Multivariate analysis of genetic data — uncovering spatial structures —

Thibaut Jombart

MRC Centre for Outbreak Analysis and Modelling
Imperial College London

Genetic data analysis with R
PR∼Statistics, Glasgow
07-08-2015

Outline

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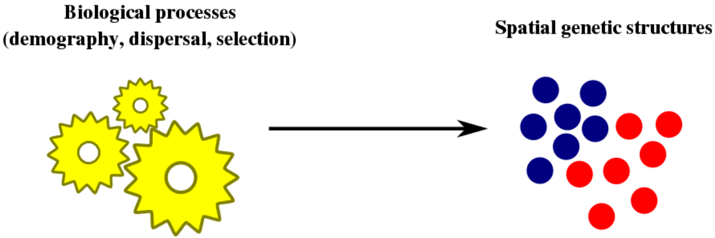
From processes to structures

Genetic structure: non-random distribution of genetic diversity.



Identify structures to infer processes.

From processes to structures

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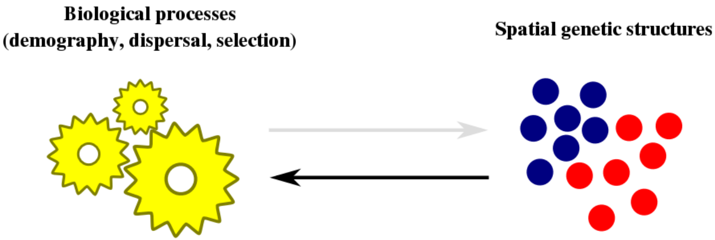
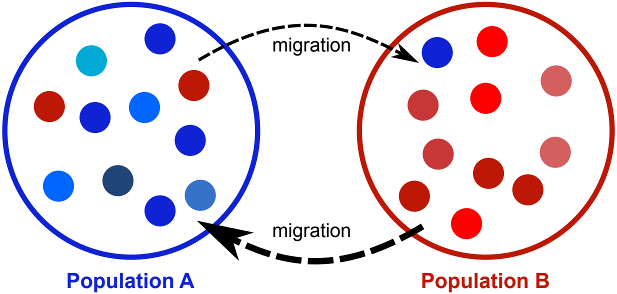


Identify structures to infer processes.

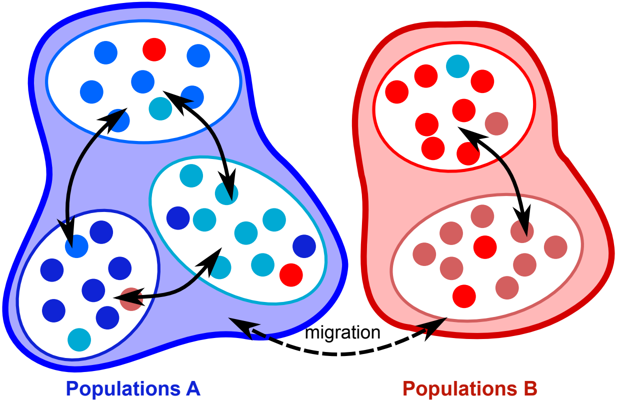
Island model

Reproduction within populations + migration.



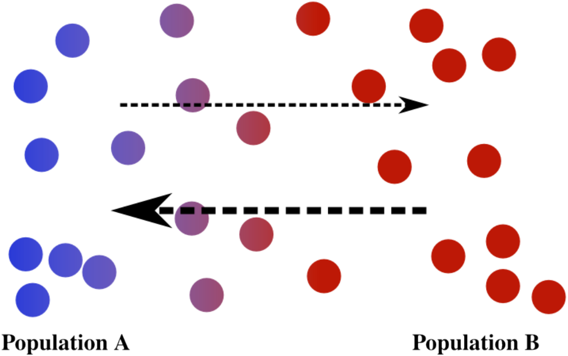
Hierarchical island model

Reproduction within subpopulations + stratified migration.



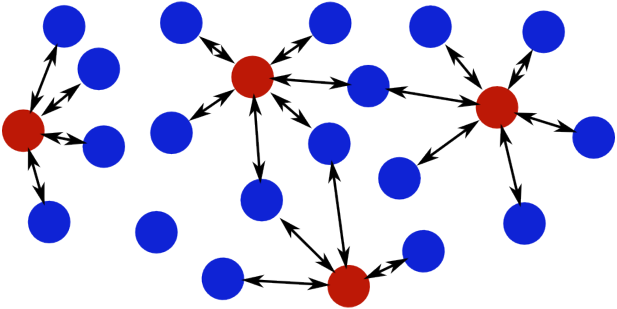
Isolation by distance (IBD)

Reproduction between neighbours → '*diffusion*' of genes



Inbreeding avoidance

Mating with individuals from another population → '*repulsion*' structure



Genetic models and spatial structures

- *island / hierarchical island model*: patches of related genotypes
- *isolation by distance (IBD)*: clines of genetic differentiation
- *inbreeding avoidance*: repulsion structure

⇒ Genetic processes often create spatial structures.
How can we reveal them?

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Introduction

Testing spatial structures
- Moran's Index
- Mantel's correlation

Multivariate analysis of spatial patterns

Spatial autocorrelation

Definitions:

- *in general*: values of a variable non independent from the corresponding spatial locations
- *in genetics*: genetic distance is correlated to spatial distance

Two types of spatial autocorrelation:

- **positive**: closer individuals are more similar than at random
- **negative**: closer individuals are more dissimilar than at random

Spatial autocorrelation

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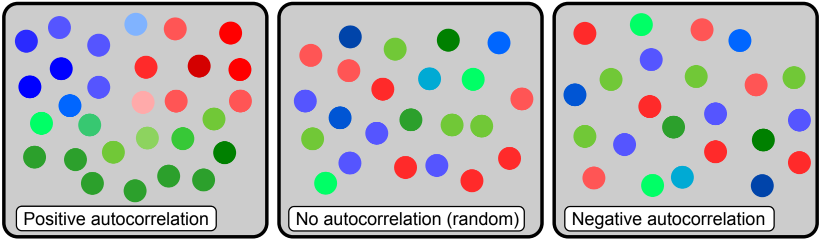
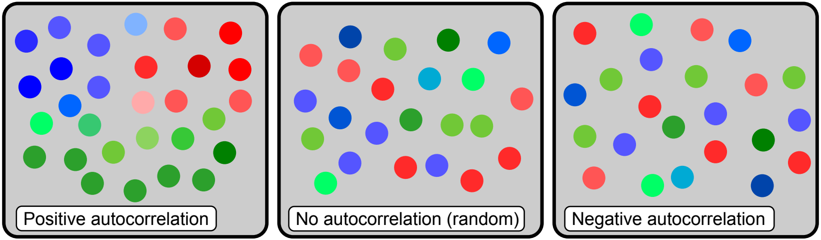
Spatial autocorrelation: illustration



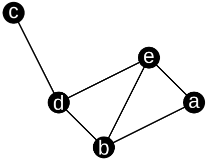
How do we measure spatial autocorrelation?

Spatial autocorrelation: illustration



How do we measure spatial autocorrelation?

From spatial coordinates to spatial weights



Matrix of spatial weights $\mathbf{L}$

Row i : uniform weights for neighbours of i.

	a	b	c	d	e
a	0.000	0.500	0.000	0.000	0.500
b	0.333	0.000	0.000	0.333	0.333
c	0.000	0.000	0.000	1.000	0.000
d	0.000	0.333	0.333	0.000	0.333
e	0.333	0.333	0.000	0.333	0.000

Let $\mathbf{x}$ be a variable with one value at each location.

The lag vector $\mathbf{Lx}$ computes mean values of neighbours.

From spatial coordinates to spatial weights

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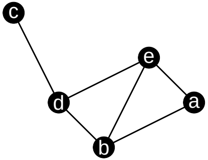

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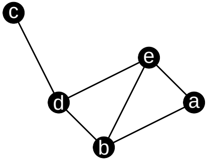

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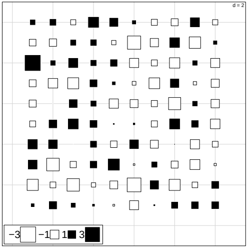
A variable and its lag-vector

Lag vector :

Random:



Regression of $\mathbf{Lx}$ onto $\mathbf{x}$:

A variable and its lag-vector

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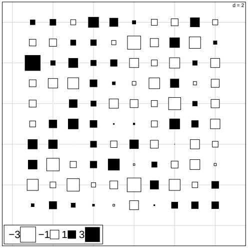
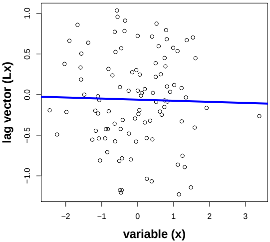


Lag vector :



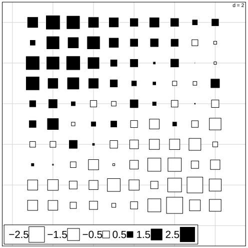
Regression of $\mathbf{Lx}$ onto $\mathbf{x}$:

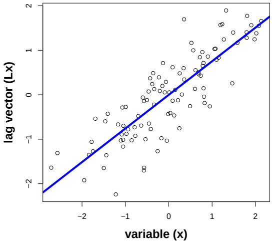
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
x	1	0.02	0.02	0.06	0.8081
Residuals	98	31.53	0.32		

A variable and its lag-vector

Lag vector :

Positive autocorrelation:





Regression of $\mathbf{Lx}$ onto $\mathbf{x}$:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
xG	1	65.91	65.91	245.69	0.0000
Residuals	98	26.29	0.27		

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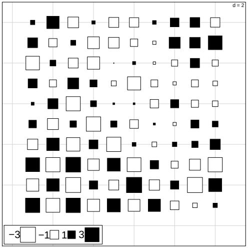
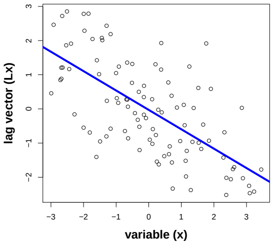
Lag vector :

Negative autocorrelation:





Regression of $\mathbf{Lx}$ onto $\mathbf{x}$:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
xL	1	87.56	87.56	77.80	0.0000
Residuals	98	110.29	1.13		

Moran's index: definition

Moran's I:

$$I(\mathbf{x}) = \frac{\mathbf{x}^T\mathbf{L}\mathbf{x}}{n}\frac{1}{\text{var}(\mathbf{x})}$$

where:

- $\mathbf{x} \in \mathbb{R}^n$: a centred variable (e.g. allele frequency, PC)
- $\mathbf{L}$: matrix of spatial weights (nxn)
- $\mathbf{Lx}$: lag vector
- $I_0 = \frac{-1}{n-1} \approx 0$: null value (no autocorrelation, i.e. random spatial distribution)

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Variable, lag-vector, Moran's I

Lag vector :

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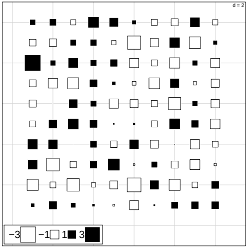

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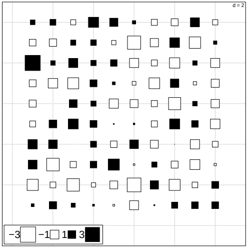

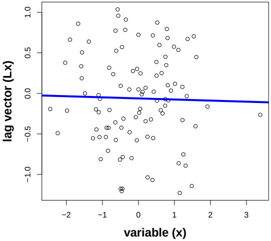

Moran's I:
$I(\mathbf{x}) \approx I_0$

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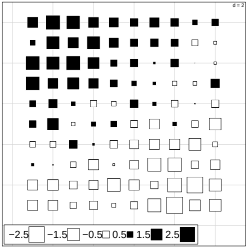

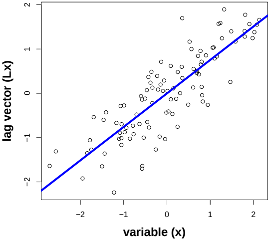

Moran's I:
$I(\mathbf{x}) > I_0$

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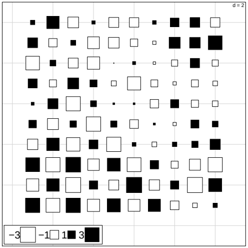
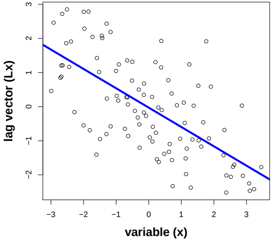
Negative autocorrelation:





Moran's I:

$I(\mathbf{x}) < I_0$

Testing Moran's I

Monte Carlo procedure:

- compute I from the data
- permute randomly the locations to get a value of I under H_0: "$\mathbf{x}$ is distributed at random across space."
- repeat this operation a large number of times to obtain a reference distribution of I under H_0
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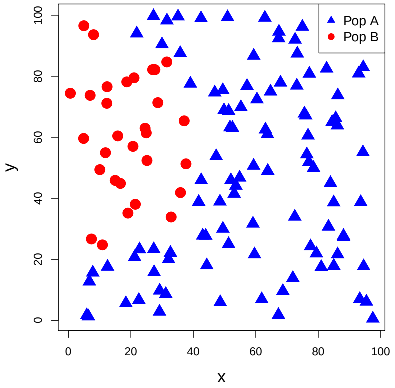
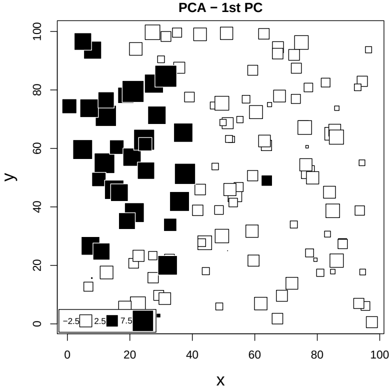
Application: testing spatial structures in principal components

Data (2 population, island model):

PCA results, PC 1:





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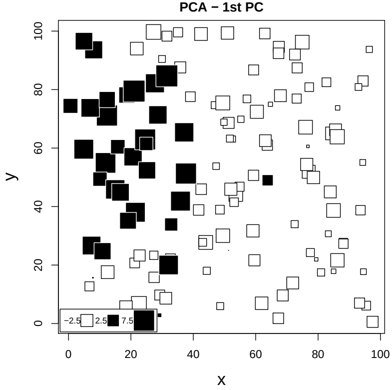
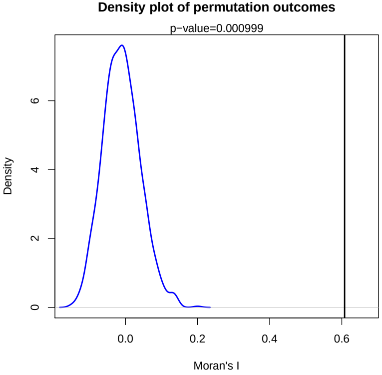


Moran's I test of PC1:



Univariate /vs/ multivariate correlation

- Moran's I is univariate
- *solution*: test a few principal components
- *problems:*
    - does not use all the genetic information
    - which PC to test?
    - correction for multiple testing

⇒ need for multivariate tests

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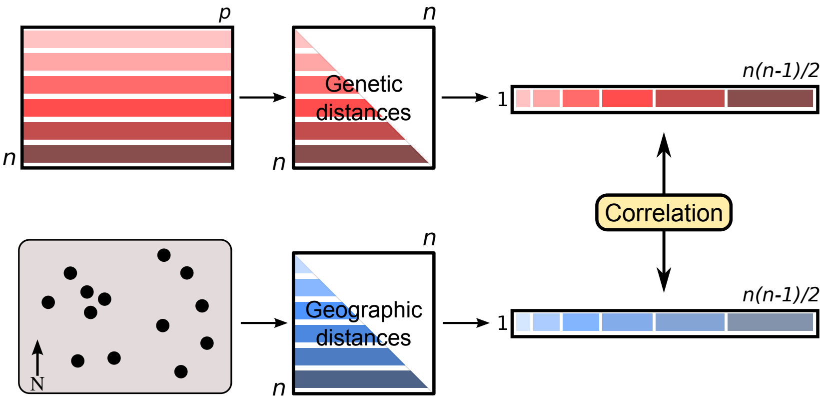
Mantel's correlation: rationale

Correlation between two unfolded distance matrices.



Mantel's correlation: definition

Notations:

- $\mathbf{X} = [x_{ij}]$ ($\mathbf{X} \in \mathbb{R}^{n \times n}$): genetic distances
- $\mathbf{Y} = [y_{ij}]$ ($\mathbf{Y} \in \mathbb{R}^{n \times n}$): geographic distances
- $\bar{x}$, $\bar{y}$: means of x and y (excepting diagonals)
- s_x, s_y: standard deviation of x and y (excepting diagonals)

Original definition (unstandardized):

$$z_{\mathsf{M}} = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} x_{ij} y_{ij}$$

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Standardized coefficient (true correlation):

$$r_{\mathsf{M}} = \frac{1}{d-1} \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} (\frac{x_{ij} - \bar{x}}{s_x})(\frac{y_{ij} - \bar{y}}{s_y})$$

Testing Mantel correlation

Monte Carlo procedure:

- compute z_{M} or r_{M} from the data
- permute randomly the rows and columns of one matrix, recompute the test statistic (i.e., under H_0: "no correlation")
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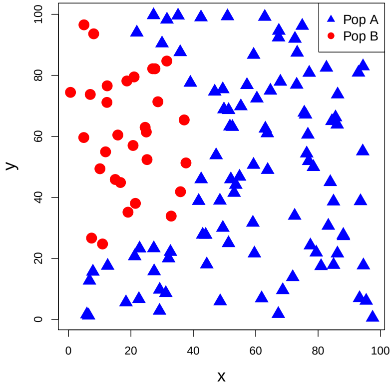
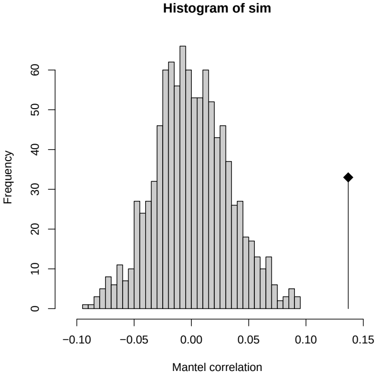


Mantel test:



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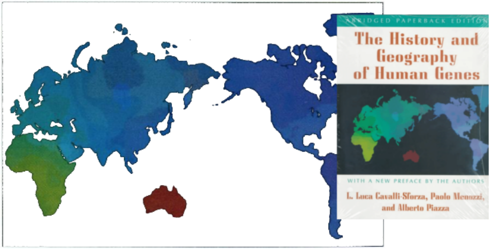
Mapping principal components

Maps of the three first principal components of PCA.



Are we actually looking for spatial patterns here?

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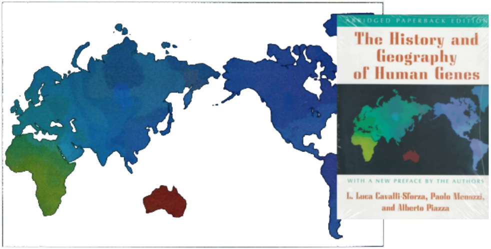

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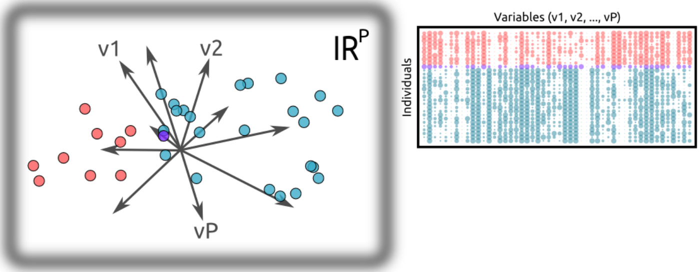

Principal components with *maximum total variance*.

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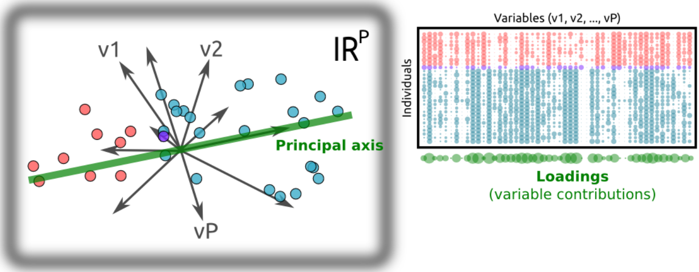

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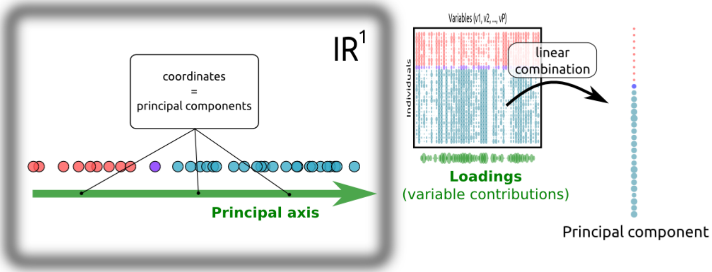

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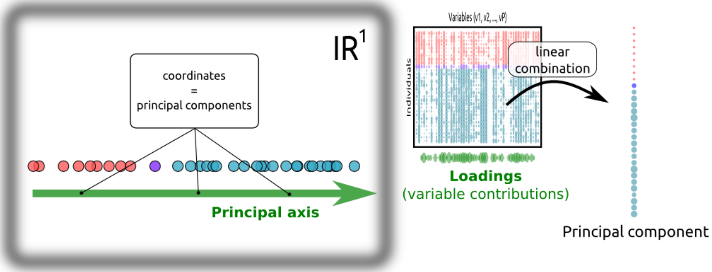

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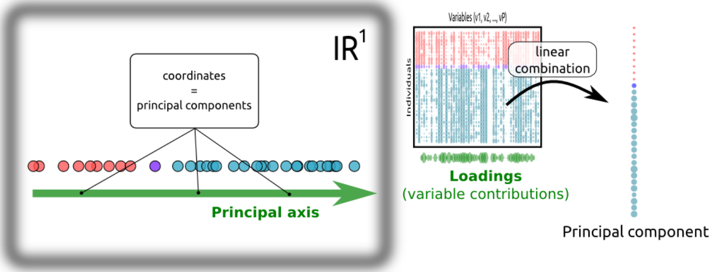

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Using spatial information

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- they may reveal obvious spatial structures, but overlook finer patterns

  ⇒ need for taking spatial information into account

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- they may reveal obvious spatial structures, but overlook finer patterns

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Spatial Principal Component Analysis (sPCA): rationale

Principal components should:

- display variability ⇒ optimize *total variance*
- display positive autocorrelation ⇒ *large Moran's I*
- (or) display negative autocorrelation ⇒ *low (negative) Moran's I*

sPCA decomposes: $(\textit{total variance}) \times (\textit{Moran's } I)$

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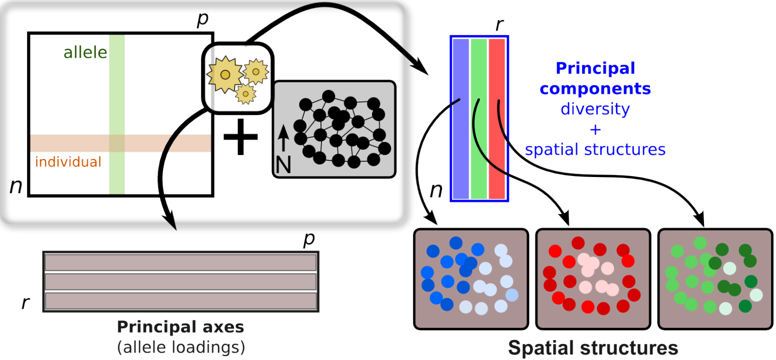
Spatial Principal Component Analysis (sPCA): outputs



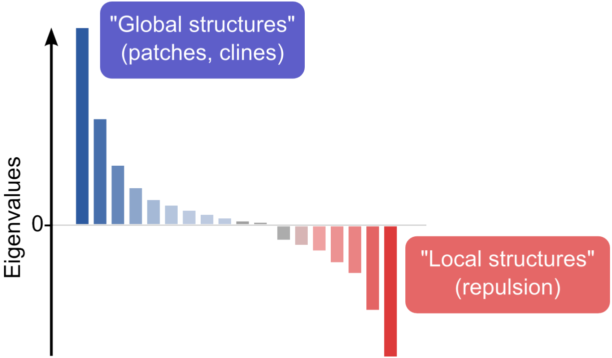
Principal components
diversity
+
spatial structures

Principal axes
(allele loadings)

Spatial structures

Global and local structures

Unlike other multivariate methods, sPCA has **positive** and **negative** eigenvalues



How do we get these in practice?

Global and local structures

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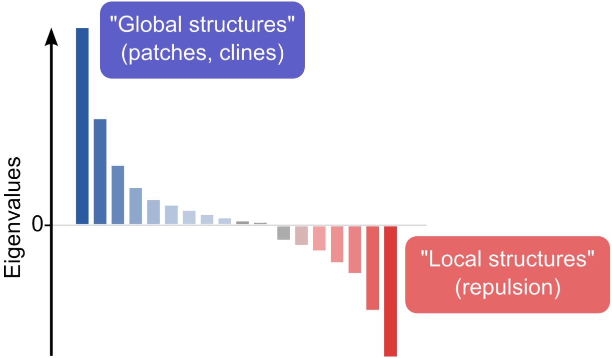

How do we get these in practice?

Time to get your hands dirty (one last time)!

The pdf of the practical is online:

`http://adegenet.r-forge.r-project.org/`

or

Google → adegenet → documents → "Workshop Glasgow, August 2015"