Statistics Applied to Bioinformatics

Multivariate analysis Introduction

Multivariate data

- Each row represents one object (also called unit)
- Each column represents one variable

	variable 1	variable 2		variable p
object 1	X ₁₁	X ₂₁	•••	X _{p1}
object 2	X ₁₂	X ₂₂	•••	X _{p2}
object 3	X ₁₃	X ₂₃	•••	Х _{р3}
object 4	X ₁₄	X ₂₄	•••	X _{p4}
object 5	X ₁₅	X ₂₅	•••	X _{p5}
object 6	X ₁₆	X ₂₆		Х _{р6}
object 7	X ₁₇	X ₂₇	•••	X _{p7}
object 8	X ₁₈	X 28		X _{p8}
	•••			
object n	X _{1n}	X _{2n}	•••	X _{pn}

Multivariate data with an outcome variable

 The outcome variable (also called criterion variable) can be quantitative or nominal

		Criterion variable			
	variable 1	variable 2	•••	variable p	variable p+1
object 1	X ₁₁	X ₂₁	•••	X _{p1}	У1
object 2	X ₁₂	X ₂₂	•••	X _{p2}	У2
object 3	X ₁₃	X ₂₃		X _{p3}	Уз
object 4	X ₁₄	X ₂₄		X _{p4}	У4
object 5	X ₁₅	X ₂₅		X _{p5}	У5
object 6	X ₁₆	X ₂₆	•••	X _{p6}	У6
object 7	X ₁₇	X ₂₇		X _{p7}	У 7
object 8	X ₁₈	X ₂₈		X _{p8}	У 8
•••		•••		•••	•••
object n	X _{1n}	X _{2n}	•••	X _{pn}	Уn

Typical questions in multivariate analysis

- No outcome variable
 - Can the objects be separated in distinct classes on the basis of the variables?
 - → Cluster analysis
 - Which variables, or combinations of variables (factors), are the most explanatory for the differences between objects?
 - → Factor analysis
- Quantitative outcome variable
 - Is the outcome variable correlated with the predictor variables?
 - → Correlation analysis
 - Can we predict the value of the outcome variable on the basis of the predictor variables?
 - → Regression analysis
- Nominal outcome variable
 - Can we predict the value of the outcome variable on the basis of the predictor variables?
 - → Discriminant analysis

Predictive approaches - Training set

- The training set is used to build a predictive function
- This function is used to predict the value of the outcome variable for new objects

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		Criterion variable			
	variable 1	variable 2	•••	variable p	variable p+1
object 1	X ₁₁	X ₂₁		X _{p1}	X _{p1}
object 2	X ₁₂	X ₂₂	•••	X _{p2}	X _{p2}
object 3	X ₁₃	X ₂₃		X _{p3}	X _{p3}
•••					
object n _{train}	X _{1n}	X _{2n}	•••	X _{pn}	X _{pn}

Predictor variables Criterion variable variable 1 variable 2 variable p variable p+1 object 1 X₁₁ X_{21} x_{p1} object 2 X₁₂ X_{22} x_{p2} object 3 X₁₃ X_{23} X_{p3} object n_{pred} x_{1n} \mathbf{X}_{2n} Xpn ...

Set to predict

Evaluation of prediction with a testing set

Training set

Testing set

Set to predict

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Criterion variable

	variable 1	variable 2	•••	variable p	variable p+1
object 1	X ₁₁	X ₂₁		X _{p1}	X _{p1}
object 2	X ₁₂	X ₂₂		X _{p2}	X _{p2}
object 3	X ₁₃	X 23		X _{p3}	X _{p3}
•••			•••		•••
object n _{train}	X _{1n}	X _{2n}	•••	X pn	Χ _{pn}

Predictor variables

Criterion variable

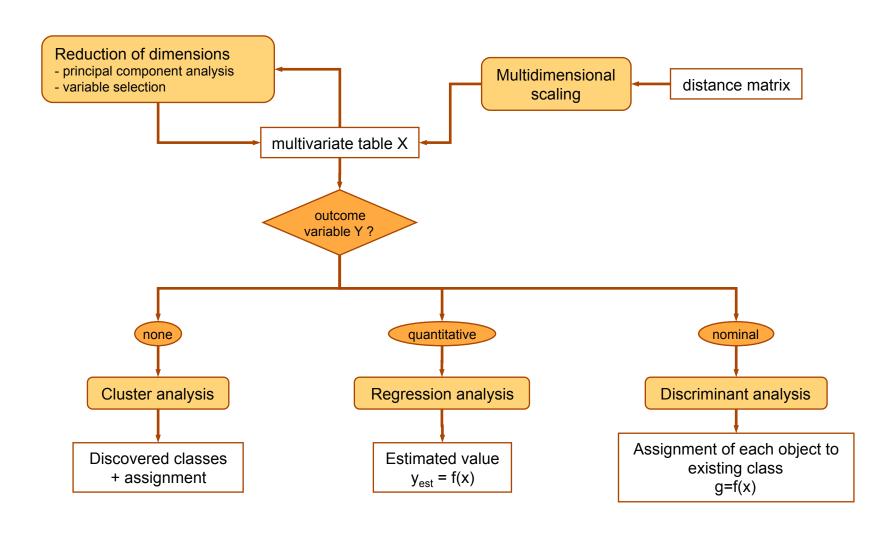
	variable 1	variable 2	variable 2 variable p		variable p+1	variable p+1	
					(known value)	(predicted)	
object 1	X ₁₁	X ₂₁		X _{p1}	X _{p1}	x' _{p1}	
object 2	X ₁₂	X ₂₂		X _{p2}	X _{p2}	x' _{p2}	
object 3	X ₁₃	X ₂₃		X _{p3}	X _{p3}	x' _{p3}	
•••					•••	•••	
object n _{test}	X _{1n}	X _{2n}		X _{pn}	X _{pn}	X' _{p5}	

Predictor variables

Criterion variable

		Official Variable			
	variable 1	variable 2	•••	variable p	variable p+1
object 1	X ₁₁	X ₂₁		X _{p1}	?
object 2	X ₁₂	X ₂₂		X _{p2}	?
object 3	X ₁₃	X 23		X _{p3}	?
•••					
object n _{pred}	X _{1n}	X _{2n}		X pn	?

Flowchart of the approaches in multivariate analysis



Conceptual work flow – RNA expression microarray analysis Legend user input Data retrieval Normalization Gene selection/ user query method/tool (TBD: single-,multi-chip) filtering result **GEO** Chip-wise selection MA5 Task ANOVA **RMA ArrayExpress** DB MAD GC-RMA Studen/Welch test Raw expression Normalized values values Selected genes Supervised classification Clustering / class discovery Training set **Training Biclustering** Sample clustering Gene clustering Testing set Trained classifier Predicting set Trained and tested Sample clusters Gene clusters classifier Functional enrichment **Evaluation** Assignmentof class membership GO categories Metabolic pathway databases Class(es) assigned **Enrichment** to each element Pathway analysis analysis Genes mapped GO-term associated onto pathways gene list