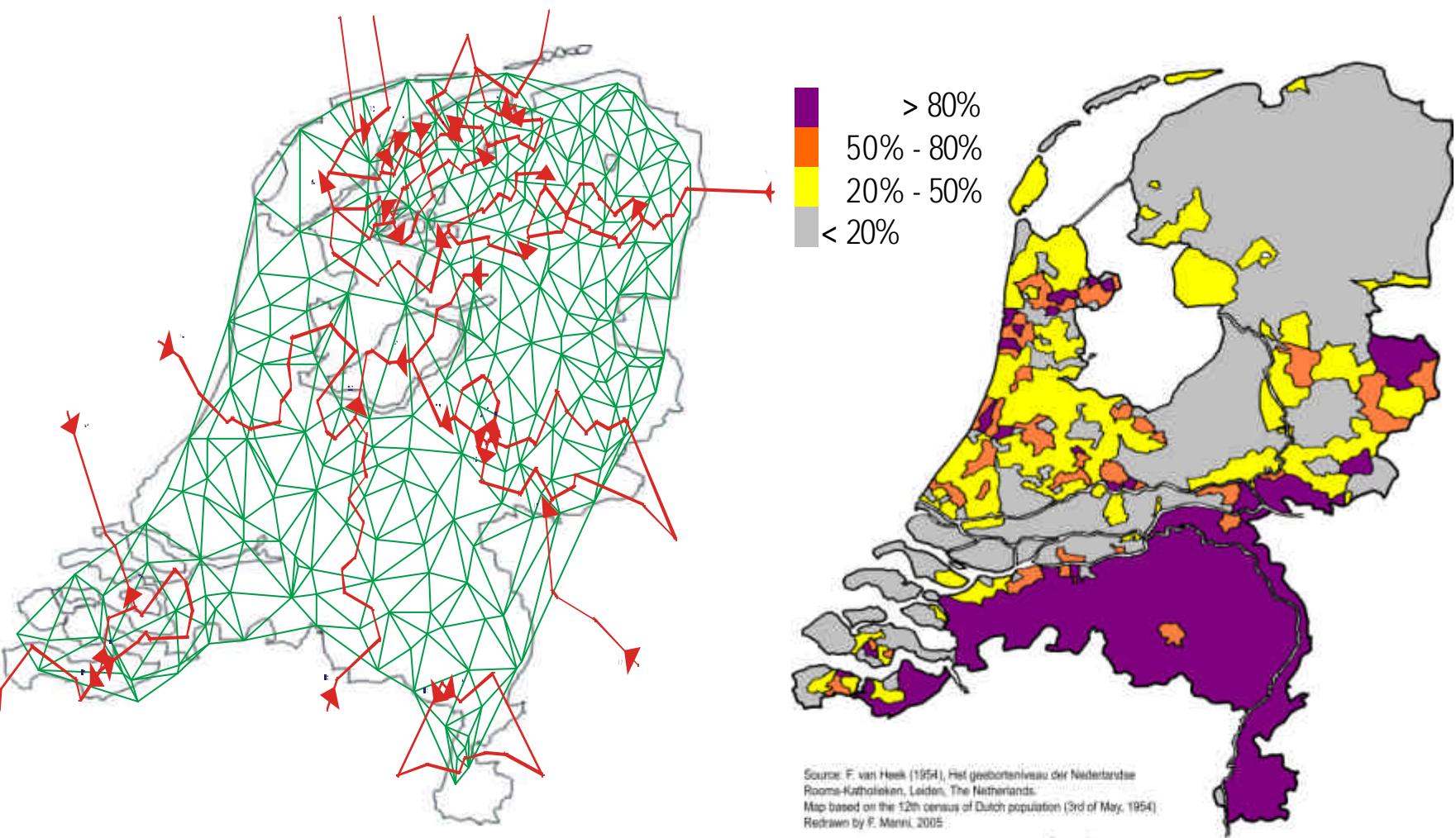
By computing the residuals for all the pairwise measures of linguistic distance we can compile a matrix of residuals and do the same kind of analysis we did before,

The new results are expected **NOT** to be conditioned by geography.

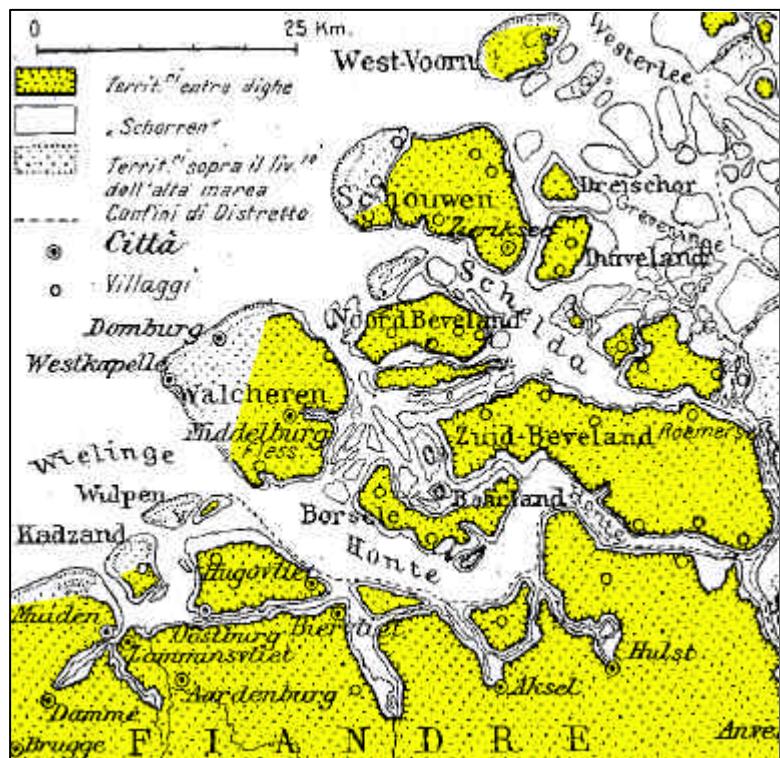
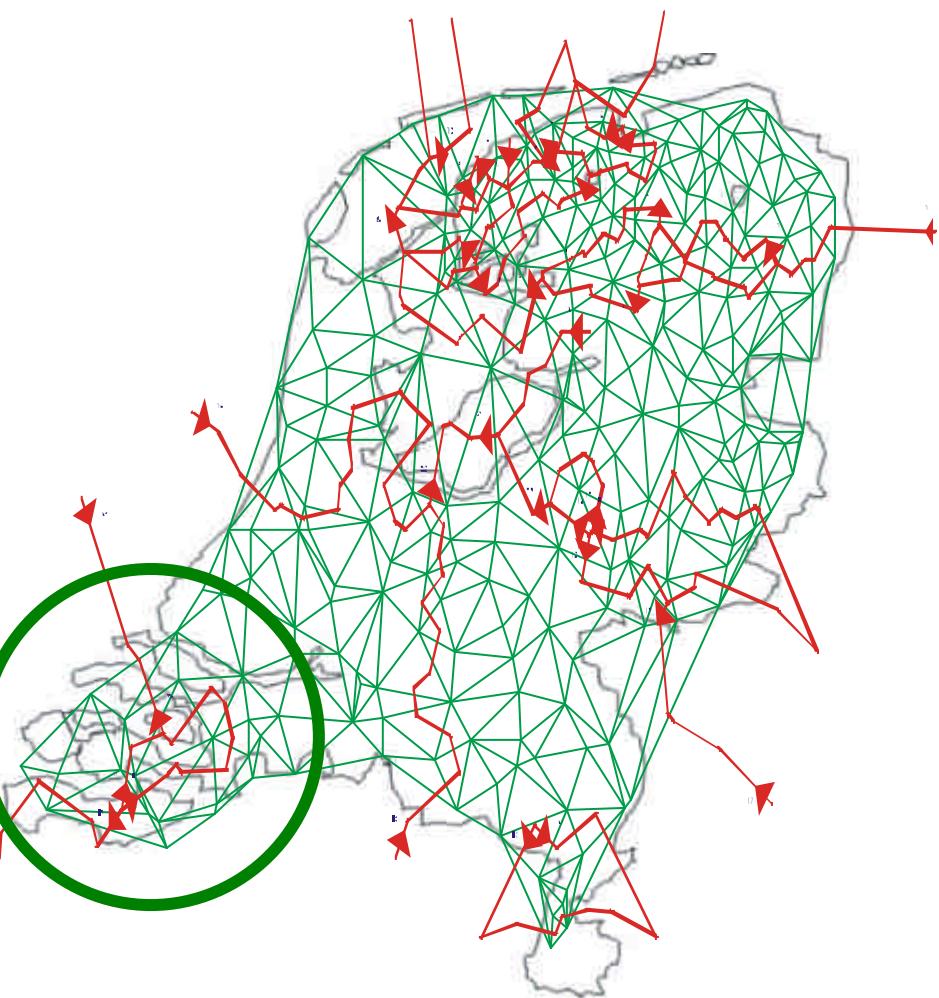
# Geographic analysis with Monmonier algorithm, «normal» vs. residuals



# Geographic analysis, *religion is NOT an explanation*



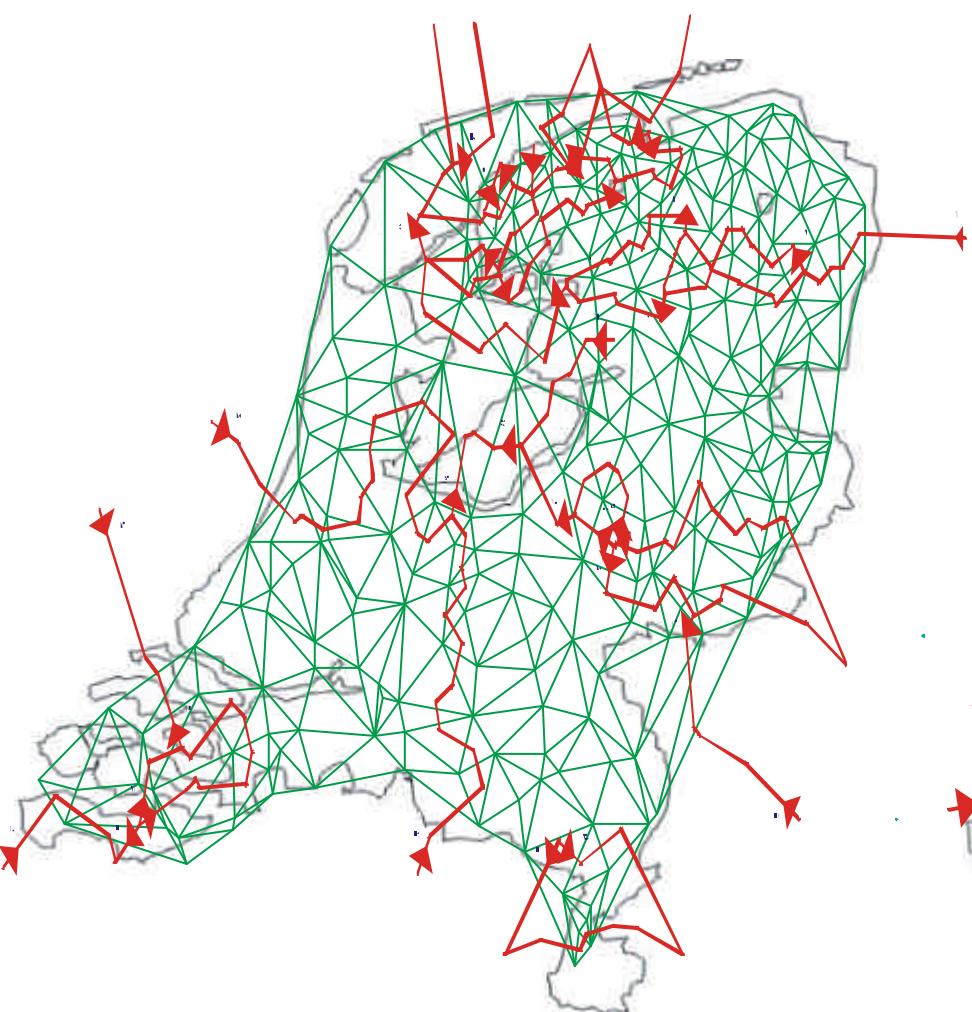
# Geographic analysis, *islands* can be an explanation



DIALECTS

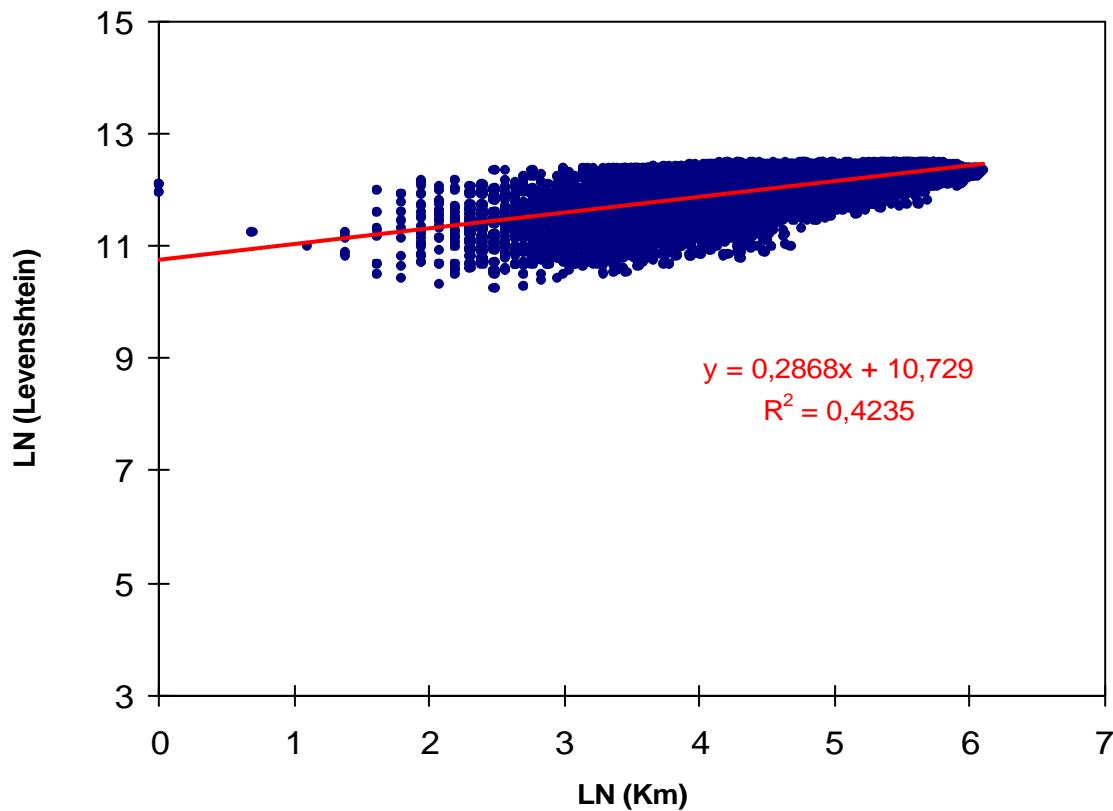
vs.

SURNAMES



*After regressions*

# DUTCH DIALECTS: excellent correlation with geography



We have seen something similar with the surnames...

# Are surnames words?

Correlation between surname and dialect dissimilarity matrices for the NL

	SURNAMES Nei	DIALECTS (72)	GEOGRAPH. DISTANCE
SURNAMES Nei	1	<b>0.298</b>	
DIALECTS 72	<b>0.298</b>	1	
GEOGRAPH. DISTANCE			

Merging dialect and surname matrices: 72 sampling points

# Are surnames words?

Correlation between surname and dialect dissimilarity matrices for the NL

	SURNAMES Nei	DIALECTS (72)	GEOGRAPH. DISTANCE
SURNAMES Nei	1	<b>0.298</b>	<b>0.565</b>
DIALECTS 72	<b>0.298</b>	1	<b>0.632</b>
GEOGRAPH. DISTANCE	<b>0.565</b>	<b>0.632</b>	1

Merging dialect and surname matrices: 72 sampling points

End of second part:

« Are Surnames words? (They are not) »

(little pause)

next:

« Surnames cooked with a spicy sauce ... »

# A New Method for Surname Studies of Ancient Patrilineal Population Structures and its Possible Application to the Improvement of Y-Chromosome Sampling

Franz MANNI, B. TOUPANCE & E. HEYER

Unité de Génétique des population - Musée de l'Homme MNHN  
17, Place du Trocadéro - 75016 Paris ([manni@mnhn.fr](mailto:manni@mnhn.fr))

# The maps of Kohonen

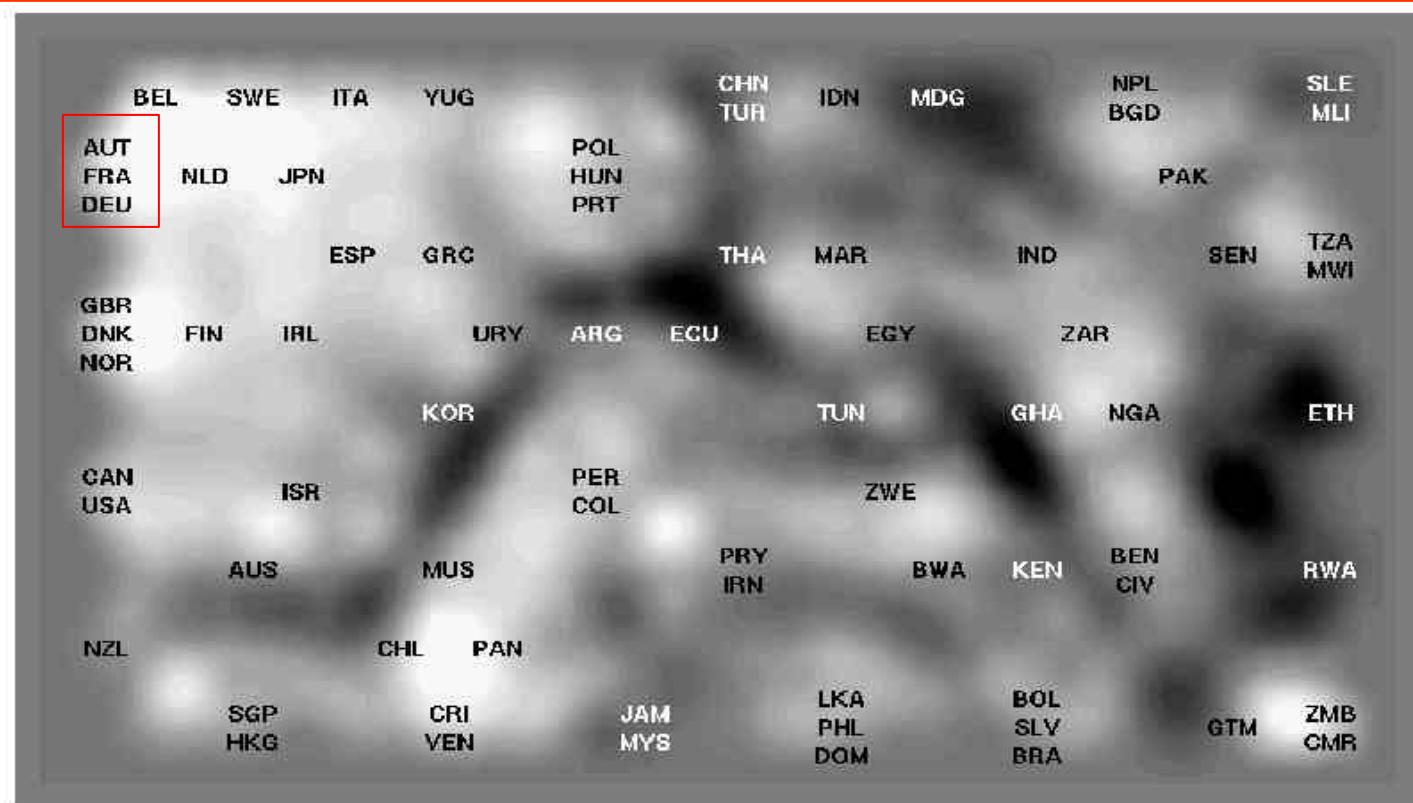


Figure 5: A map display constructed using the SOM algorithm. The overall order of the countries seems to correspond fairly closely to the Sammon's mapping of the same data set (Fig. 4). The most prominent clustering structures are also visible in both displays. Details on how the map was constructed are presented in Publication 2. The size of the map was 13 by 9 units.

### *Example : poverty in the world*

# Comparing different methods

*Example : poverty in the world*

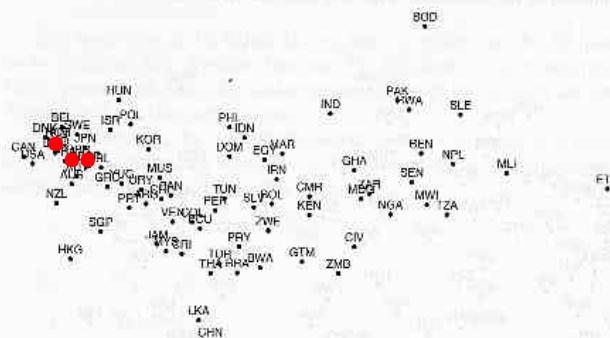


Fig. 1.7. A nonlinear projection constructed using nonmetric MDS [1.27]. The data set is the same as in Fig. 1.5 and Fig. 1.6. Missing data values were treated by the following simple method which has been demonstrated to produce good results at least in the pattern recognition context [1.37]. When computing the distance between a pair of data items, only the (squared) differences between component values that are available are computed. The rest of the differences are then set to the average of the computed differences.

MDS

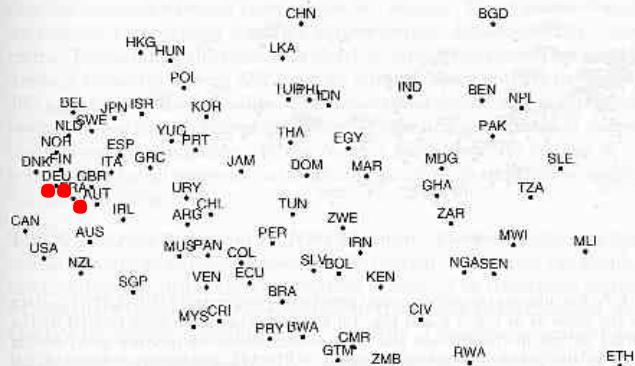


Fig. 1.6. Sammon's mapping of the same data set that was projected using the PCA in Fig. 1.5 [1.27]

Sommon's mapping



Figure 2: A dataset projected linearly onto the two-dimensional subspace obtained with PCA. Each 39-dimensional data item describes different aspects of the welfare and poverty of one country. The data set consisting of 77 countries, used also in Publication 2, was picked up from the World Development Report published by the World Bank (1992). Missing data values were neglected when computing the principal components; and same when forming the projections. A key to the abbreviated country names is given in the Appendix.

ACP

# A discrete classification

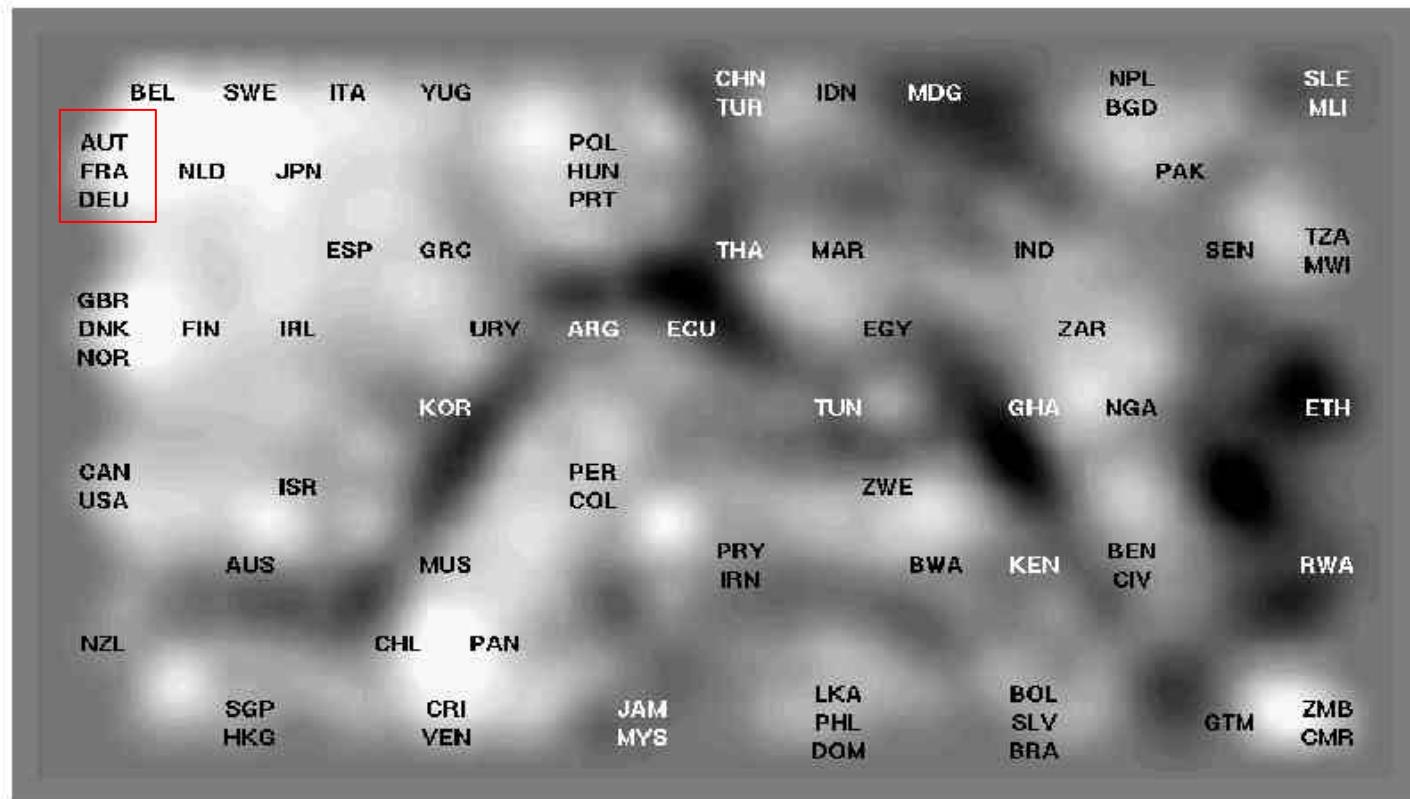
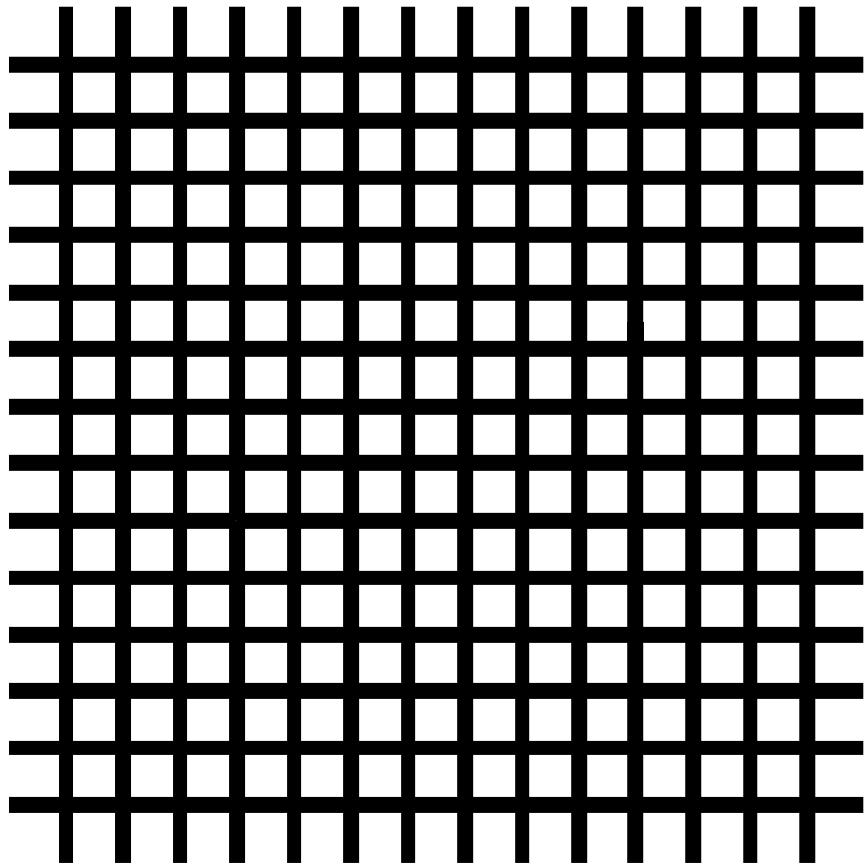


Figure 5: A map display constructed using the SOM algorithm. The overall order of the countries seems to correspond fairly closely to the Sammon's mapping of the same data set (Fig. 4). The most prominent clustering structures are also visible in both displays. Details on how the map was constructed are presented in Publication 2. The size of the map was 13 by 9 units.

*Example : poverty in the world*

# Surnames: *Cluster analysis*

	Surname 1	Surname 2	Surname 3	Surname 4	...
Town1	1	1	1	1	...
Town2	0	0	0	0	
Town3	1	1	1	1	
Town4	0	0	0	0	
...	...	...	...	...	
Town5	0	0	0	0	

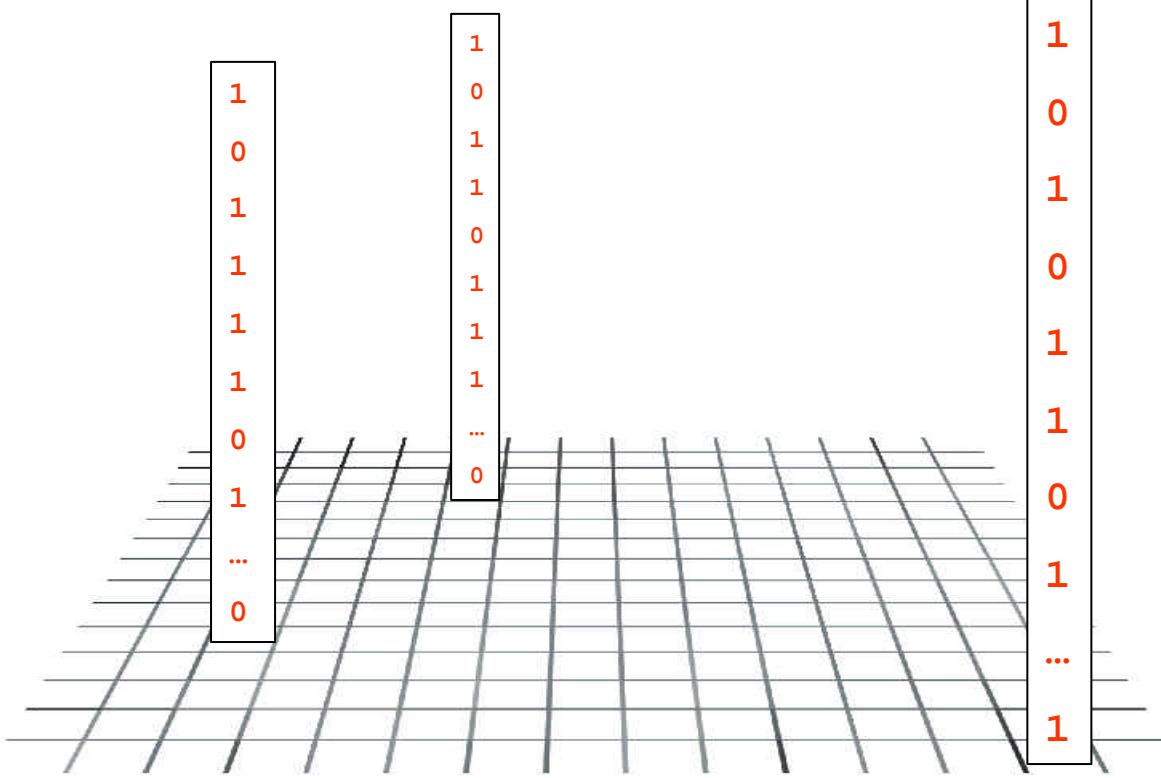


15 x 15

# Surnames : *How it works* 1

AAAAAA  
BBBBBB

1	1
0	0
1	1
1	1
1	0
1	1
0	1
1	1
...	...
0	0



Surnames

Reference vectors on the map

# Surnames : *How it works* 2

AAAAAA  
BBBBBB

1	1
0	0
1	1
1	1
1	0
1	1
0	1
1	1
...	...
0	0

=

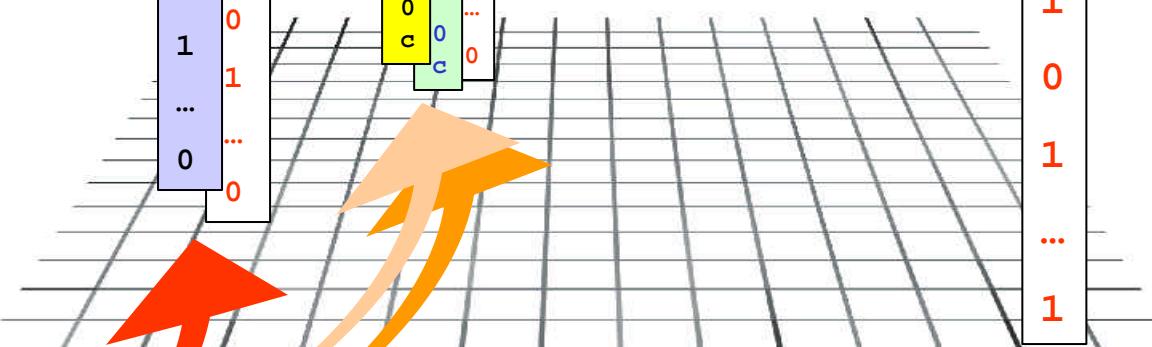
WWWWWW

1	1
0	1
1	1
1	0
1	1
0	1
1	1
1	1
...	...
0	0

1	1
0	0
1	1
1	1
1	0
1	1
0	0
1	1
...	...
0	0

1	1
0	0
1	1
1	0
1	1
0	0
1	1
1	1
...	...
0	0

1
0
1
0
1
1
0
0
...
1

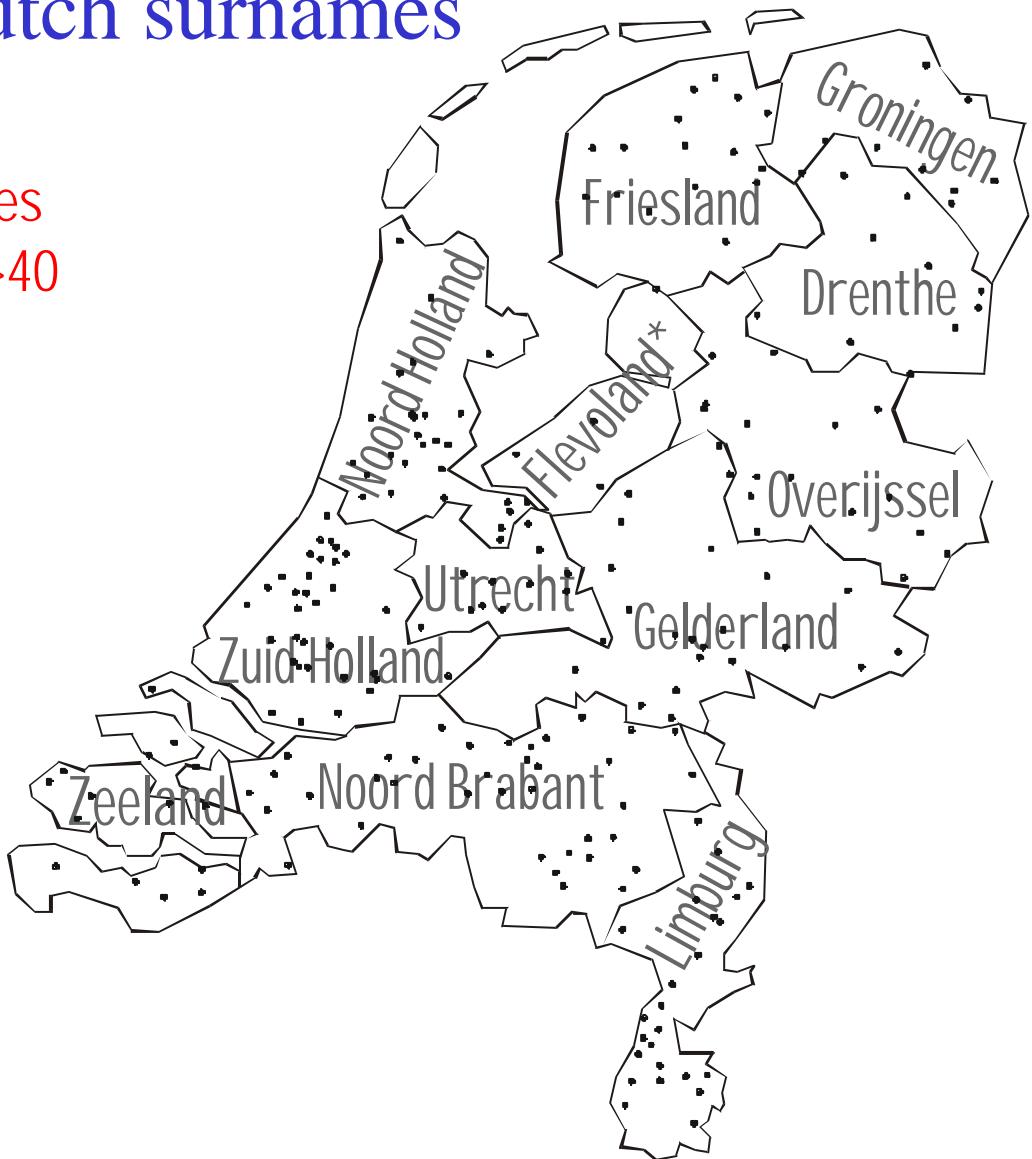


## Kohonen maps: *advantages*

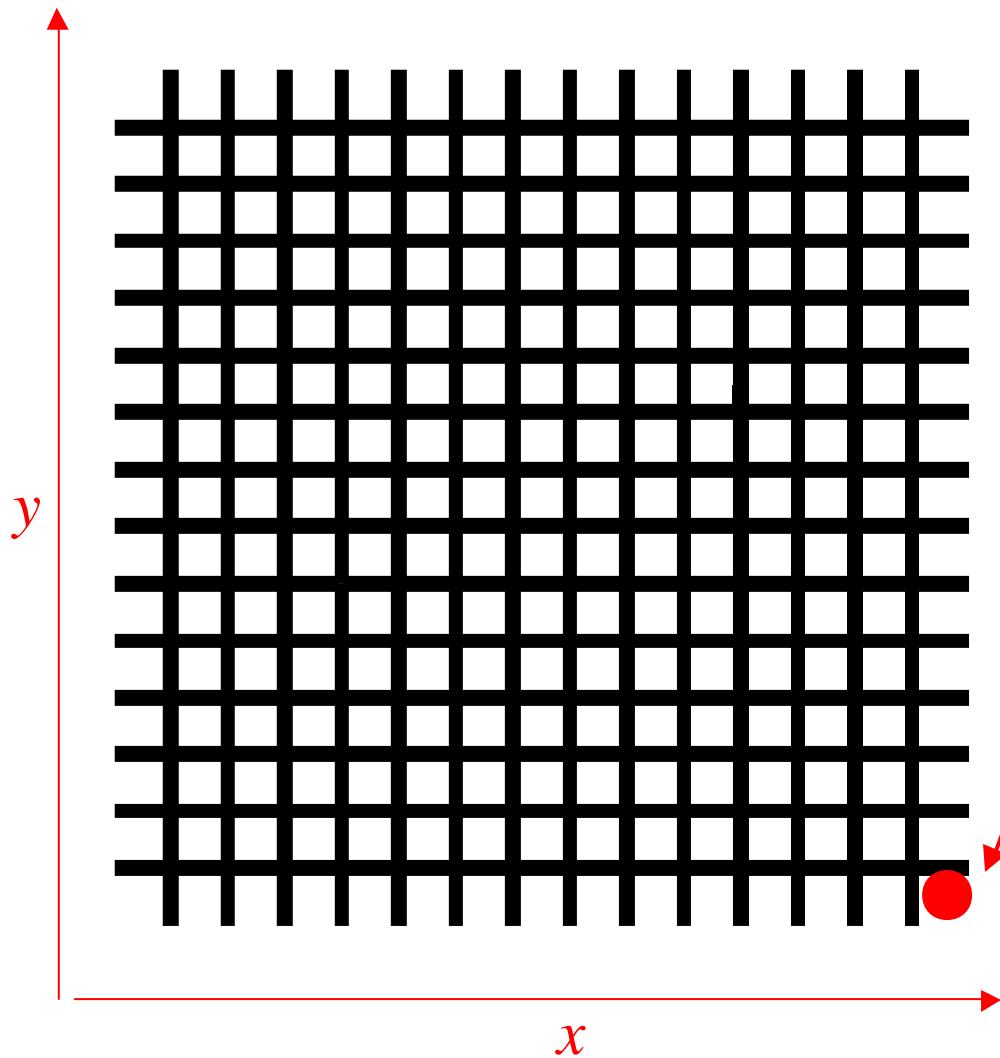
1. Can handle **missing values** (vectors)
2. It has been shown that the **topology** is more exact than in MDS or PCA representation.
3. As a consequence, the relations between **weakly differentiated** populations are more clear.
4. Softwares are very stable and can handle up to **10.000 vectors (surnames) in 226 dimensions (towns)** (Pentium II, 1000 MHz, 256 Mo RAM).

# Application to Dutch surnames

- 9,929 different surnames  
(1,642,354 families)  $f > 40$
- 226 towns and cities
- 15 x 15 cells map  
(225 clusters)



# How results look like...

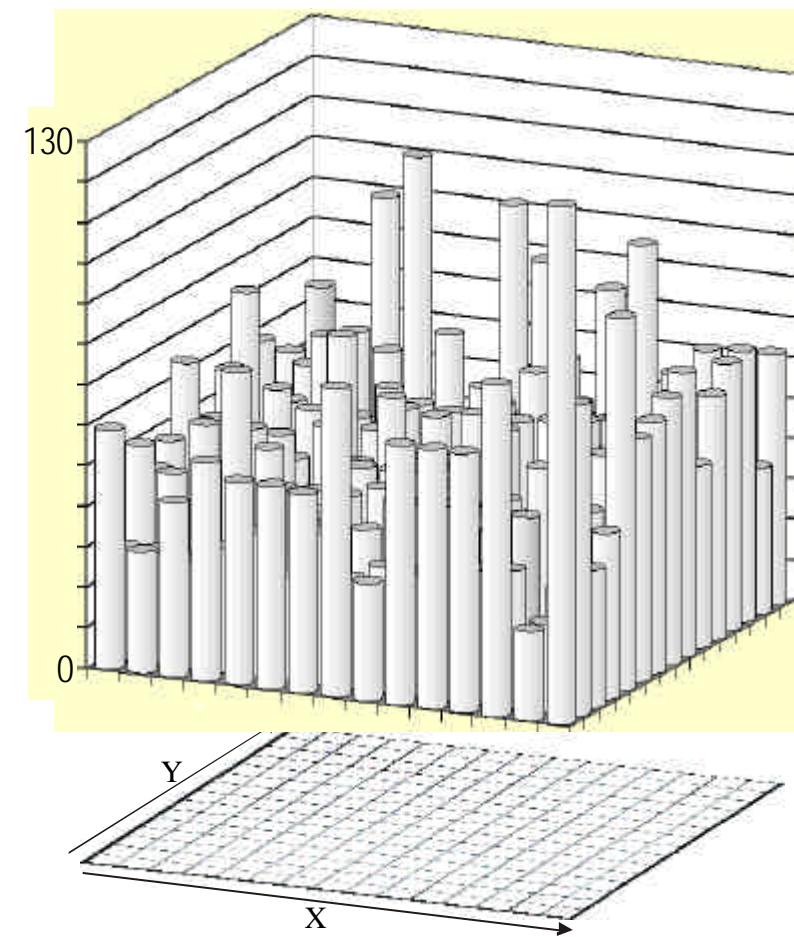


*36 surnames:*

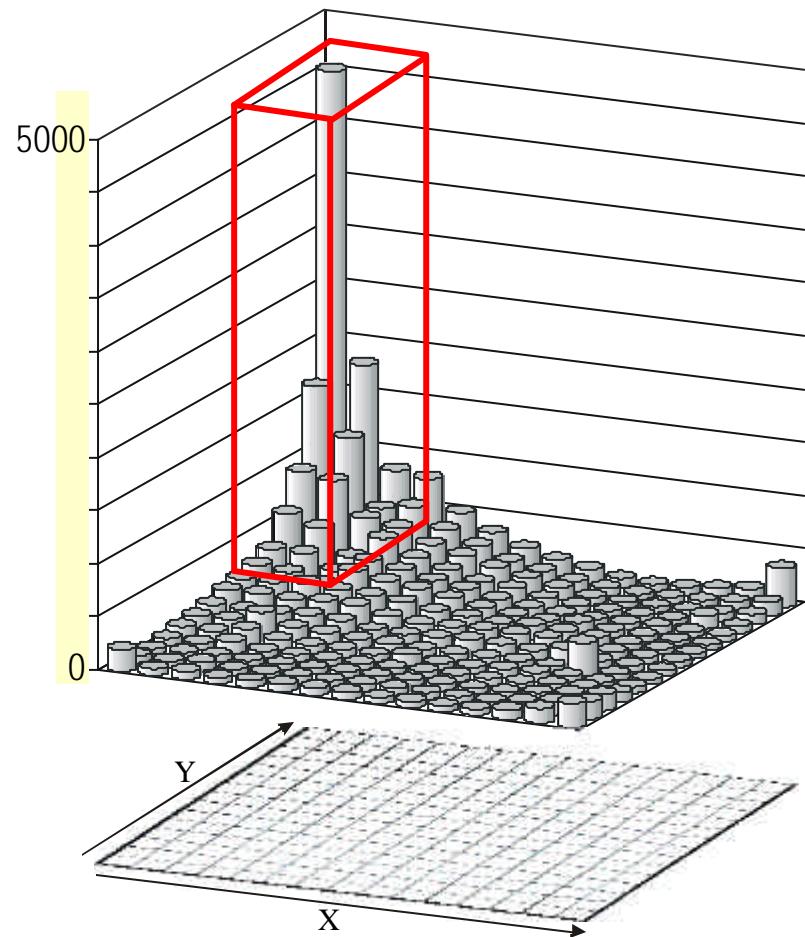
Abma, Algra, Anema, Attema, Baarda, Betten, Bonnema, Bontekoe, Bottema, Brinksma, Clossen, Cuperus, Damstra, Deelstra, Duiker, Haitsma, Hengst, Hoeksma, Huitema, Hylkema, Iedema, Jelsma, Kammen, Kooiker, Kuiken, Minnema, Mollema, Monsma, Numan, Piersma, Popma, Rienstra, Schaper, Sinnema, Steensma, Vlietstra

Surnames grouped in a same cell will be considered as if they were a single  
**SUPER – SURNAME (GSSGD)**  
(families having a similar migration history)

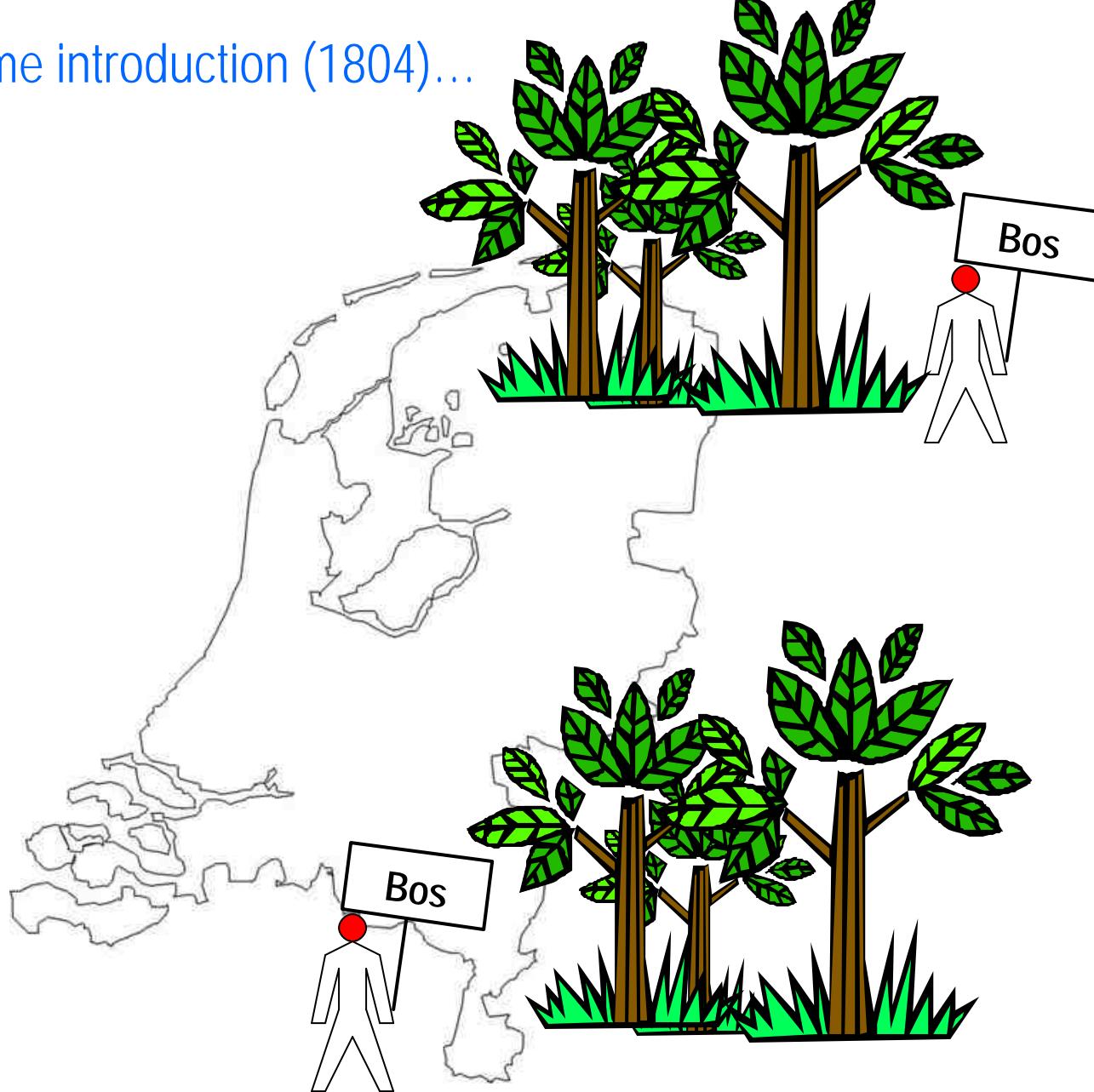
Absolute frequency of surnames per cell (cluster) ...



Average number of families sharing such surnames...



At the time of surname introduction (1804)...



*Polyphyletism*

Surnames' frequency vectors undergo a correction by the size of the town/city...

Surname	City 1 ( <i>200,000 hbt.</i> )	City 2 ( <i>5,000 hbt.</i> )	
<i>Johnsson</i>	<b>1000</b>	<b>56</b>	<b>1556</b>
	$1000 / 200000 = \underline{0.5}$	$30 / 5000 = \underline{0.65}$	<u>1.15</u>
	$0.50 / 1.15 = \underline{0.43}$	$0.65 / 1.15 = \underline{0.56}$	<u>1.00</u>
	<b>43 %</b>	<b>56 %</b>	

# Polyphyletism: its signature...

(24% of individuals)

Everywhere...



X=1  
Y=15

No where...



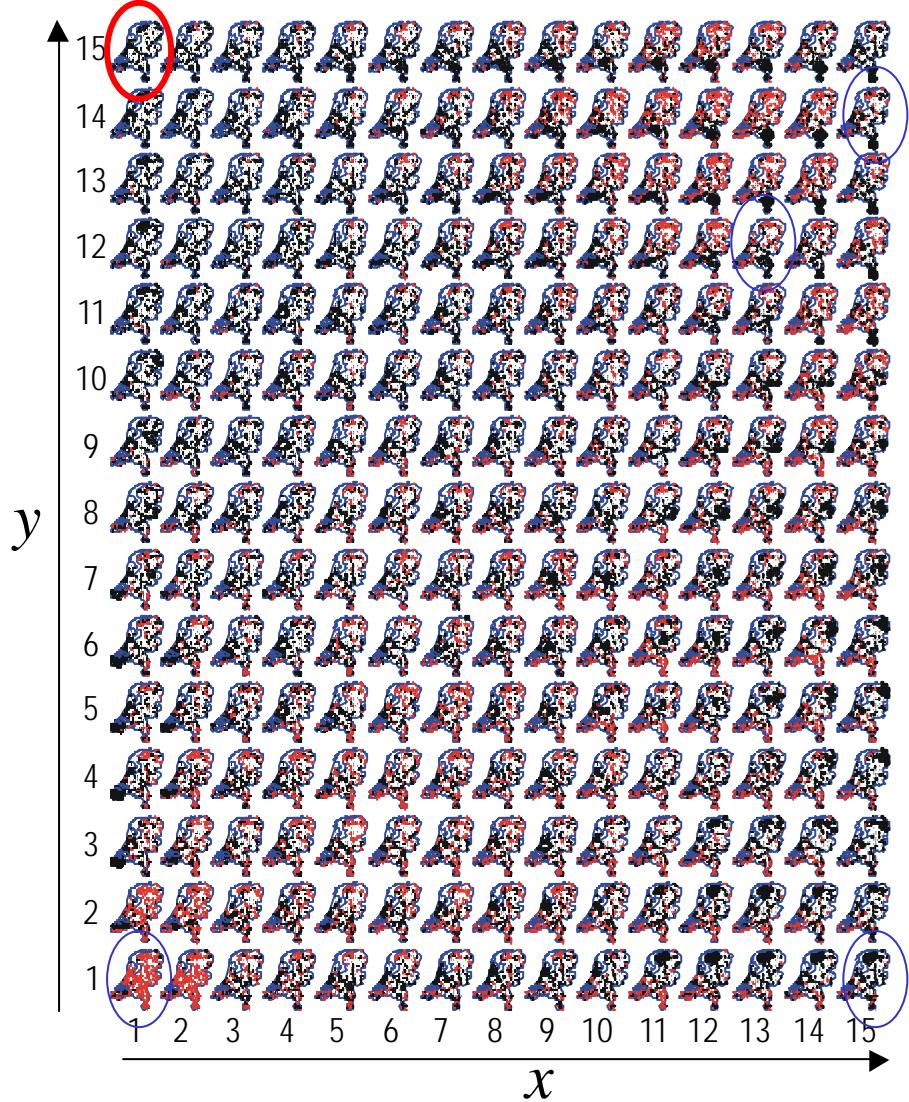
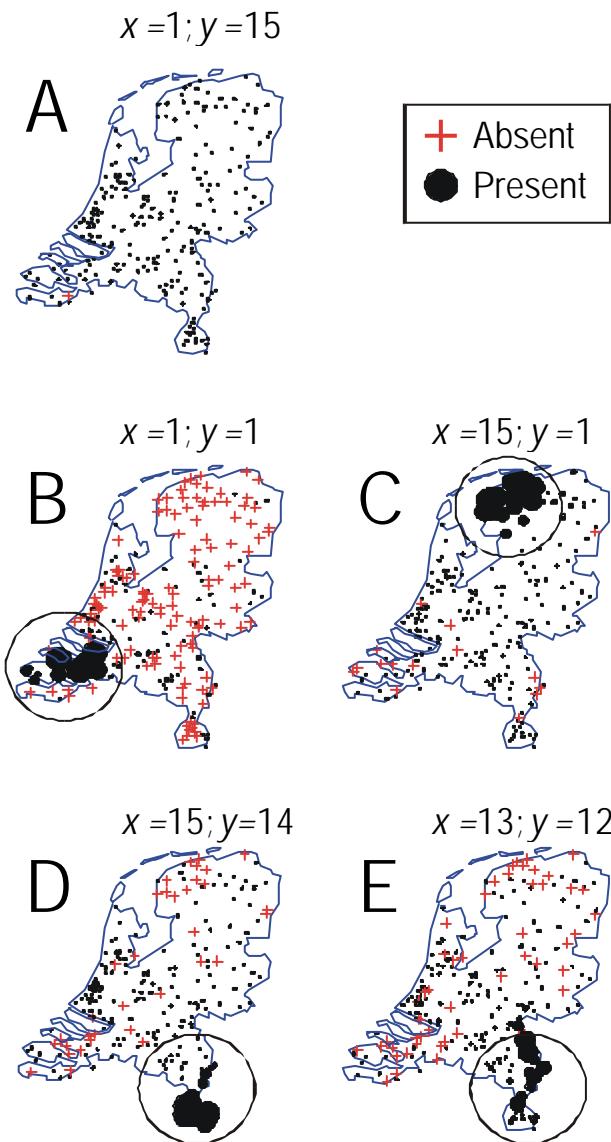
correction

68 surnames:

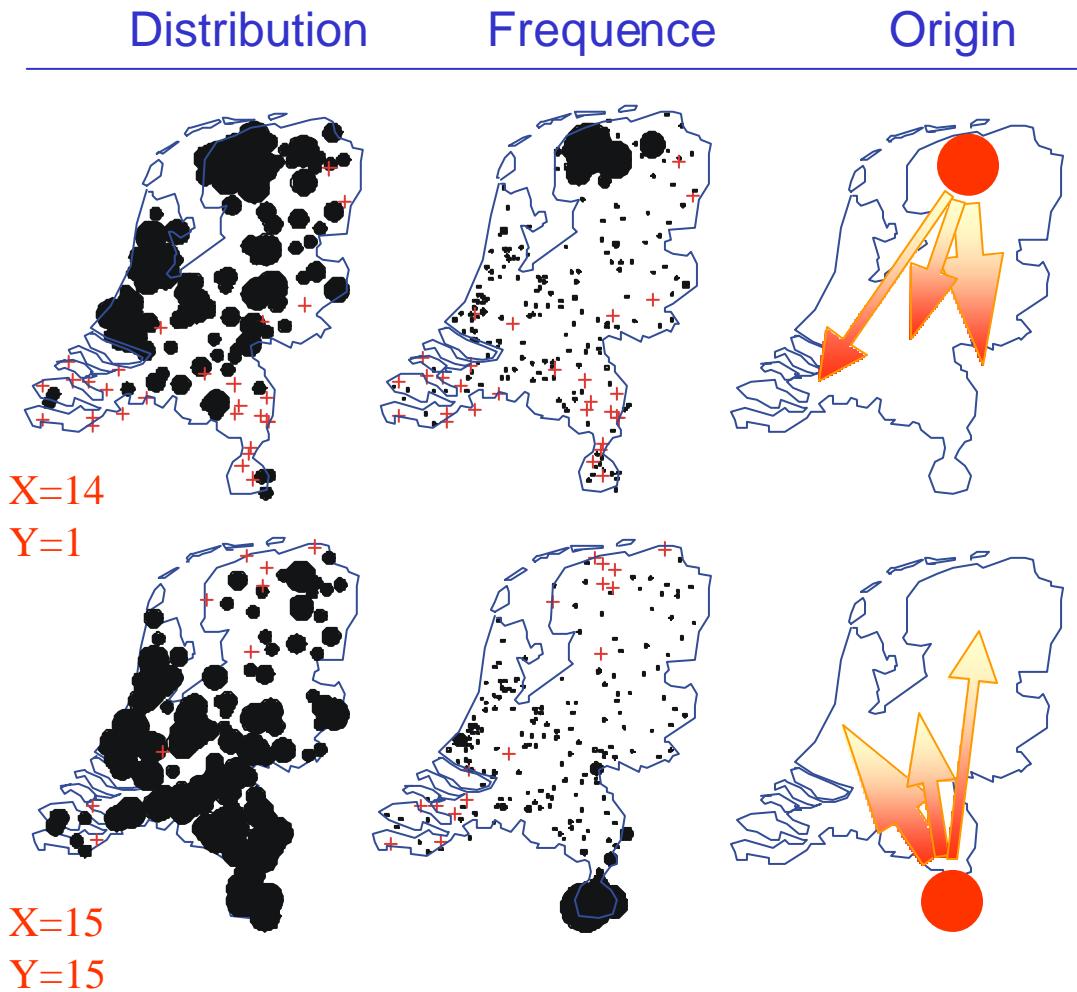
Beek, Berg, Bijl, Blom, Boer, Bos, Bosch, Bosman, Brink, Broek, Brouwer, Dam, Dekker, Dijk, Dijkstra, Graaf, Groot, Haan, Hendriks, Hoek, Horst, Huisman, Jager, Jansen, Janssen, Jong, Jonge, Kamp, Kok, Koning, Koster, Kramer, Kroon, Kuipers, Laan, Lange, Leeuw, Leeuwen, Linden, Meer, Meijer, Mulder, Peters, Post, Roos, Ruiter, Smits, Valk, Veen, Velde, Vermeulen, Visser, Vliet, Vonk, Vos, Vries, Wal, Wijk.

② Paesant; Wood; «From the wood»; King; Brewer; Hunter; «From the dam»;  
Chevalier; Fisherman; Big; Young; The young...

# Geographic origin...



# Migrations: *How many? Where from? Where to?*



36 surnames:

Abma, Algra, Anema, Attema, Baarda, Betten, Bonnema, Bontekoe, Bottema, Brinksma, Clossen, Cuperus, Damstra, Deelstra, Duiker, Haitsma, Hengst, Hoeksma, Huitema, Hylkema, Iedema, Jelsma, Kammen, Kooiker, Kuiken, Minnema, Mollema, Monsma, Numan, Piersma, Popma, Rienstra, Schaper, Sinnema, Steensma, Vlietstra

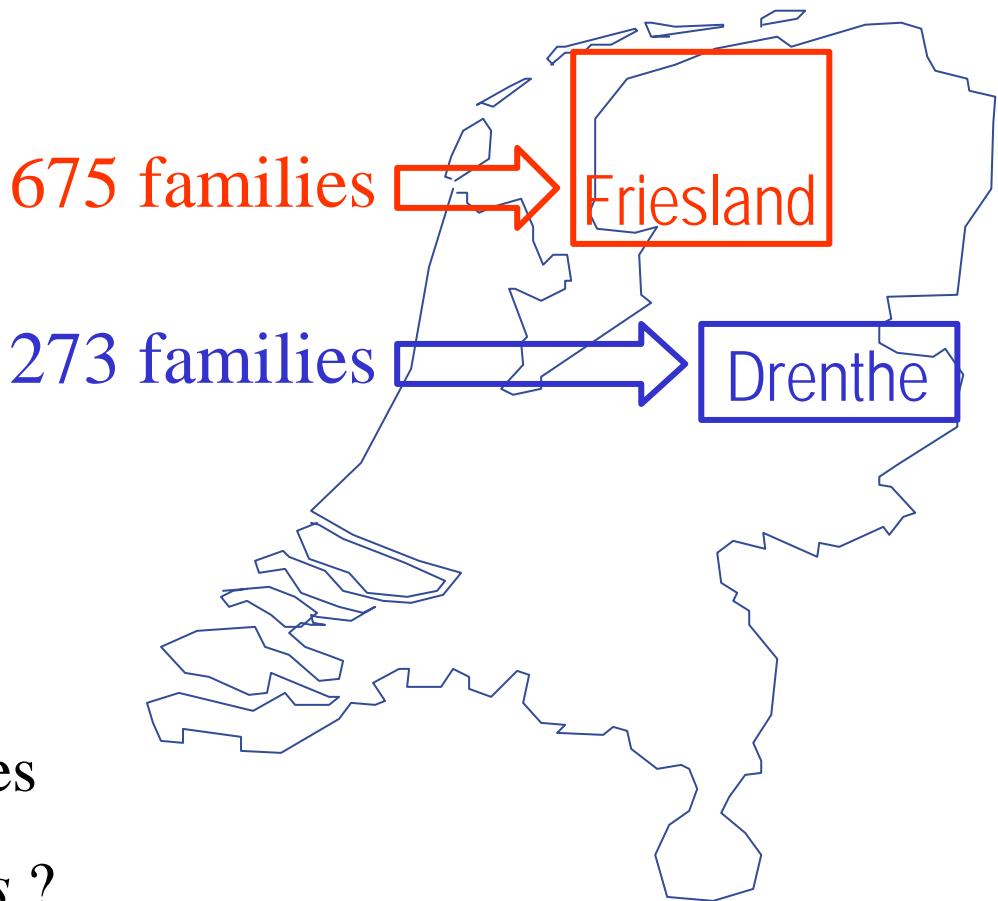
2

65 surnames:

Beurskens, Bisschops, Boonen, Breuer, Brouns, **Claassens**, **Claessen**, Cleef, Coenders, Coumans, Creemers, **Cuijpers**, Custers, **Cuypers**, Daemen, Daniels, Dassen, Dohmen, Eyck, Frenken, Gerards, Gijsen, Godschalk, Gubbels, Habets, Haenen, Hermens, Heynen, Hillen, Houwen, Jetten, Jeurissen, Knippenberg, Knops, Kurvers, Lenssen, Leurs, Maessen, Mans, Megen, Meuwissen, Michiels, Mommers, Palmen, **Paulissen**, **Paulussen**, Puts, Ramaekers, Ramakers, Reynders, Rijks, Rongen, Sassen, Schendel, Schols, Seuren, Sieben, Theelen, Thissen, Tummers, Verheggen, Verlinden, Vinken, Vroomen, Weerts

3

# *A well identified population:*

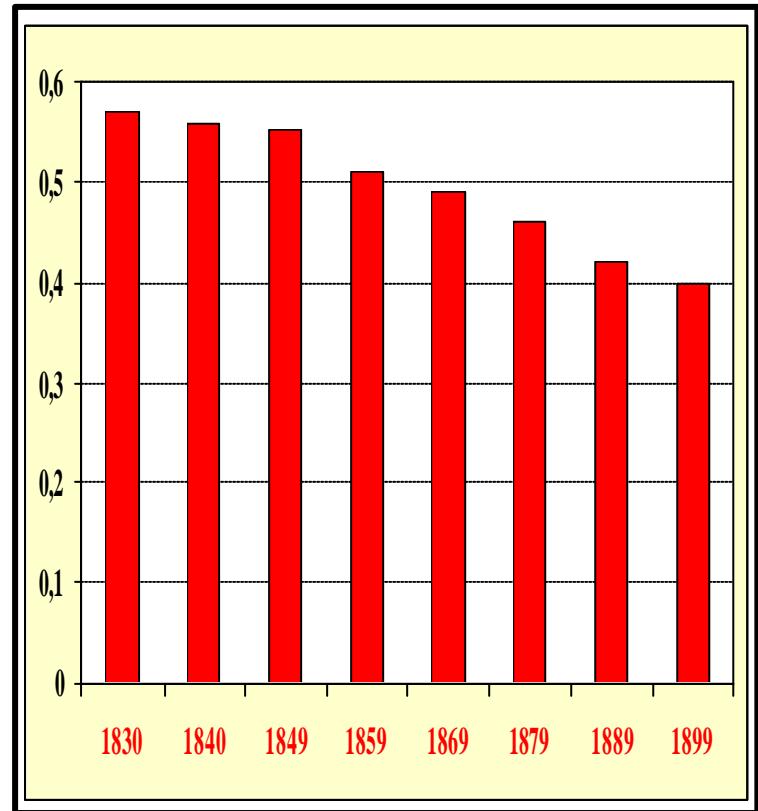


- Extinction of surnames
- Size of families: *clans* ?
- We only considered those surnames  $f > 40$  individuals

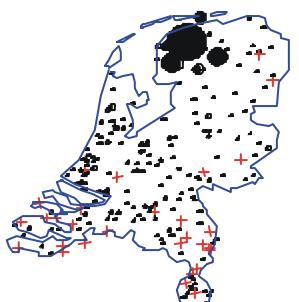
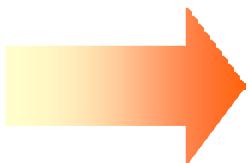
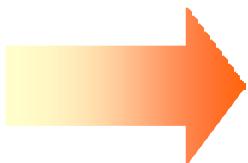
# Correlations with census data

4

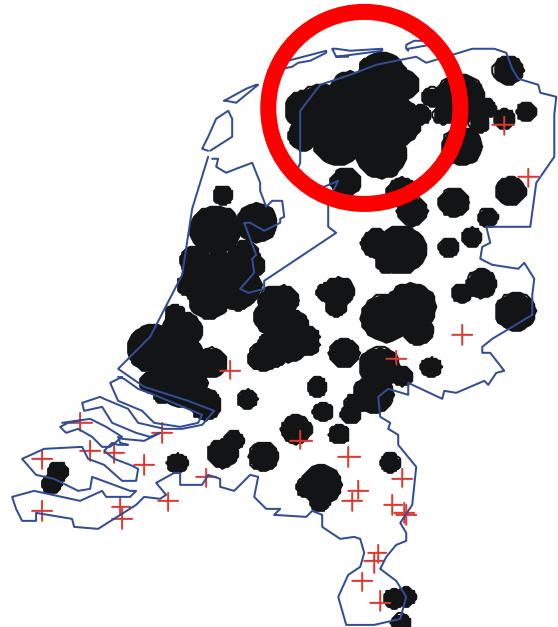
	<i>1830</i>	
	<i>census</i>	<i>SOMs</i>
Drenthe	21,328	273
Friesland	64,841	675
Gelderland	101,594	716
Groningen	50,161	345
Limburg	60,527	1,025
Noord Brabant	116,244	1,193
Noord Holland	117,971	610
Overijssel	58,344	699
Utrecht	41,814	399
Zeeland	42,824	864
Zuid Holland	141,41	1,035
<i>Total</i>	<i>817,058</i>	<i>7,834</i>



# How many didn't move? (with reference to the time of surnames' origin)

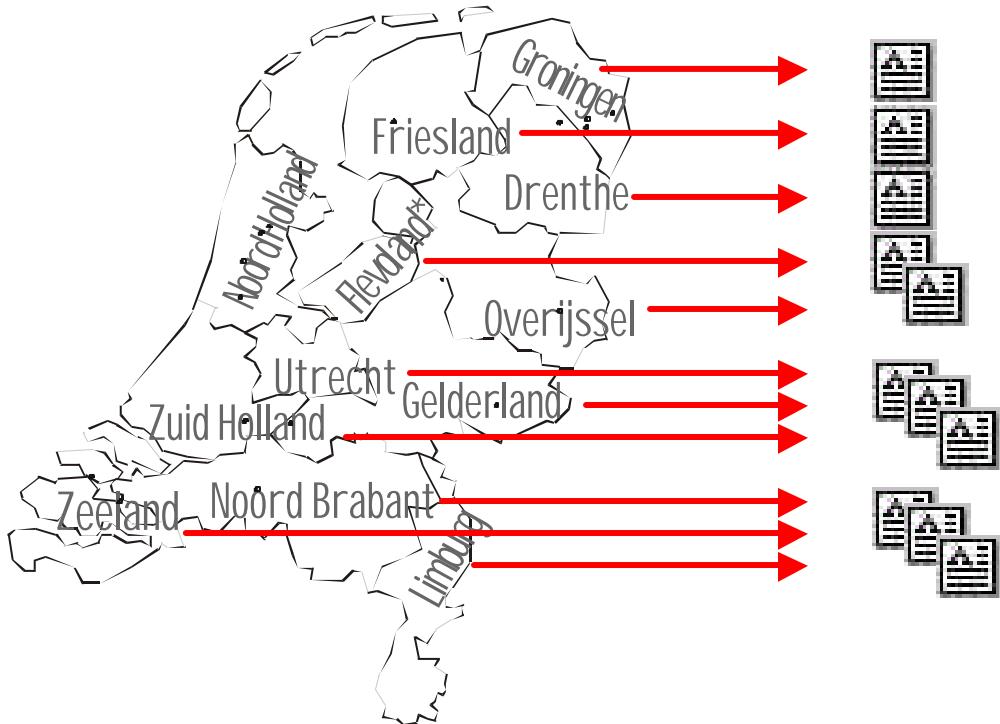


Abma, Algra, Anema, Attema,  
Baarda, Betten, Bonnema, Bontekoe,  
Bottema, Brinksma, Cnossen,  
Cuperus, Damstra, Deelstra, Duiker,  
Haitsma, Hengst, Hoeksma,  
Huitema, Hylkema, Iedema, Jelsma,  
Kammen, Kooiker, Kuiken,  
Minnema, Mollema, Monsma,  
Numan, Piersma, Popma, Rienstra,  
Schaper, Sinnema, Steensma,  
Vlietstra Beurskens, Bisschops,  
Boonen, Breuer, Brouns, Claassens,  
Claessen, Cleef, Coenders,  
Coumans, Creemers, Cuijpers,  
Custers, Cuypers, Daemen, Daniels,  
Dassen, Dohmen, Eyck, Frenken,  
Gerards, Gijzen, Godschalk,  
Gubbels, Habets, Haenen, Hermens,  
Heynen, Hillen, Houwen, Jetten,  
Jeurissen, Knippenberg, Knops,  
Kurvers, Lenssen, Leurs, Maessen,  
Mans, Megen, Meuwissen, Michiels,  
Mommers, Palmen, Paulissen,  
Paulussen, Puts, Ramaekers,  
Ramakers, Reynders, Rijks, Rongen,  
Sassen, Schendel, Schols, Seuren,  
Sieben, Theelen, Thissen, Tummers,  
Verheggen, Verlinden, Vinken,  
Vroomen, Weerts ...



20 %

# Improving the quality of Y chromosome samplings ...



Since we know which individuals live where their ancestors lived two centuries ago, then we can sample **only** corresponding families (surnames) !!!

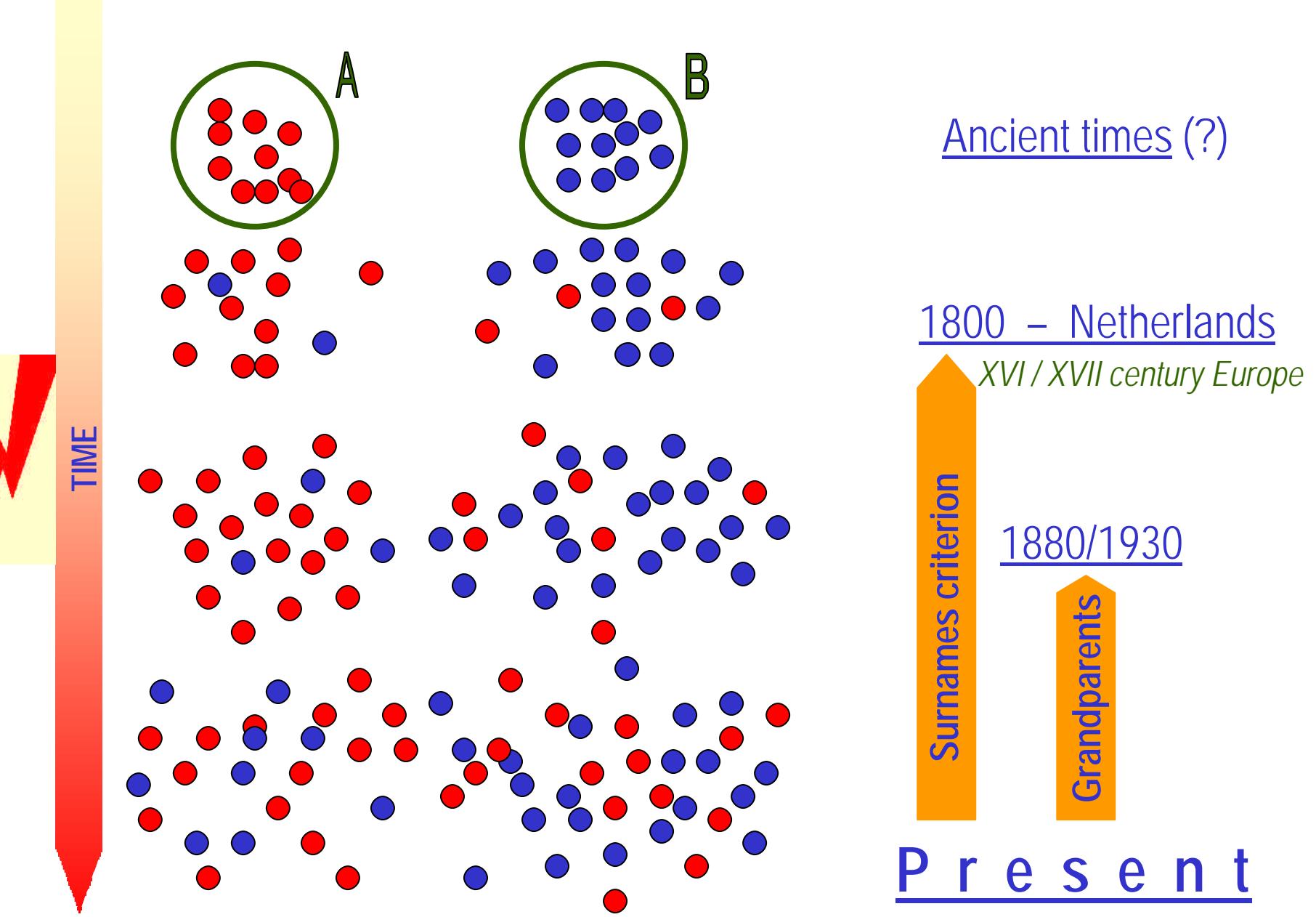
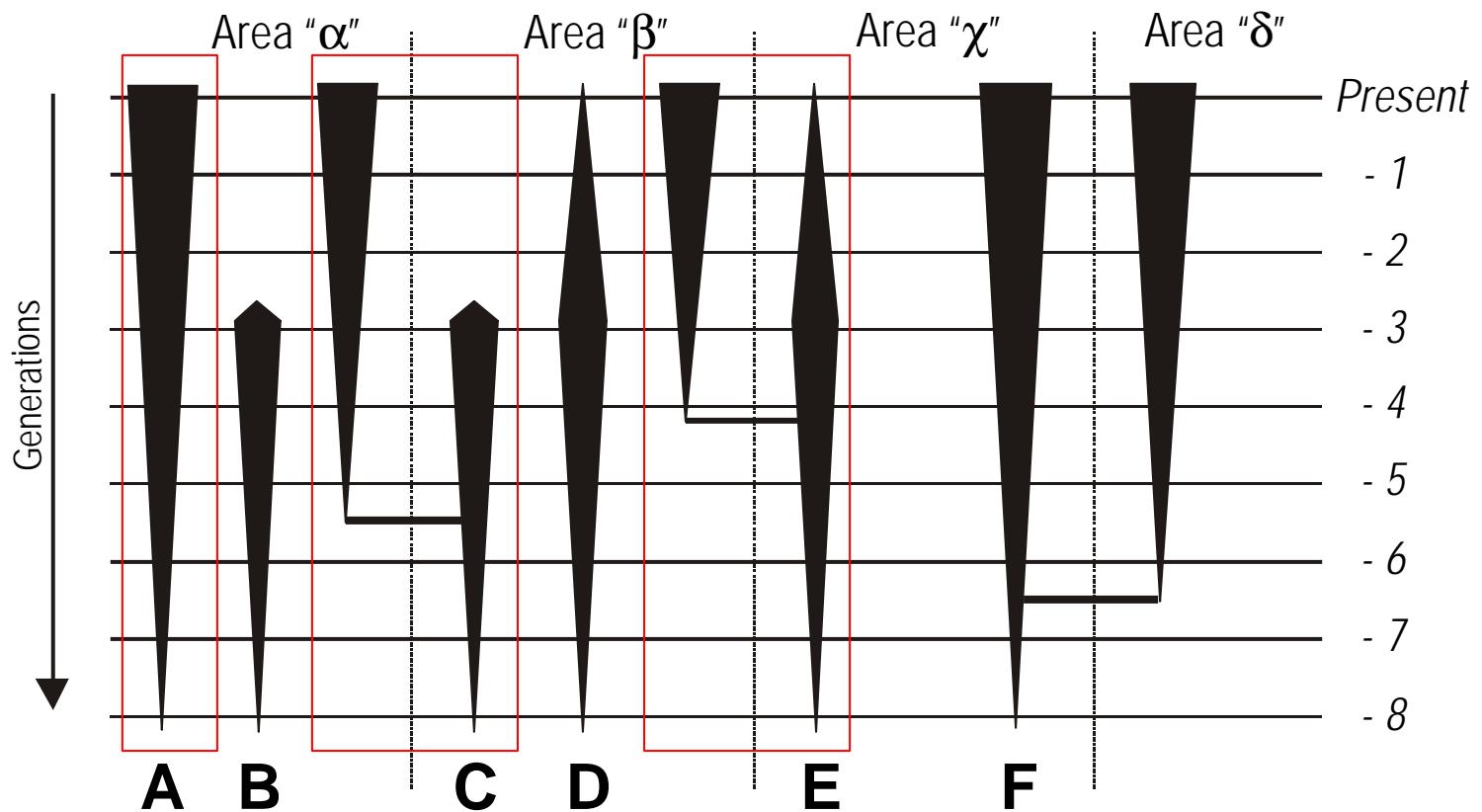


Fig. 5



# New Method for Surname Studies of Ancient Patrilineal Population Structures, and Possible Application to Improvement of Y-Chromosome Sampling

Franz Manni,\* Bruno Toupance, Audrey Sabbagh, and Evelyne Heyer



The Wenner-Gren Foundation  
supporting worldwide research in all branches of anthropology

# Leidse Wetenschappers professoren

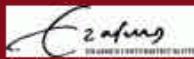
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**Prof.dr. P. de Knijff (Peter)**

**Prof. dr. Manfred Kayser**

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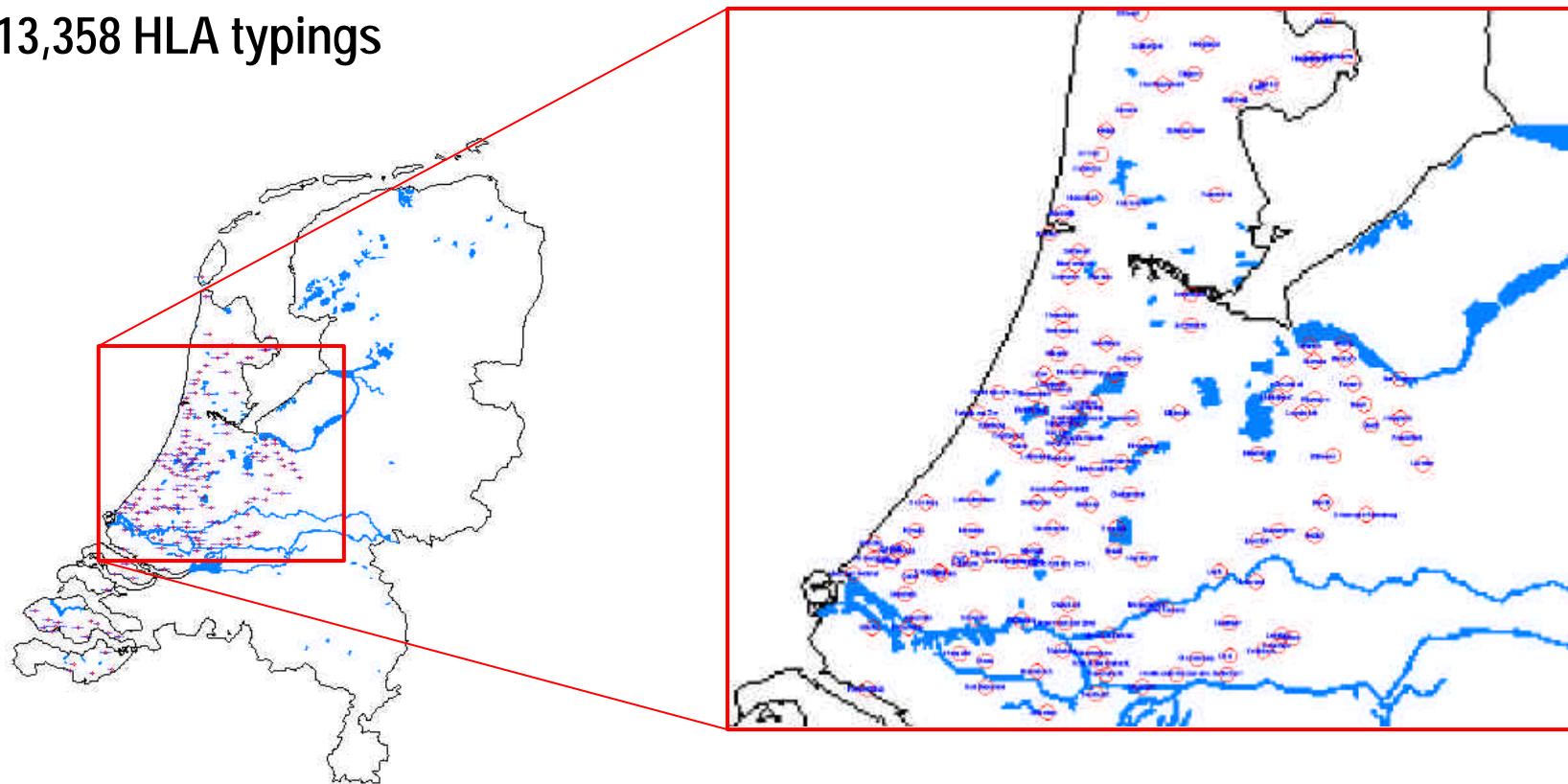


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supporting worldwide research in all branches of anthropology

We would like to compare a random sample of the Dutch population with a sample selected according to surnames specific of given locations.

13,358 HLA typings



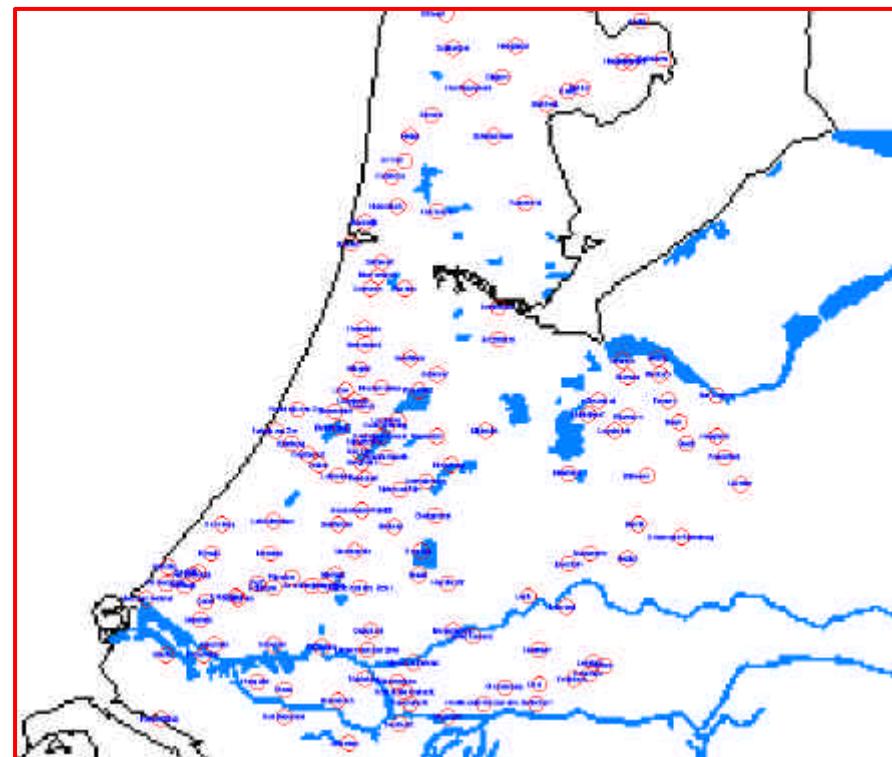


We would like to compare a random sample of the Dutch population with a sample selected according to surnames specific of given locations.

13,358 HLA typings

210 locations

Province	Locations	Individuals
N. Holland	60	2007
Z Holland	104	10,582
Utrecht	22	301
Zeeland	24	468





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13,358 HLA typings

210 locations

Province	Locations	Individuals
N. Holland	60	2007
Z Holland	104	10,582
Utrecht	22	301
Zeeland	24	468

People with a surname really from Noord Holland, Zuid Holland, Utrecht and Zeeland: 1310

We compared such 1310 individuals with the resting 12,048 ones

There is a statistically significant difference

Wait a second, please...





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New editorship (october 2008)

Evelyne Heyer

Editor-in-Chief

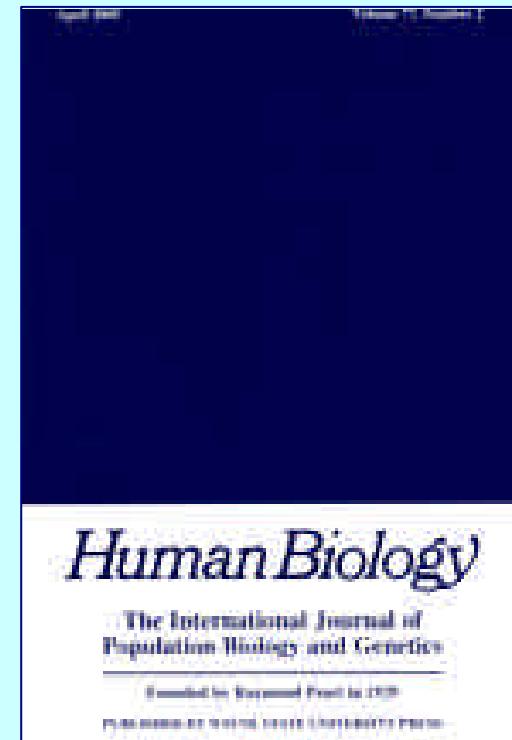
Franz Manni

Executive Editor

Guido Barbujani

Associate Editor

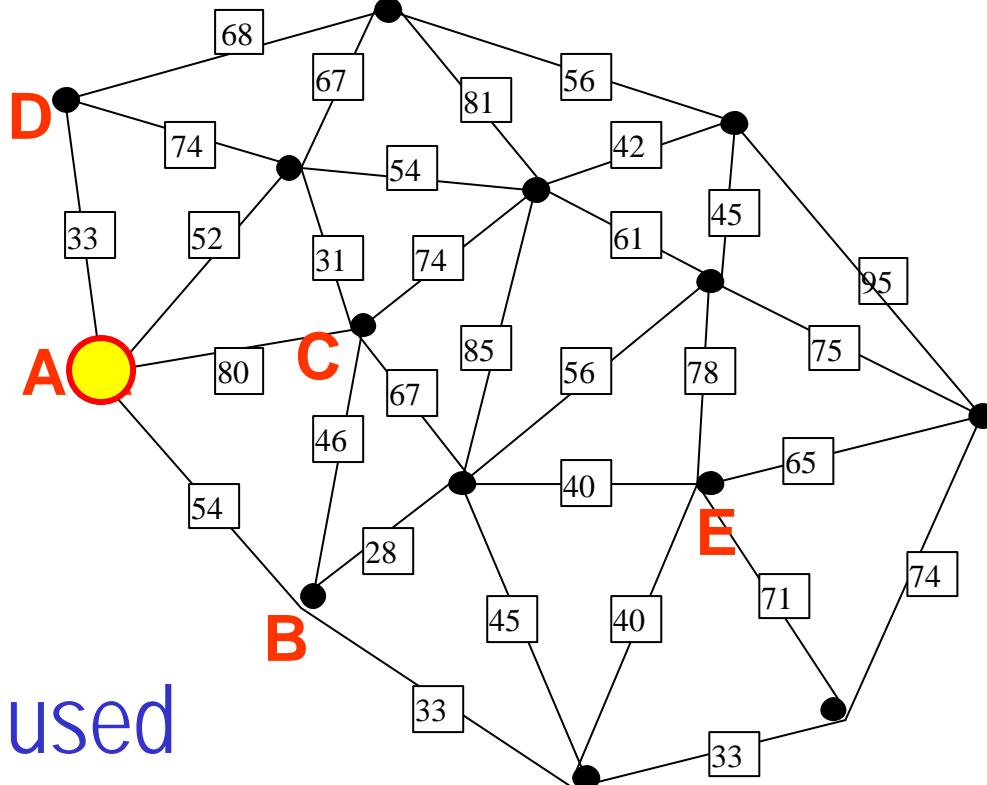
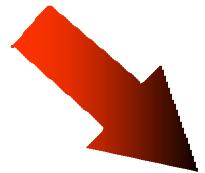
*Interdisciplinary papers* : population genetics,  
cultural evolution, demography, anthropology...





	A	B	C	D	E
A	0				
B	54	0			
C	80	38	0		
D	33	61	78	0	
E	40	28	74	33	0

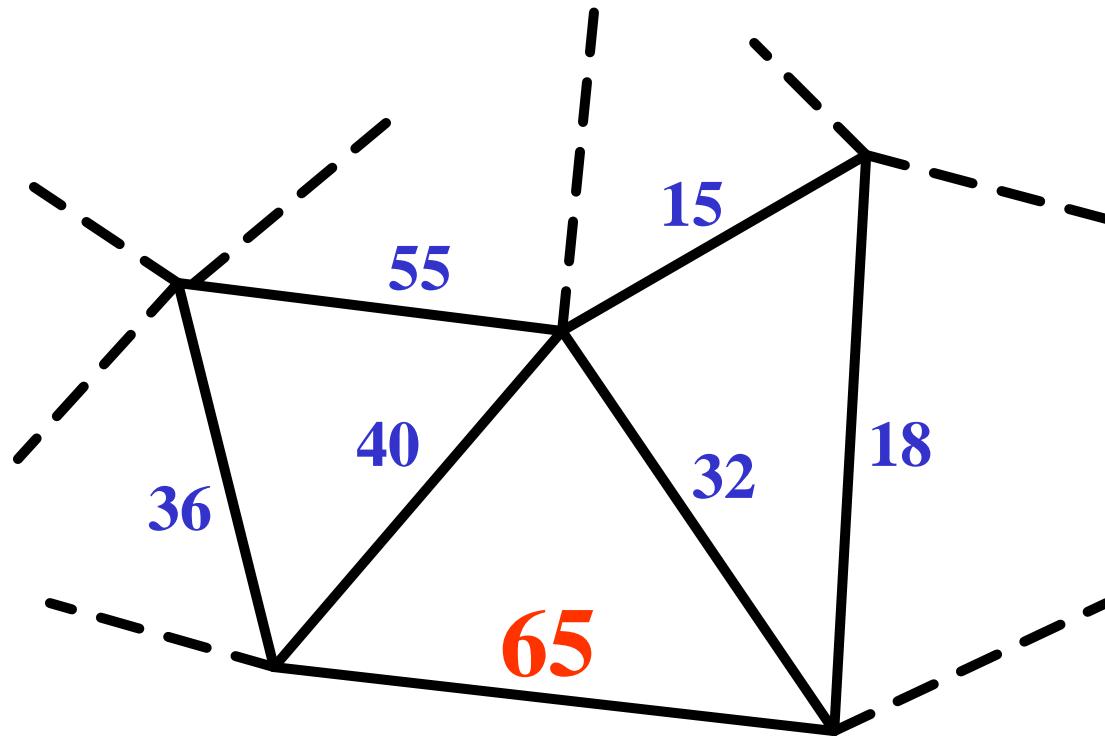
...



The matrix is partially used

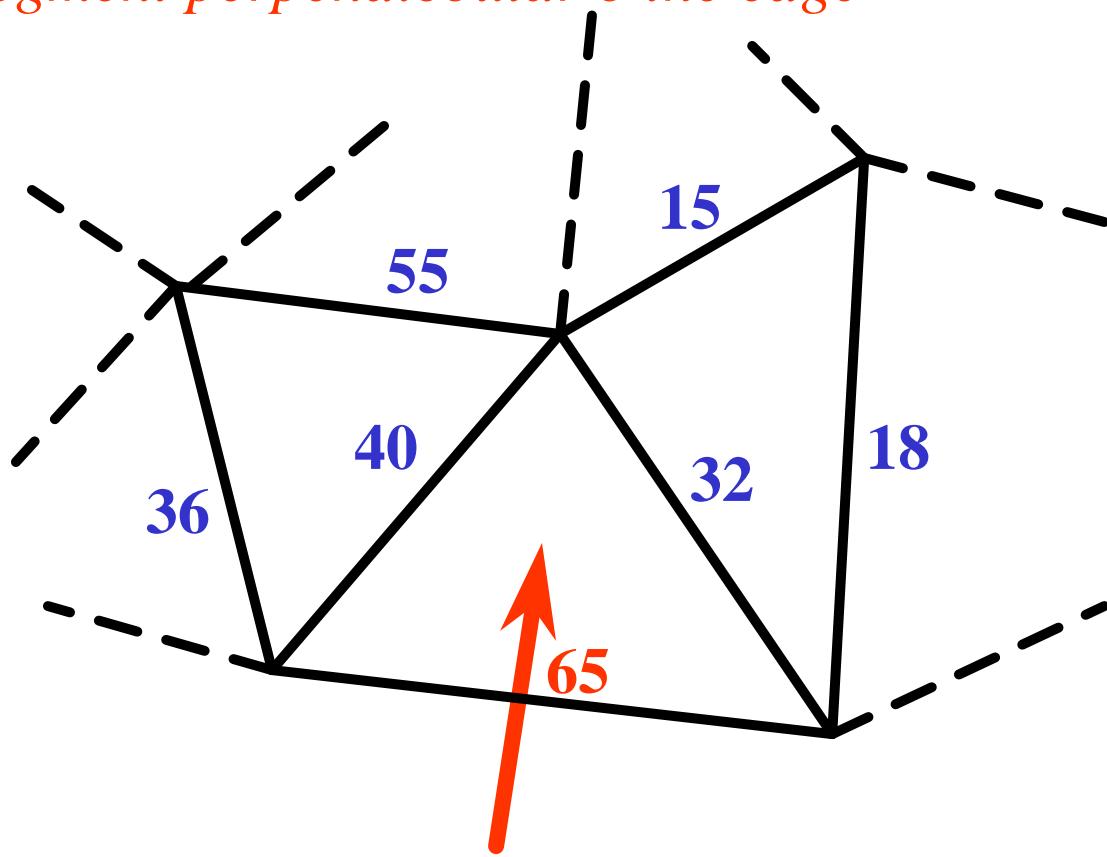
# Monmonier algorythm

1) Search for the higher distance value



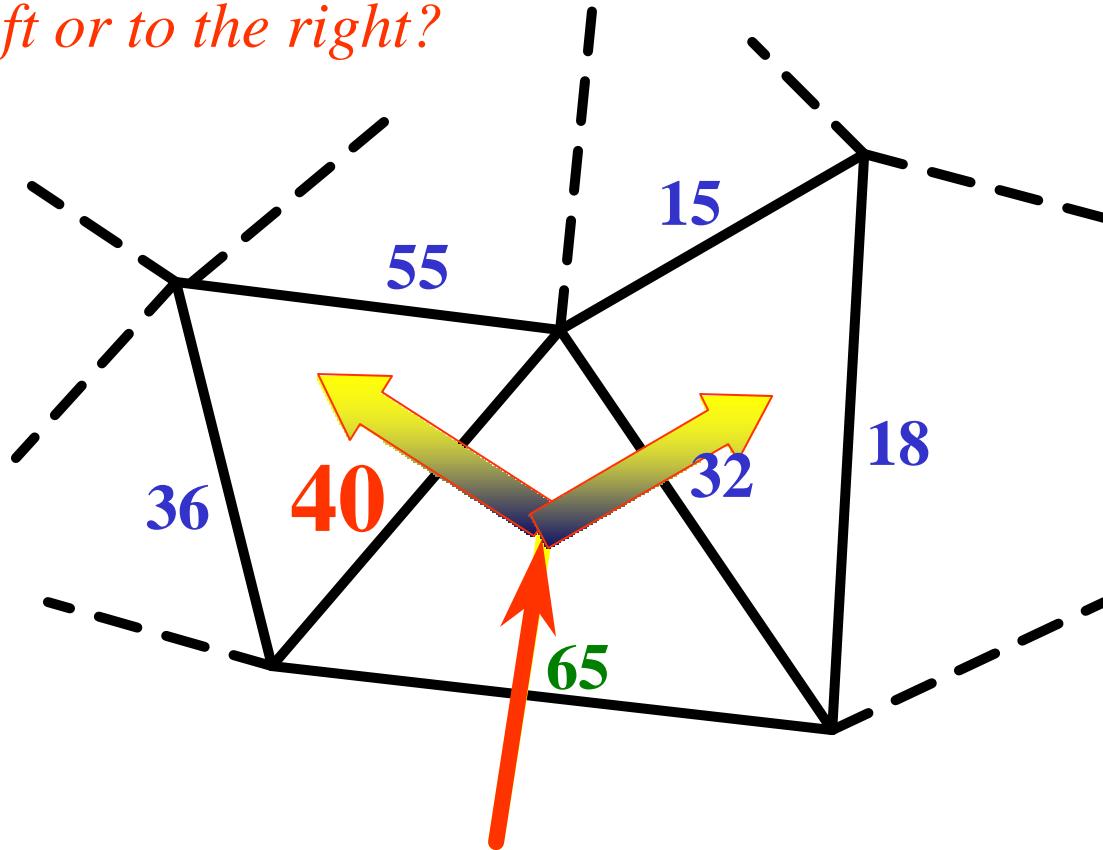
# Monmonier algorythm

- 1) Search for the higher
- 2) Trace a segment perpendicular o the edge



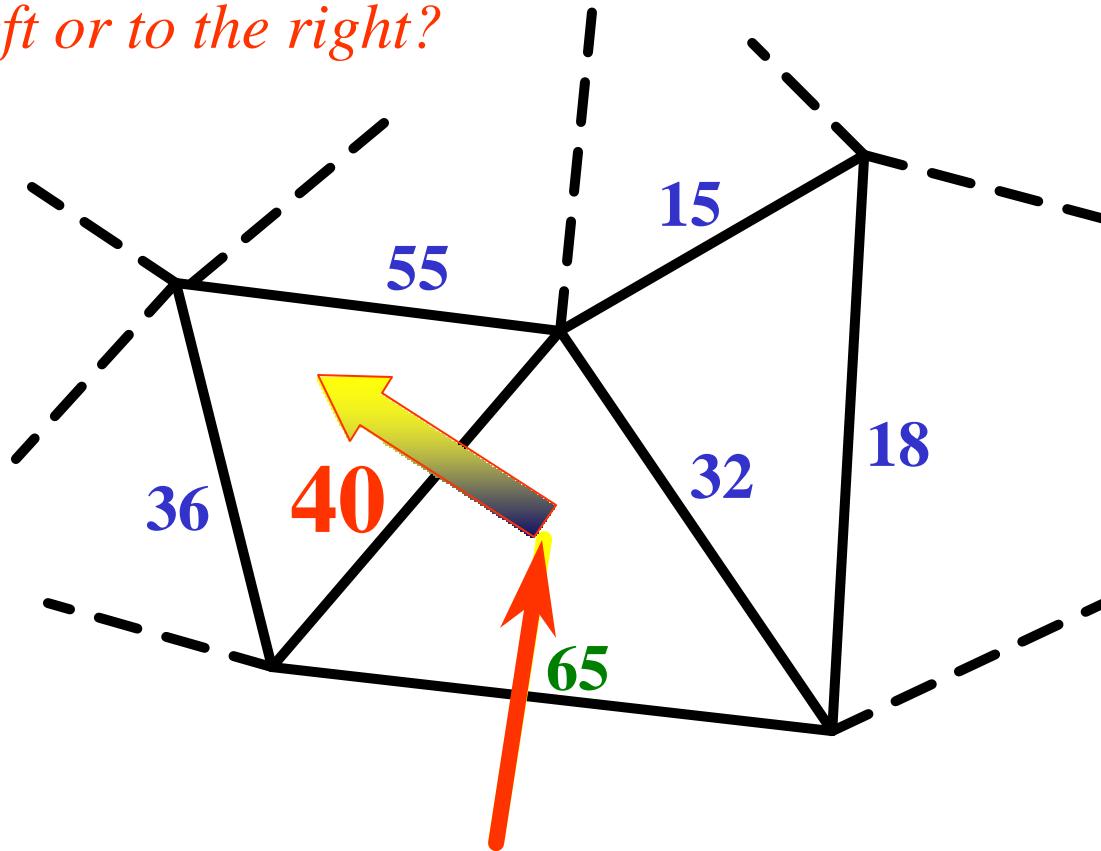
# Monmonier algorythm

- 1) Search for the highest distance value
- 2) Trace a segment perpendicular to the edge of triangle
- 3) To the left or to the right?



# Monmonier algorythm

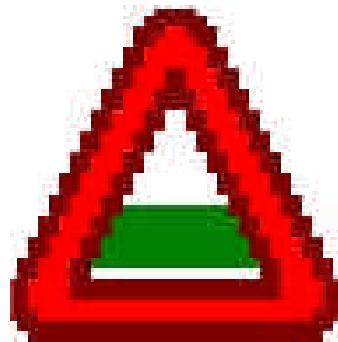
- 1) Search for the highest distance value
- 2) Trace a segment perpendicular to the edge
- 3) To the left or to the right?



## **Barrier vs. 2.2 for MS Windows**

a software to compute geographic barriers from a distance matrix

By F. Manni and E. Guérard



**Google** Nederland : **"barrier" "2.2"**