



Co-structure of two tables

Application to a clinical study designed to demonstrate the superiority of drug A over drug B in reducing pre-existing coronary atherosclerosis in T2DM patients

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Clinical Trial	<i>Main analysis, Baseline values</i>
1. PCA	} <i>Principles, Applications</i>
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Conclusion	<i>MVA, R, graphics</i>

Aims of this talk

1. **Multivariate statistical analysis**
2. **Variety of graphics**
3. **Statistical language R**



List of Abbreviations

- . PCA = Principal Component Analysis
- . LDA = Linear Discriminant Analysis
- . MVA = Multivariate Analysis
- . T2DM = Type 2 Diabetes Mellitus
- . CHD = Coronary Heart Disease



What is R ?

« A Programming Environment for Data Analysis and Graphics »

Basic package

+

Specific Packages

- linear and non linear modelling,
- classical statistical tests,
- time-series analysis,
- classification,
- clustering,
- ...

Free Software under the terms of the GNU General Public License

<http://www.r-project.org/>

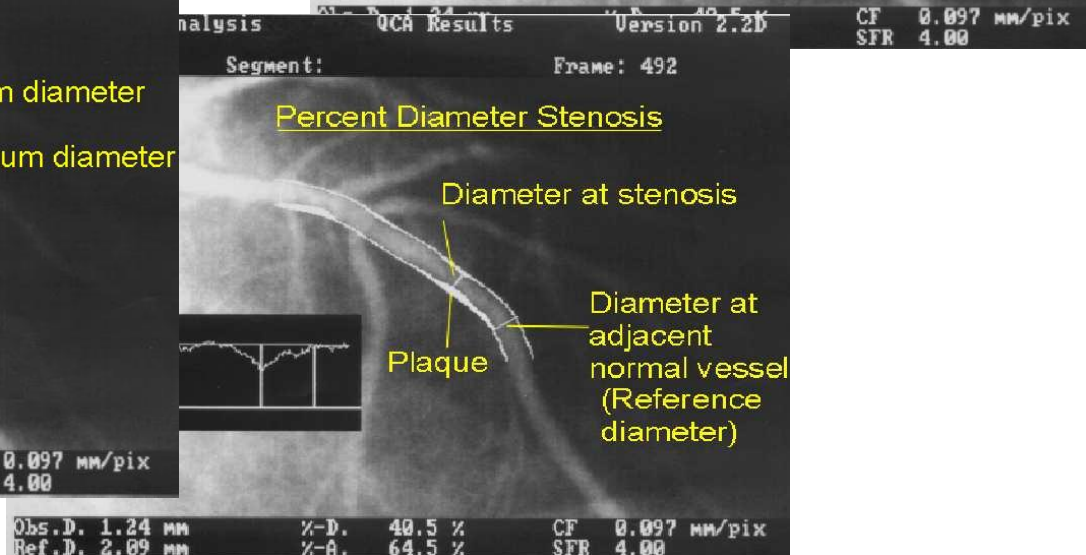
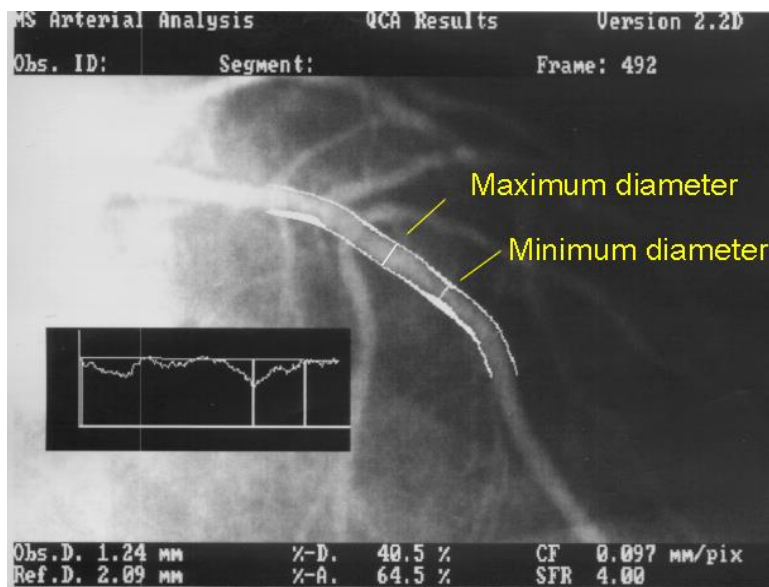
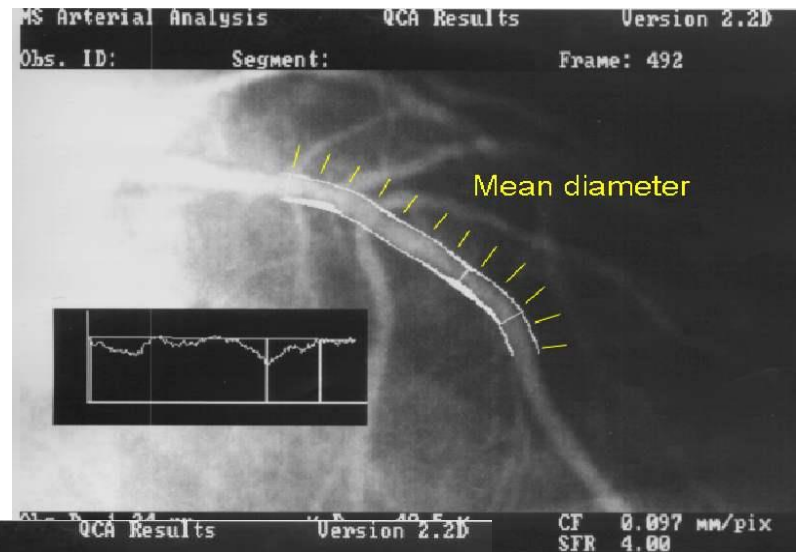


Lipid lowering drugs in T2DM

- NCEP/ATP III guidelines consider diabetes as a CHD risk equivalent, in part because its frequent association with multiple risk factors



Angiography





Synopsis

- Randomised, double-blind, two parallel arms : drug A *vs.* drug B
- N=418 randomized patients, 305 males, 113 females
- Mean Treatment Duration ~ 3 years
- Mean Age at Baseline ~ 57 years
- n=379 non missing data

« To compare the average diameter between groups »

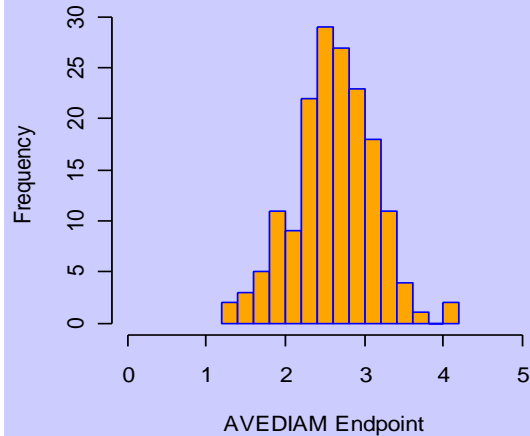
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TC, HDL-C, IDL-C, cLDL-C, qLDL-C, VLDL-C, TG, IDL-TG, VLDL-TG,
Apo AI, Apo CIII, Apo B, Lp a, Lp AI, Lp AII

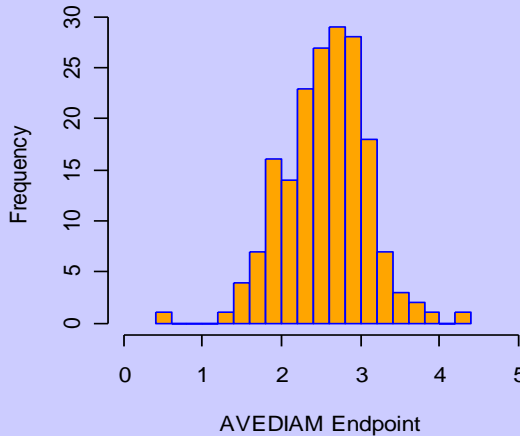
Average diameter, Minimum diameter, %Stenosis, %New lesions,
%Progressing segments, %Regressing or Stable segments



Histogram for drug A

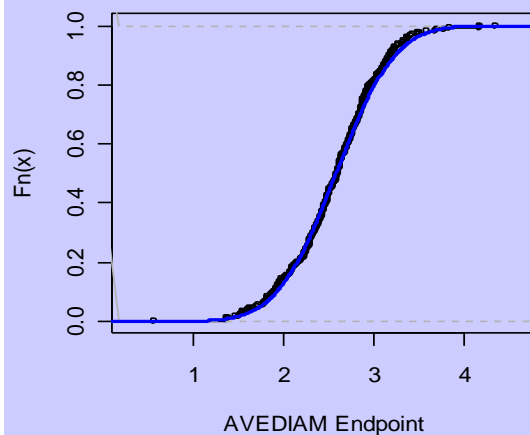


Histogram for drug B



Main analysis on
Average diameter

ECDF



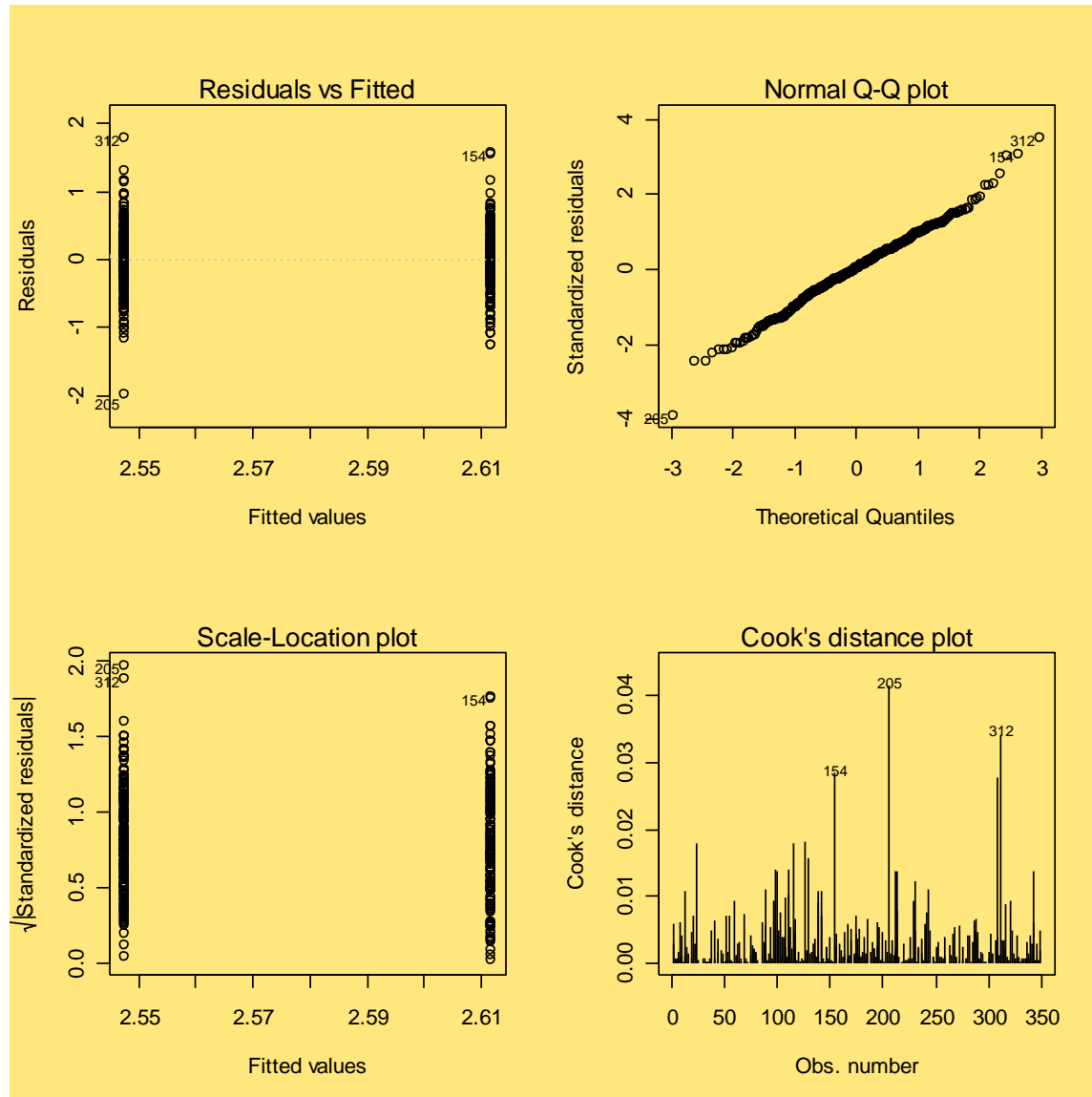
Analysis of Variance Table

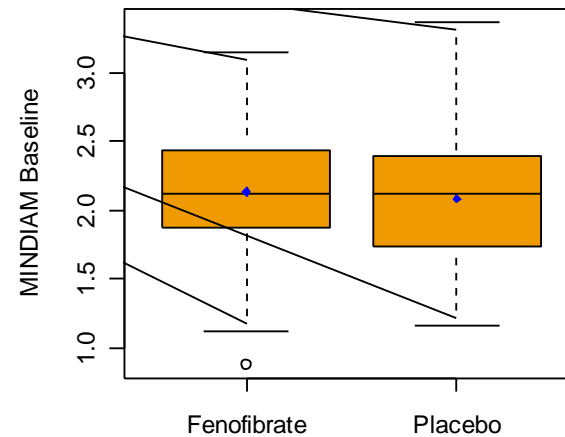
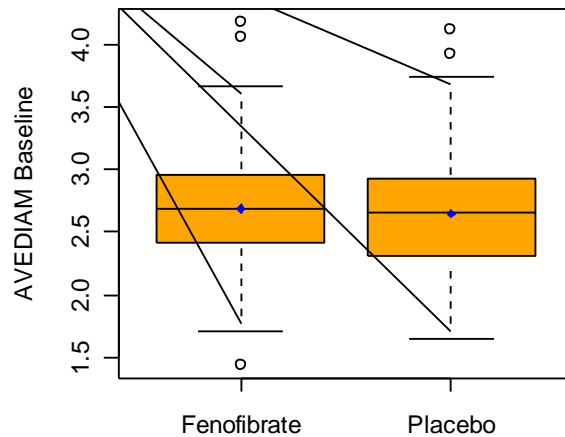
Response: AVEDIAM

	Df	Sum	Sq Mean	Sq F	Value Pr(>F)
groups	1	0.360	0.360	1.3694	0.2427
Residuals	347	91.100	0.263		

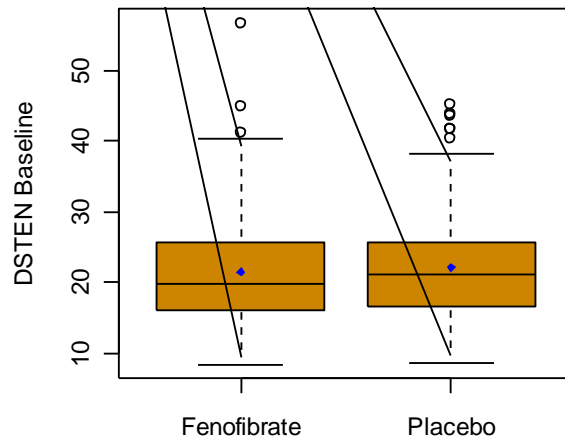


Diagnostics for linear model

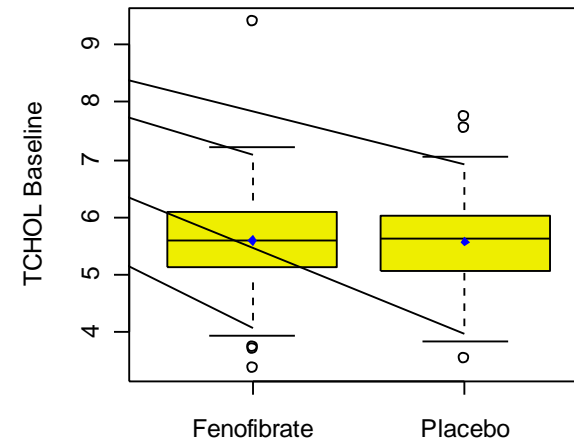
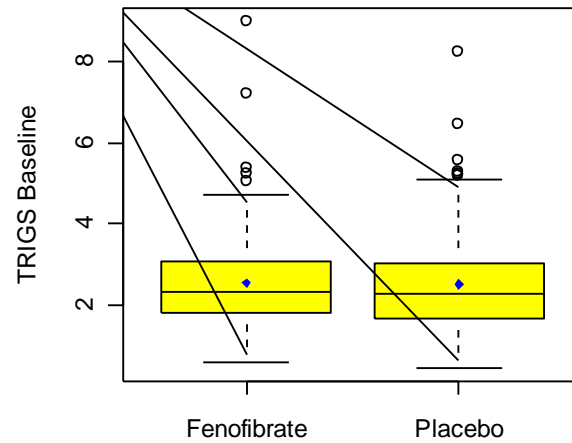




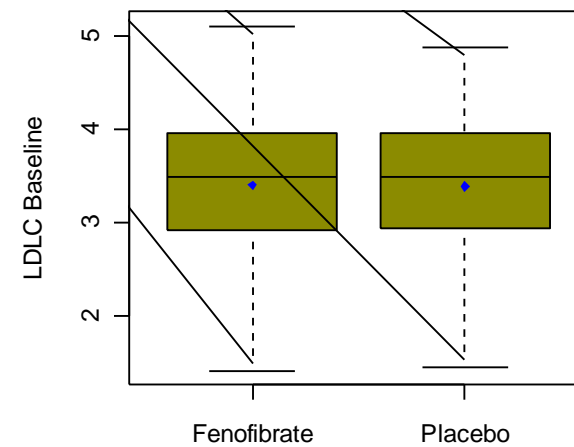
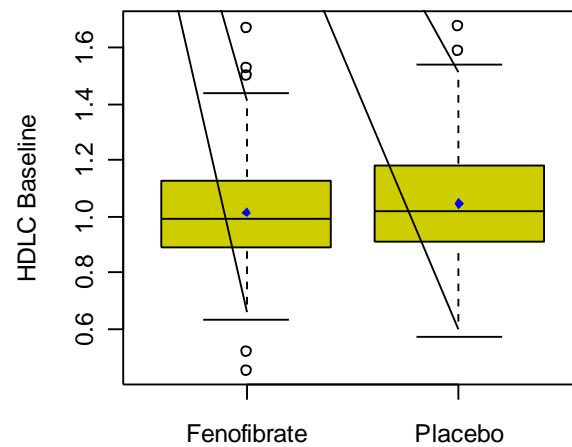
Assessment of main angios at baseline

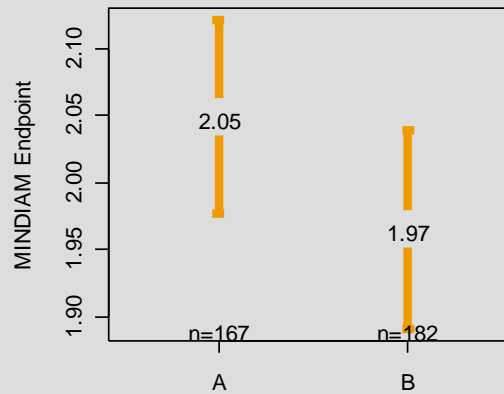
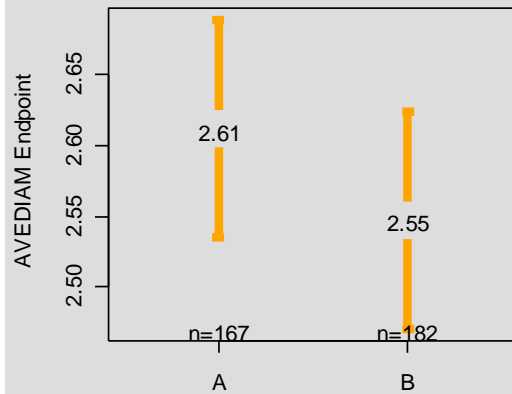


```
boxmoy<-function(x, gp, thecol, yaxlab)
{
  thebox<-boxplot(x~gp, col=thecol, ylab=yaxlab)
  meang<-tapply(x, gp, mean)
  xi<-seq(thebox$n)
  points(xi, meang, col="blue", pch=18, cex=1)
}
```

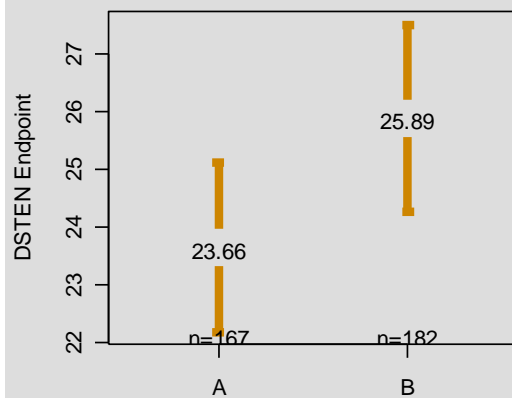


Assessment of main lipids at baseline

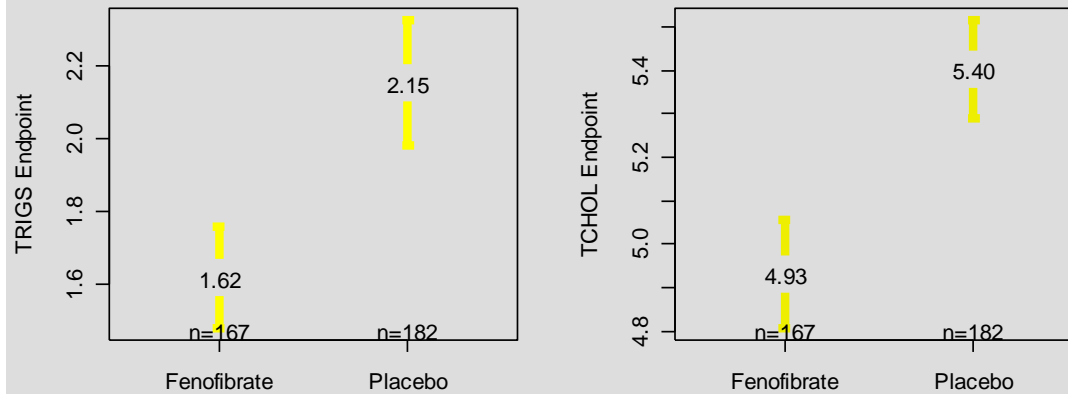




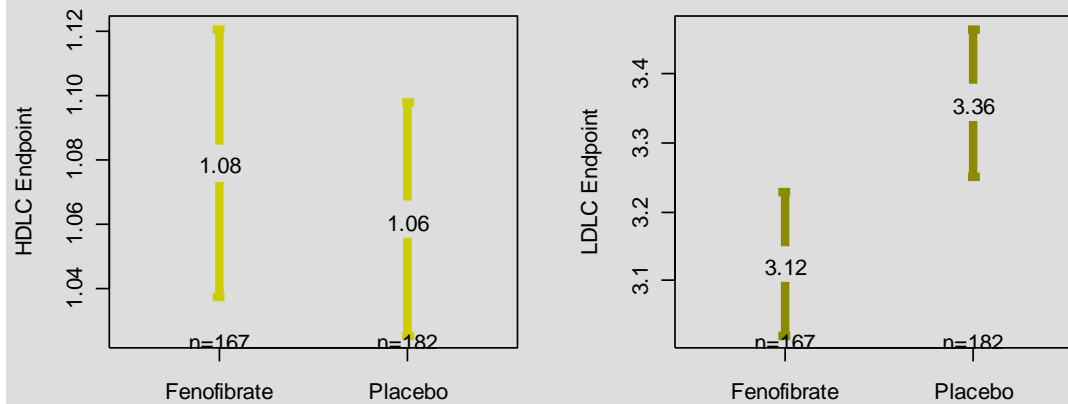
Assessment of main angios at endpoint



```
plotmeans (AVEDIAMF~groups, barcol="orange1",  
barwidth=5, xlab="", ylab=" AVEDIAM Endpoint",  
n.label=T, mean.label=T, digits=2, connect=F)
```



Assessment of main lipids at endpoint





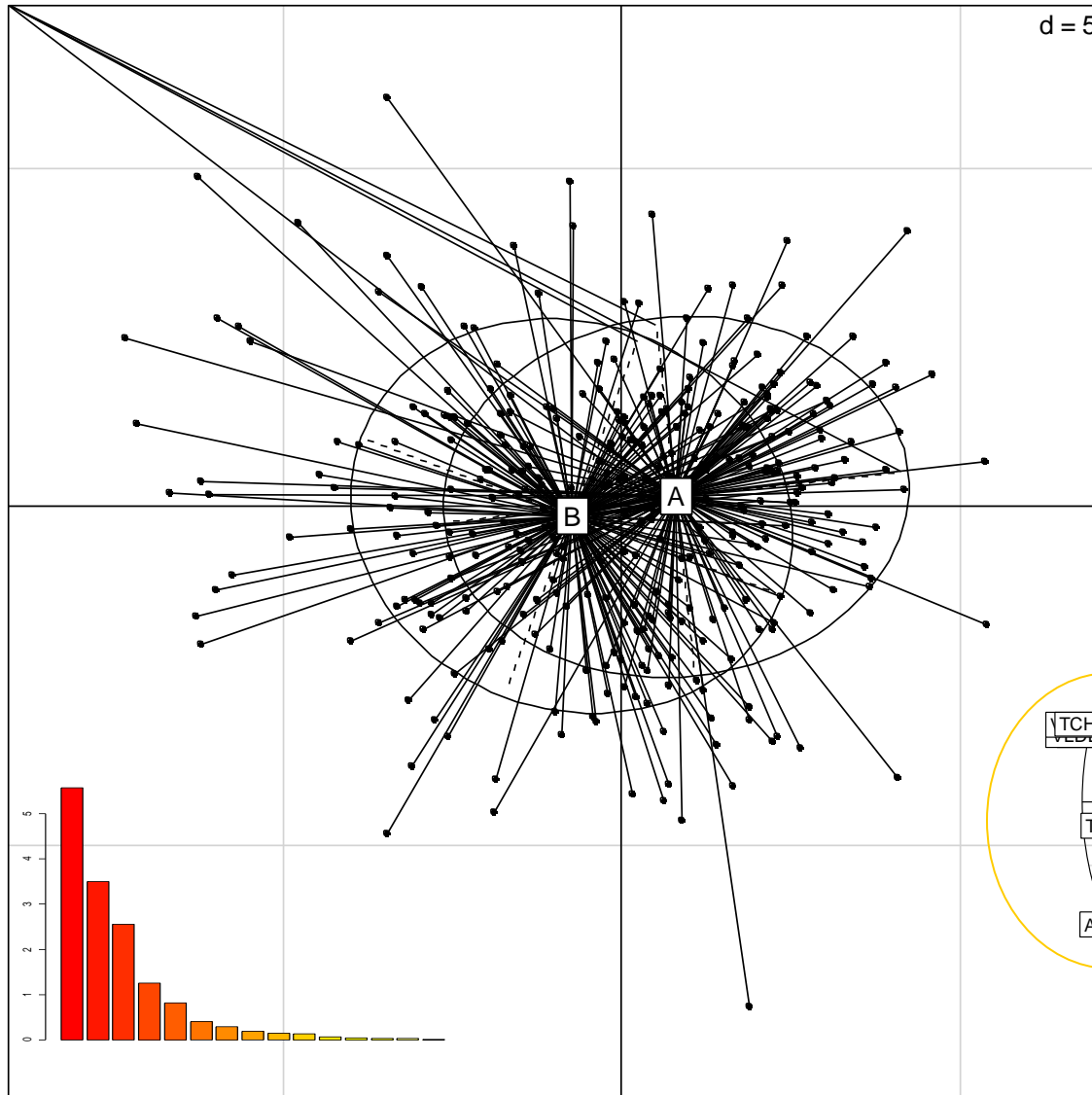
Principal Component Analysis

Principle

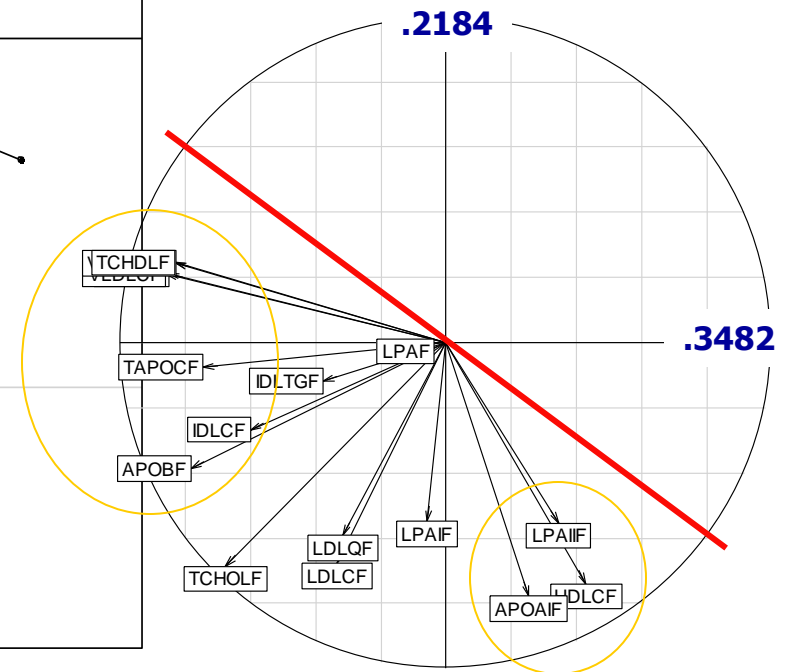
Randtest



Principal Component Analysis

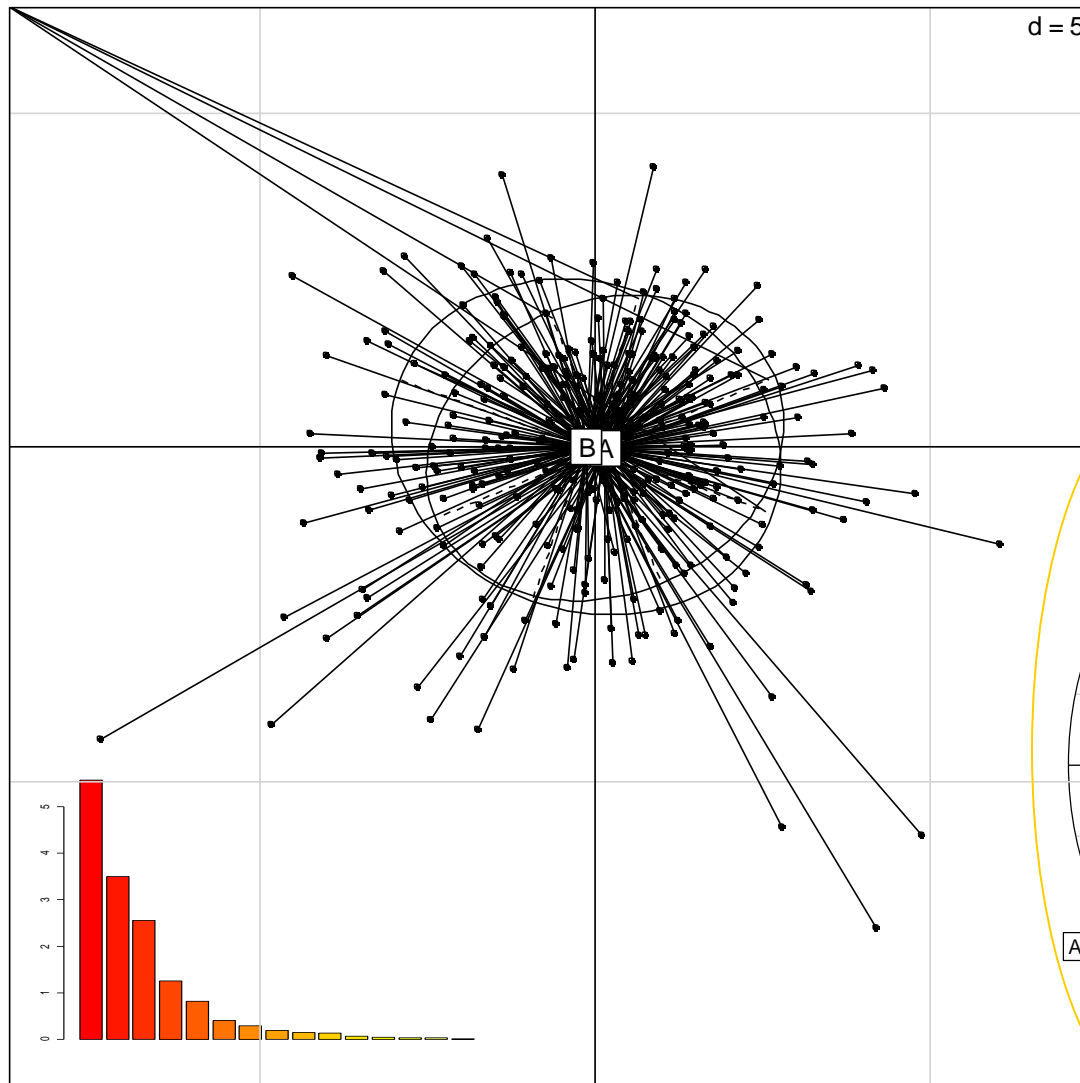


PCA on lipids
at endpoint
Axes 1+2

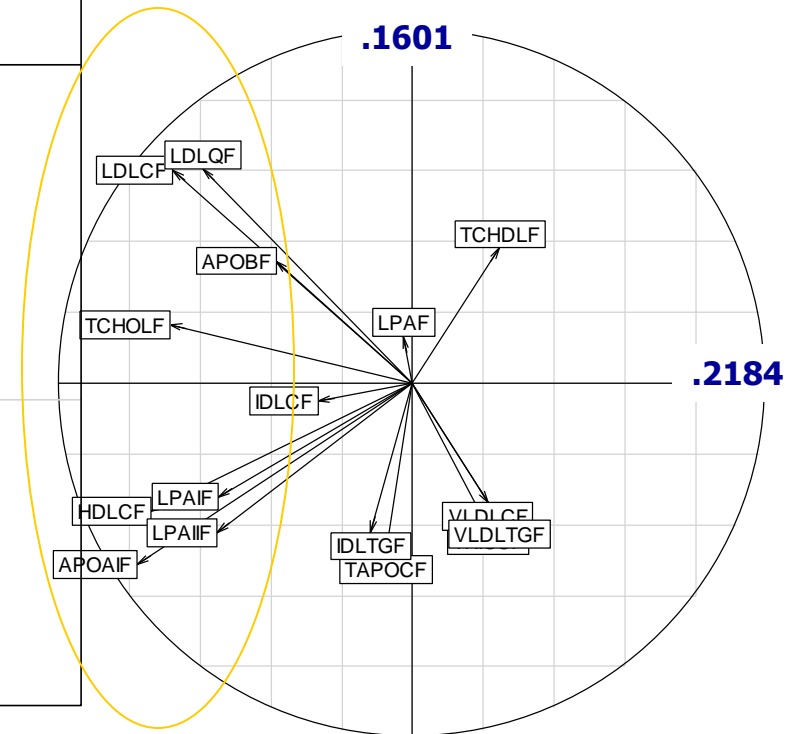




Principal Component Analysis

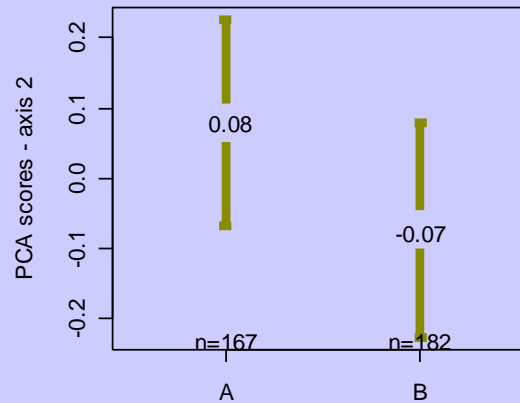
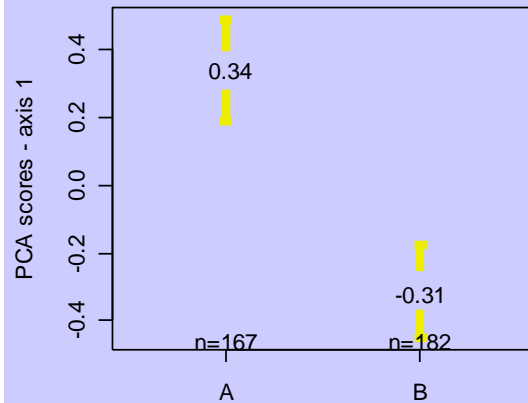


PCA on lipids
at endpoint
Axes 2+3

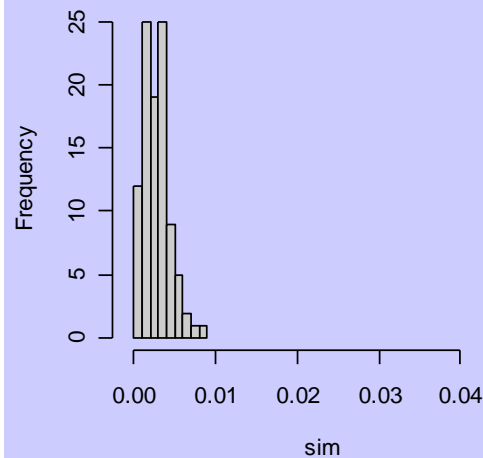




Principal Component Analysis



Monte-Carlo test



95% CI on PCA scores for lipids
Axes 1+2

Monte-Carlo test

Observation: 0.04591039

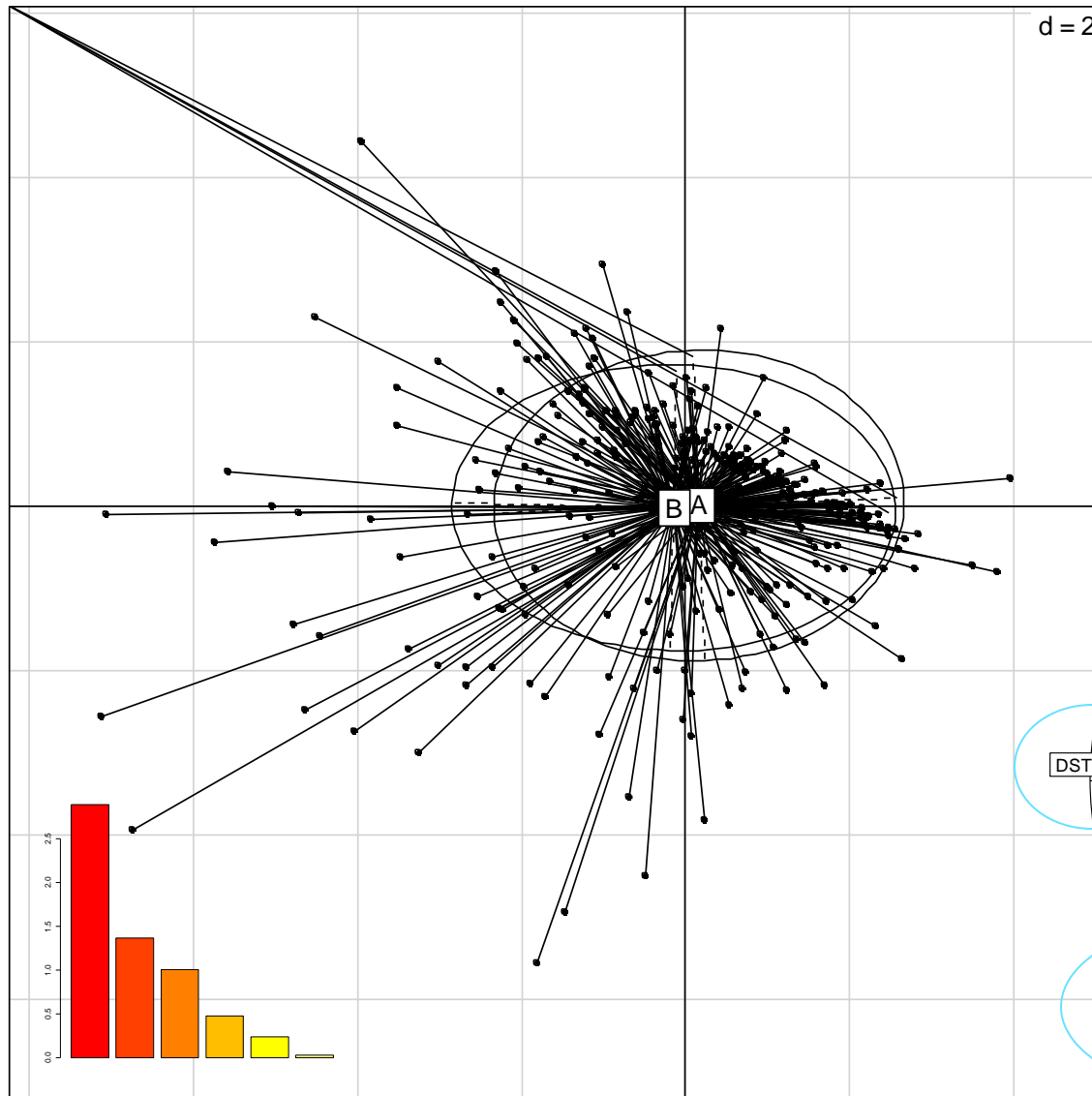
Call: `as.rtest(sim = sim, obs = obs)`

Based on 99 replicates

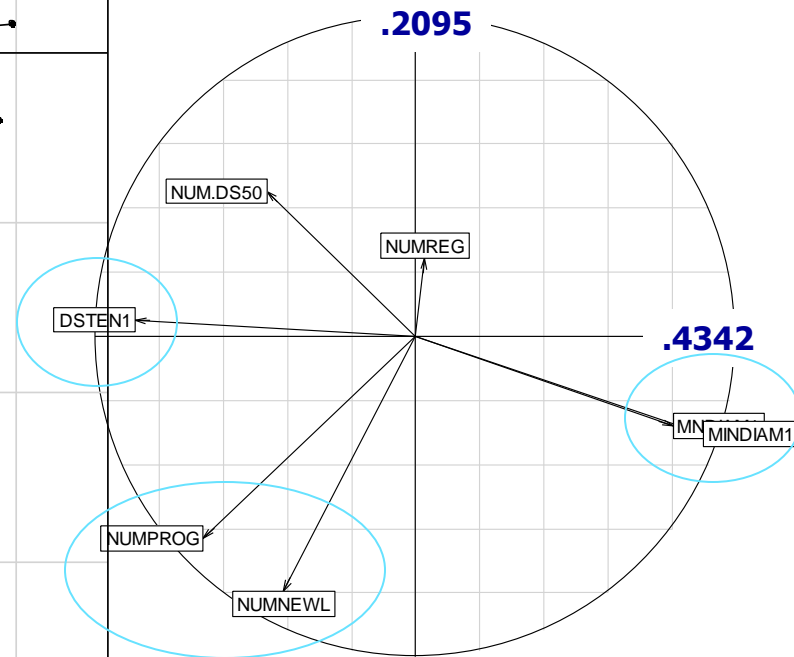
Simulated p-value: 0.01



Principal Component Analysis

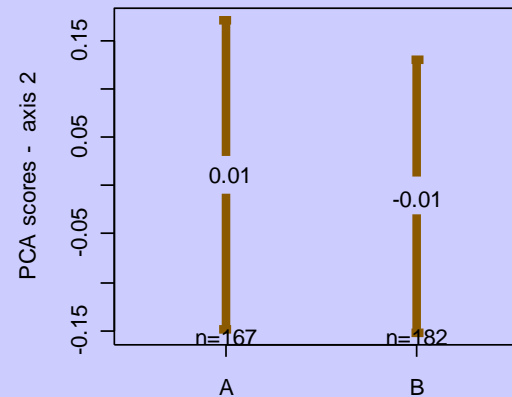
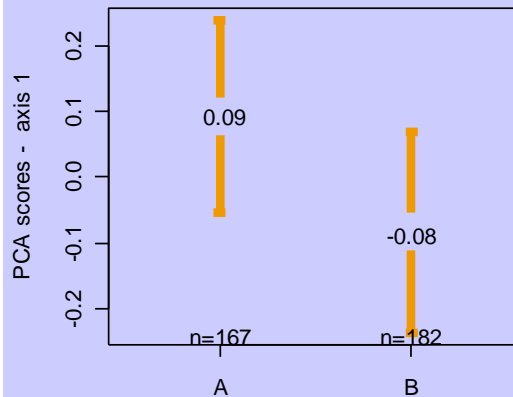


PCA on angios
at endpoint
Axes 1+2

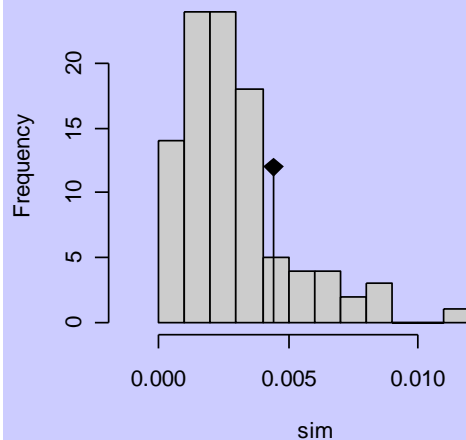




Principal Component Analysis



Monte-Carlo test



95% CI on PCA scores for angios
Axes 1+2

Monte-Carlo test

Observation: 0.004432635

Call: `as.rtest(sim = sim, obs = obs)`

Based on 99 replicates

Simulated p-value: 0.17



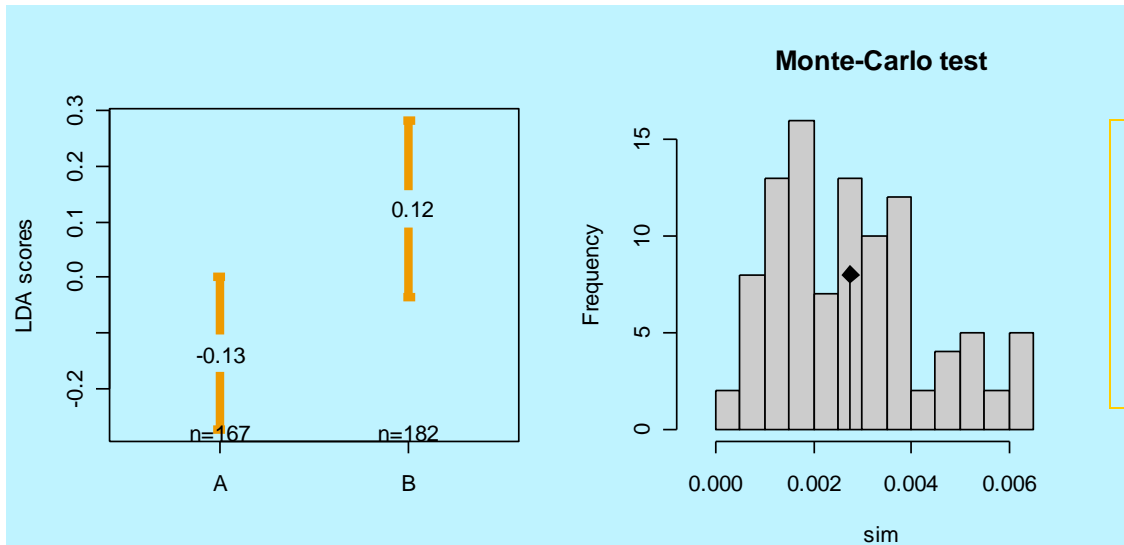
Linear Discriminant Analysis

Principle

Randtest



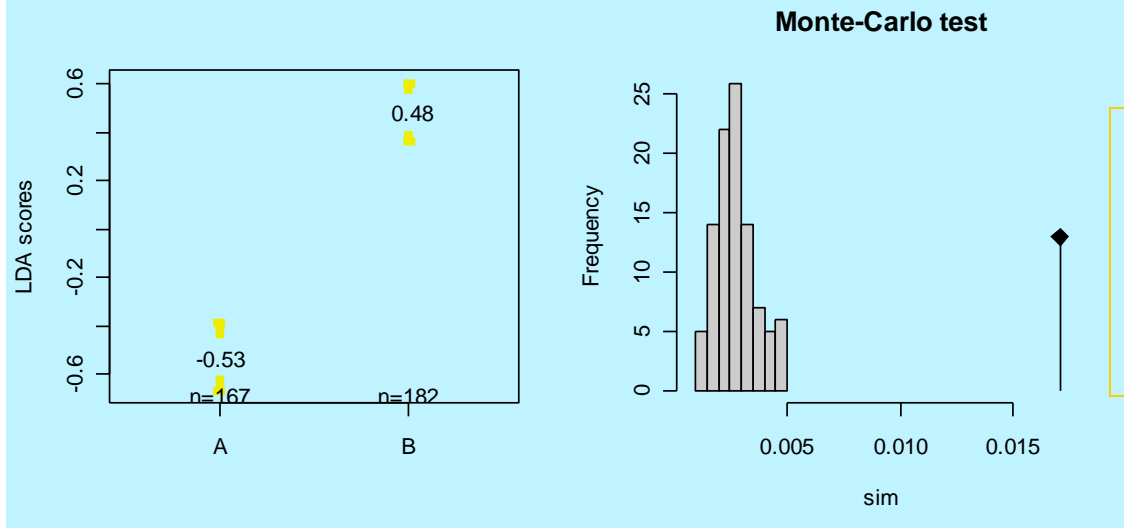
Linear Discriminant Analysis



Monte-Carlo test

Observation: 0.002760904
Call: `as.rtest(sim = sim, obs = obs)`
Based on 99 replicates
Simulated p-value: 0.49

ANGIOS



Monte-Carlo test

Observation: 0.01706249
Call: `as.rtest(sim = sim, obs = obs)`
Based on 99 replicates
Simulated p-value: 0.01

LIPIDS

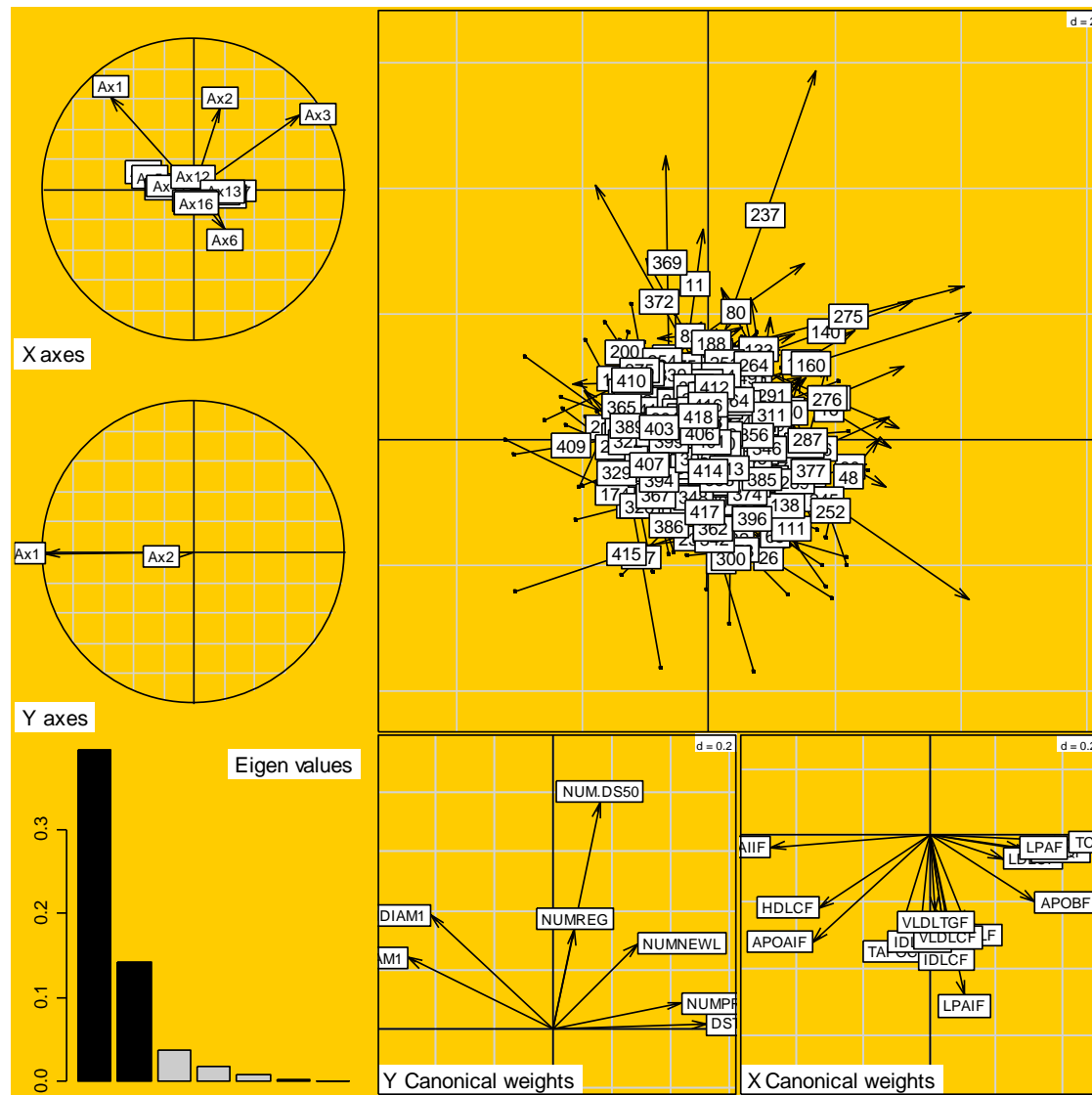


Principle

Randtest



Co-inertia





Eigenvalues decomposition:

	eig	covar	sdX	sdY	corr
1	0.3958632	0.6291766	1.794465	1.7269392	0.2030302
2	0.1430298	0.3781928	1.947764	0.9554333	0.2032247

Inertia & coinertia X (lipids):

	inertia	max	ratio
1	3.220104	5.571867	0.5779219
12	7.013889	9.066556	0.7736001

Inertia & coinertia Y (angios):

	inertia	max	ratio
1	2.982319	3.039098	0.9813171
12	3.895172	4.505455	0.8645457

RV:

0.02254131





ON MVA :

-



ON R :

-



ON THE CLINICAL TRIAL :

- The idea is to capitalize on the clinical knowledge of the evaluation criteria, their relationships,
- To build a model as narrow as possible from the data,
-