Perceptual mapping based on three-way binary data

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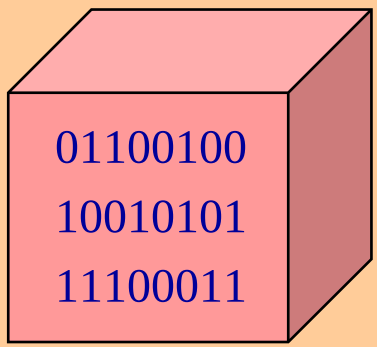
Perceptual Mapping

Based on Three-Way Binary Data



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Perceptual Mapping - 1

- **Perceptual mapping: Graphical display summarizing consumers' perceptions of multi-attribute objects.**

- **Example: Displaying brands in a product class together with their attributes**
  e.g. brands for treating stomach problems.

- **Brunswik's (1955) Lens Model:**
  Theoretical foundation for understanding the importance of perceptions in consumer purchases

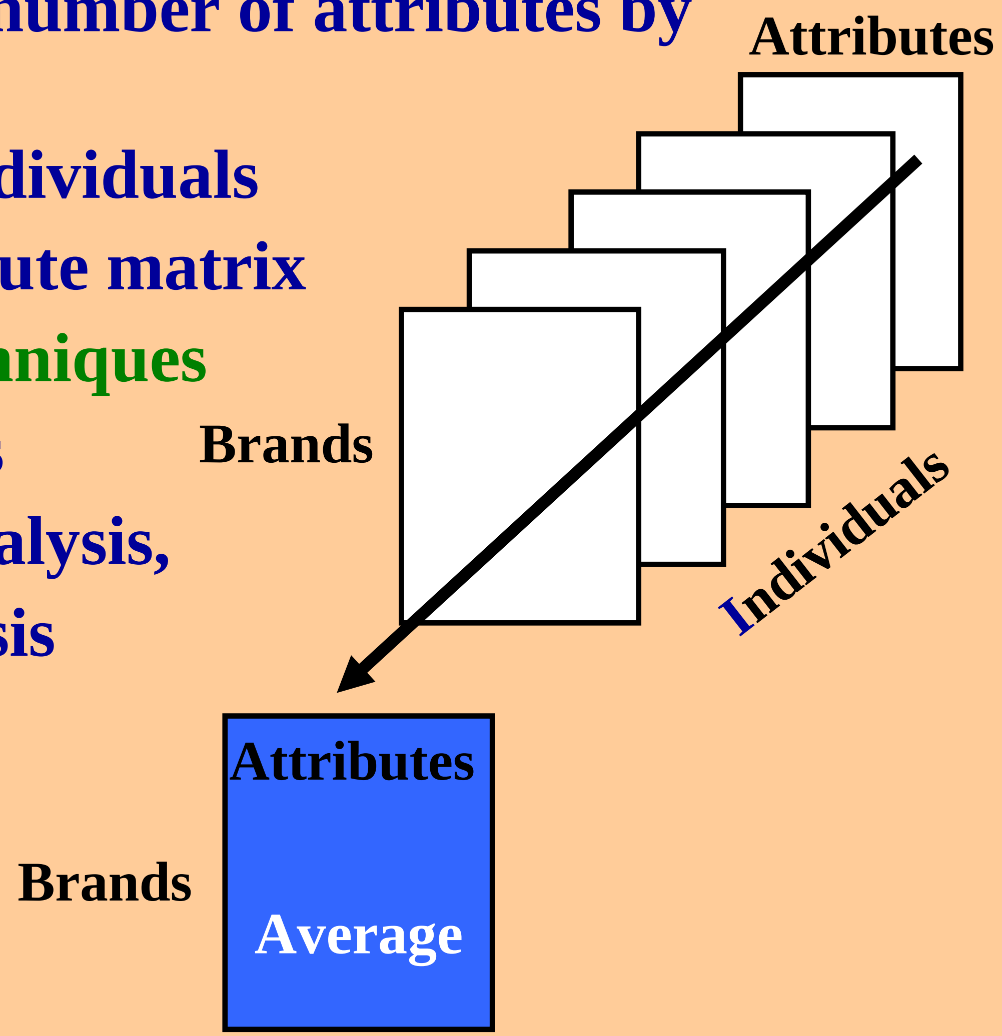
  Perceptions → ***Preferences*** → ***Choice***

Perceptual Mapping - 2

- Goals perceptual mapping
  - Aid for strategic marketing decisions
  - Summarizing nature and degree of competition among a set brands via key product attributes.
- Common application areas
  - product positioning
  - identification of market gaps for new product development.

Perceptual Mapping - 3

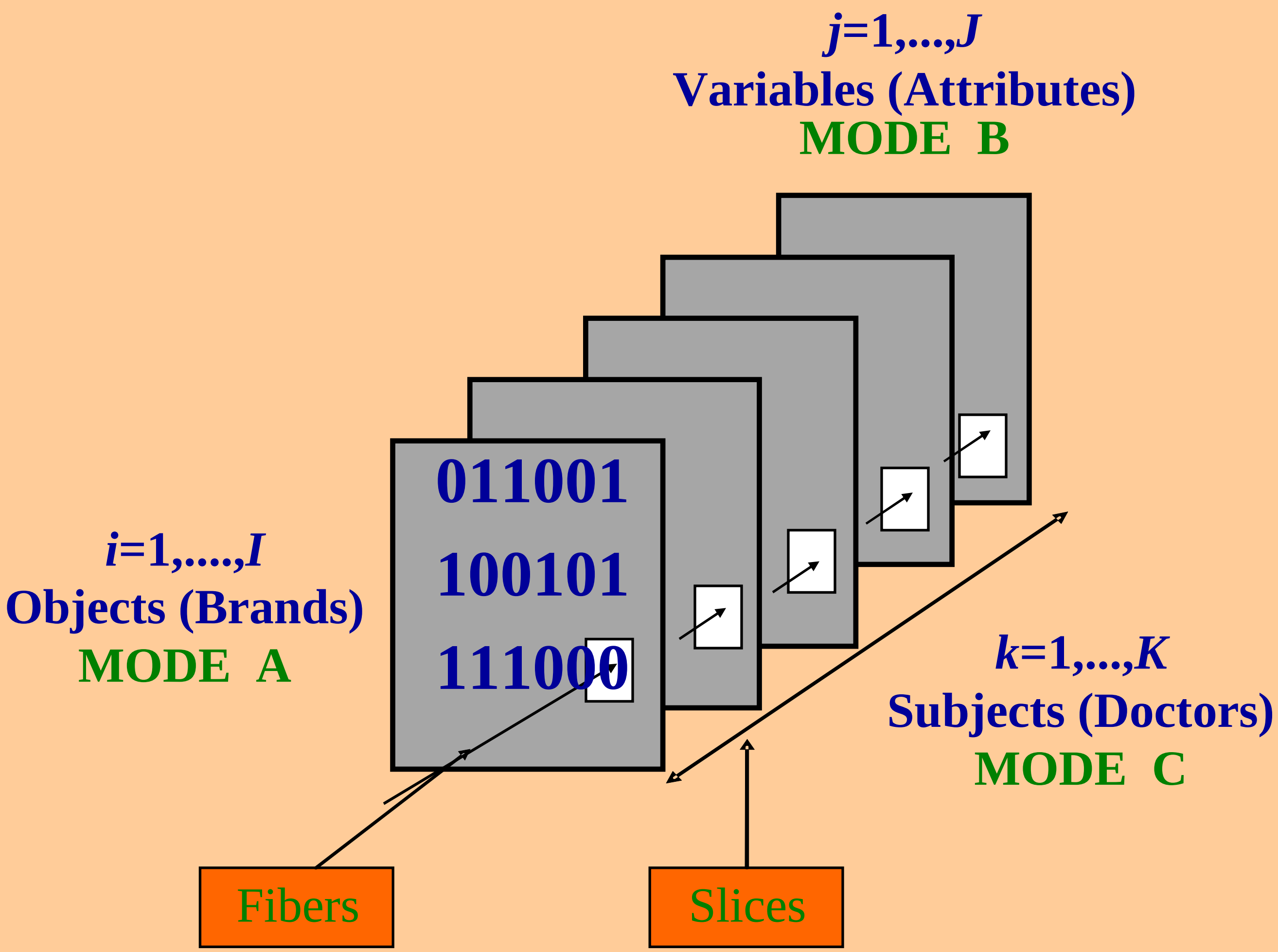
- Basic data
  - Brands are scored on a number of attributes by several individuals
  - Scores averaged over individuals
  - Result: Brand by Attribute matrix
- Common data analysis techniques
  - correspondence analysis
  - principal component analysis,
  - multidimensional analysis
  - discriminant analysis
  - factor analysis



Perceptual Mapping - 4

- Basic data
  - Doctor thinks a brand posesses an attribute => score = 1 , if not: score = 0
  - Three-way binary data: Brands $\times$ Attributes $\times$ Doctors
  - Why average over doctors?
  - Different doctors may be sensitive to different attributes
- Three-way data analysis techniques
  - Three-mode binary hierarchical cluster analysis
  - Three-mode principal component analysis (numerical)

The Binary Data Cube



Stacked Two-Way Data

Columns: Attributes
1 through J

Doctor 1 (k=1)

010001
101101
111010

Rows: Brands 1 through I

Doctor 2 (k=2)

010001
010101
110001

Rows: Brands 1 through I

Doctor K (k=K)

011001
100101
111000

Rows: Brands 1 through I

HICLAS3: Algebraic Representation

(Tucker3-HICLAS)

- **Hiclas3 model (uses Boolean algebra)**

$$\hat{x}_{ijk} = m_{ijk} = \bigoplus_{p=1}^{P} \bigoplus_{q=1}^{Q} \bigoplus_{r=1}^{R} \tilde{a}_{ip} \tilde{b}_{jq} \tilde{c}_{kr} \tilde{g}_{pqr}$$

- **m_{ijk} =1 iff $\tilde{a}_{ip}$= 1 and $\tilde{b}_{jq}$= 1 and $\tilde{c}_{kr}$ = 1 and $\tilde{g}_{pqr}$ = 1 for at least one combination of *p*, *q*, and *r*;**
- **$\tilde{a}_{ip}$, $\tilde{b}_{jq}$, $\tilde{c}_{kr}$: elements binary component matrices A, B, and C, respectively (brands, attributes, doctors).**
- **$\tilde{g}_{pqr}$: element of the $P \times Q \times R$ three-way binary core array $\mathcal{G}$, indicates links between binary components of the three modes**

HICLAS3 – Pictorial Representation

brands

A

1	1	1
2	0	1
3	0	1
4	1	0
5	0	1
6	0	0
7	1	1
8	1	0

attributes

B

1	1
0	1
0	1
1	0
0	1
1	0
1	0

doctors

C

1	0
1	1
0	1
1	0
0	1

core array

c1

	a1	a2
b1	1	0
b2	0	1

G_1

c2

	a1	a2
b1	0	1
b2	0	1

G_2

$m_{211} = 1$ **as** $a_{22}b_{12}c_{11}g_{221} = 1 \times 1 \times 1 \times 1$ **(all other 7 combinations contain a zero)**

Three-Mode Component Analysis

- **Tucker3 model (numerical)**

$$\hat{x}_{ijk} = m_{ijk} = \sum_{p=1}^{P} \sum_{q=1}^{Q} \sum_{r=1}^{R} a_{ip} b_{jq} c_{kr} g_{pqr}$$

  - ***i*=1,...,*I* (brands); *j*=1,...,*J* (attributes); *k*=1,...,*K* (doctors);**
  - **m_{ijk} is the model matrix or structural image**
  - **a_{ip}, b_{jq}, c_{kr} : elements loading matrices A, B, and C, respectively (brands, attributes, doctors).**
  - **g_{pqr} : element of the $P \times Q \times R$ three-way core array $\mathcal{G}$; indicates strength of the link between the components of the three modes**

Three-Mode Binary Analysis in Action

Perceptions of Medical Doctors
w.r.t.
Gastro-Intestinal Drugs

Perceptions of Medical Doctors

Gastro-Intestinal Drugs

- Tagamet
- Zantac
- Pepcid
- Axid
- Sulcrate
- Cytotec
- Losec

Attributes

Adjectives [Binary answers– no (0) or yes (1)]

• Relieves Pain	RelPain
• Does not have serious side effects	NoSideEf
• Relatively safe w.r.t. potential interactions with other drugs	Safe
• Flexible in terms of dosage	FlexDose
• Not too costly for the patient	LowCost
• Relieves symptoms	RelSymptoms
• Promotes healing	Heals
• Prophylactic	Prophylactic

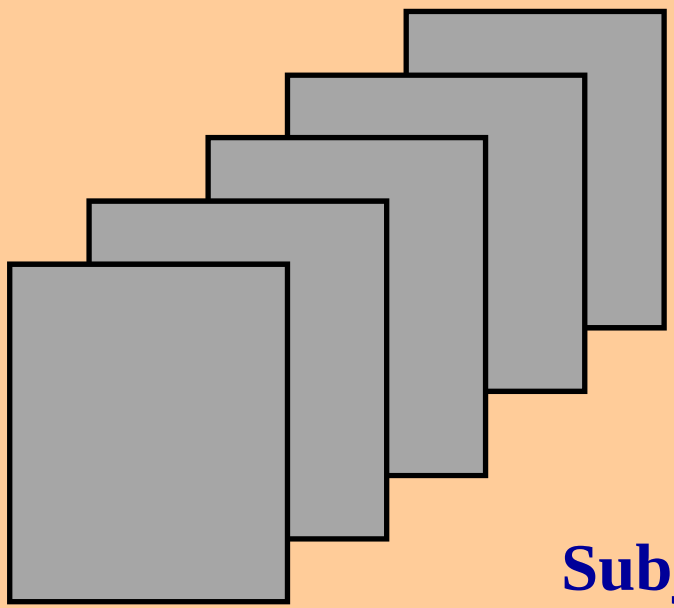
Data: Brands × Attributes × Doctors

(7×8×283)

***j*=1,...,8**

Variables (Attributes)

MODE B



***i*=1,....,7**

Objects (Brands)

MODE A

***k*=1,...,283**

Subjects (Doctors)

MODE C

Perceptions of Medical Doctors

Central questions

- What is the position of brands w.r.t. each other?
- Which attributes are related to this positioning?
- Do doctors differ in their perceptions in which brands have which attributes?

HiClas3 Model

Tucker3 hierarchical classes model

Basic elements

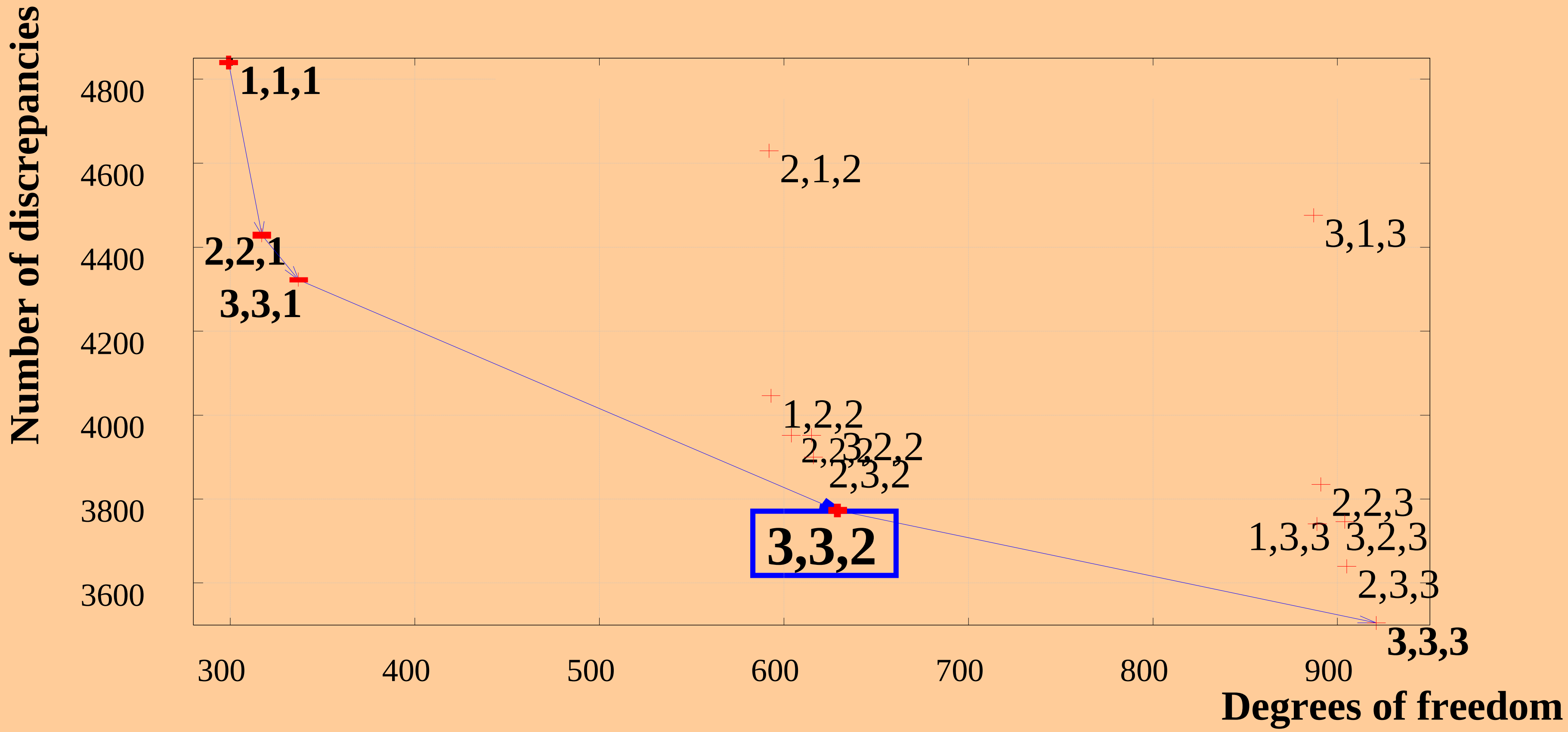
- Binary components for all three modes (doctors, brands and attributes)
- Plus linkage information about the components

Basic literature

- Papers by Ceulemans, Van Mechelen in *Psychometrika* (Catholic University Leuven, Belgium)

HiClas3 – Choosing a Model

Brands × Attributes × Doctors



Model complexity: **(3,3,2) = (Brands = 3 components ; Attr = 3; Docs = 2)**

Discrepancy : Data have a 1, model matrix a 0 and vice versa

Binary Component Matrices

(brands; attributes)

Brand	Discre-pancies	Fit	B1	B2	B3
Sulcrate	659	0.626	1	0	1
Cytotec	645	0.564	1	0	0
Zantac	488	0.709	0	0	1
Pepcid	388	0.743	0	0	1
Axid	467	0.691	0	0	1
Losec	499	0.665	0	0	1
Tagamet	627	0.589	0	1	0

B1 = Cytoprotective agent

B2 = Tagamet (Oldest)

B3 = Histamines; H-2 blocker

Attribute	Discre-pancies	Fit	A1	A2	A3
Relieves Pain	369	0.79	1	1	1
Relieves Symptoms	330	0.82	1	1	1
Promotes Health	406	0.77	1	1	1
No Side Effects	517	0.60	0	0	1
Relatively Safe	542	0.57	0	0	1
Flexible Dose	632	0.52	0	1	0
Prophylatic	500	0.61	1	0	0
Low Cost	477	0.00	0	0	0

A1 = Primary medical

A2 = Use in practice

A3 = Secondary medical

Low Cost had no relations with other attributes

Binary Component Matrices
(doctors)

Doctors	MD1	MD2	*f*	*Prop. 1s*
Doctor Type 1	1	1	70	.73
Doctor Type 2	1	0	69	.50
Doctor Type 3	0	1	98	.61
Doctor Type 4	0	0	46	.28

Average sd = .09

Doctor Type 4 (0,0) has no links with other doctors

Binary Core Array

Dr2 (1 0)

	A1 Prim. Med.	A2 Practice	A3 Secon. Med.
B1 (Cytoprotective)	1	0	0
B2 (Tagamet)	1	1	0
B3 (Histamines)	1	0	0

Dr3 (0 1)

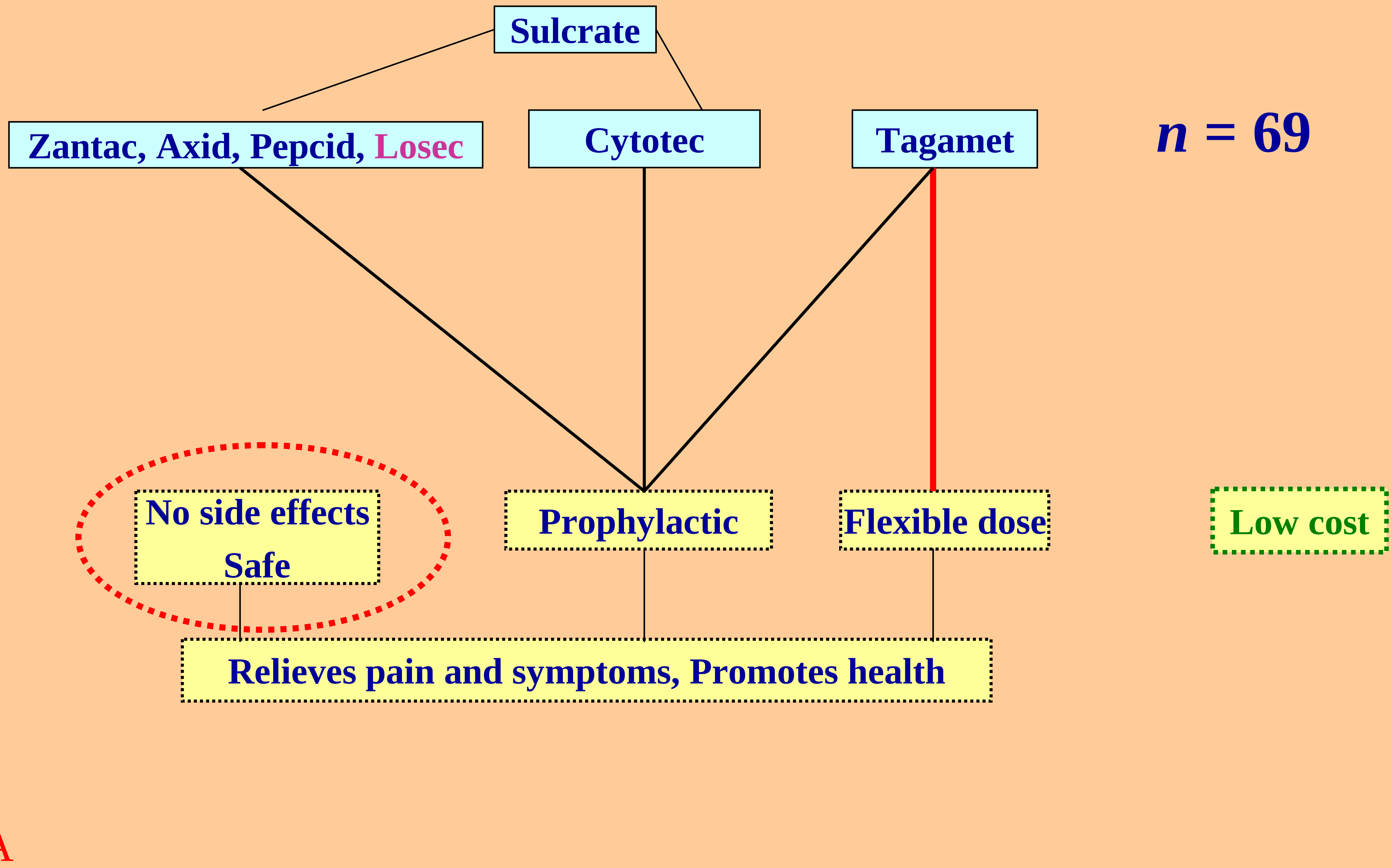
	A1 Prim. Med.	A2 Practice	A3 Secon. Med.
B1 (Cytoprotective)	1	0	1
B2 (Tagamet)	0	1	0
B3 (Histamines)	0	1	1

Dr1 =

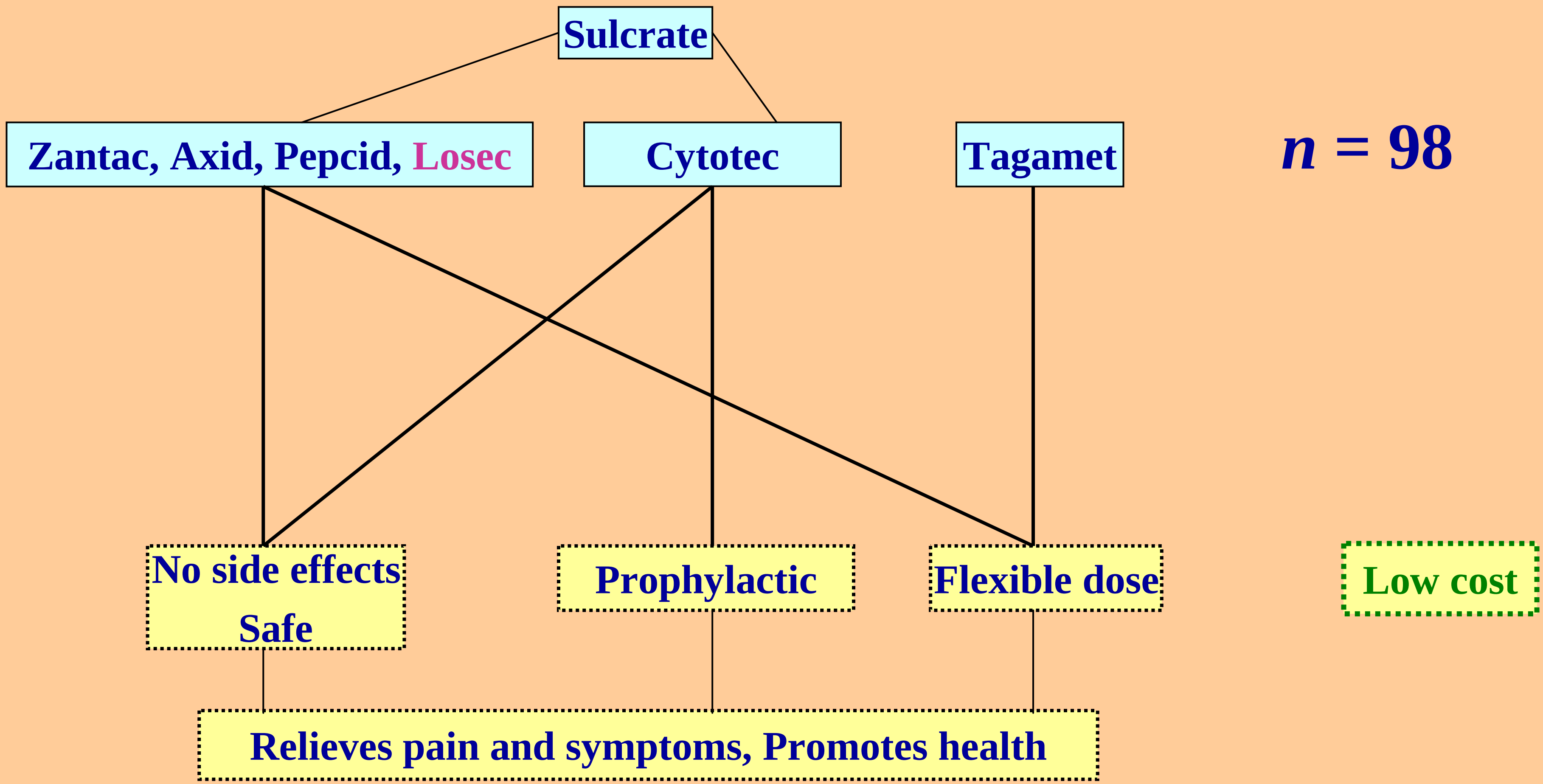
Dr2 + Dr3

1 : a link exists between components of the three modes

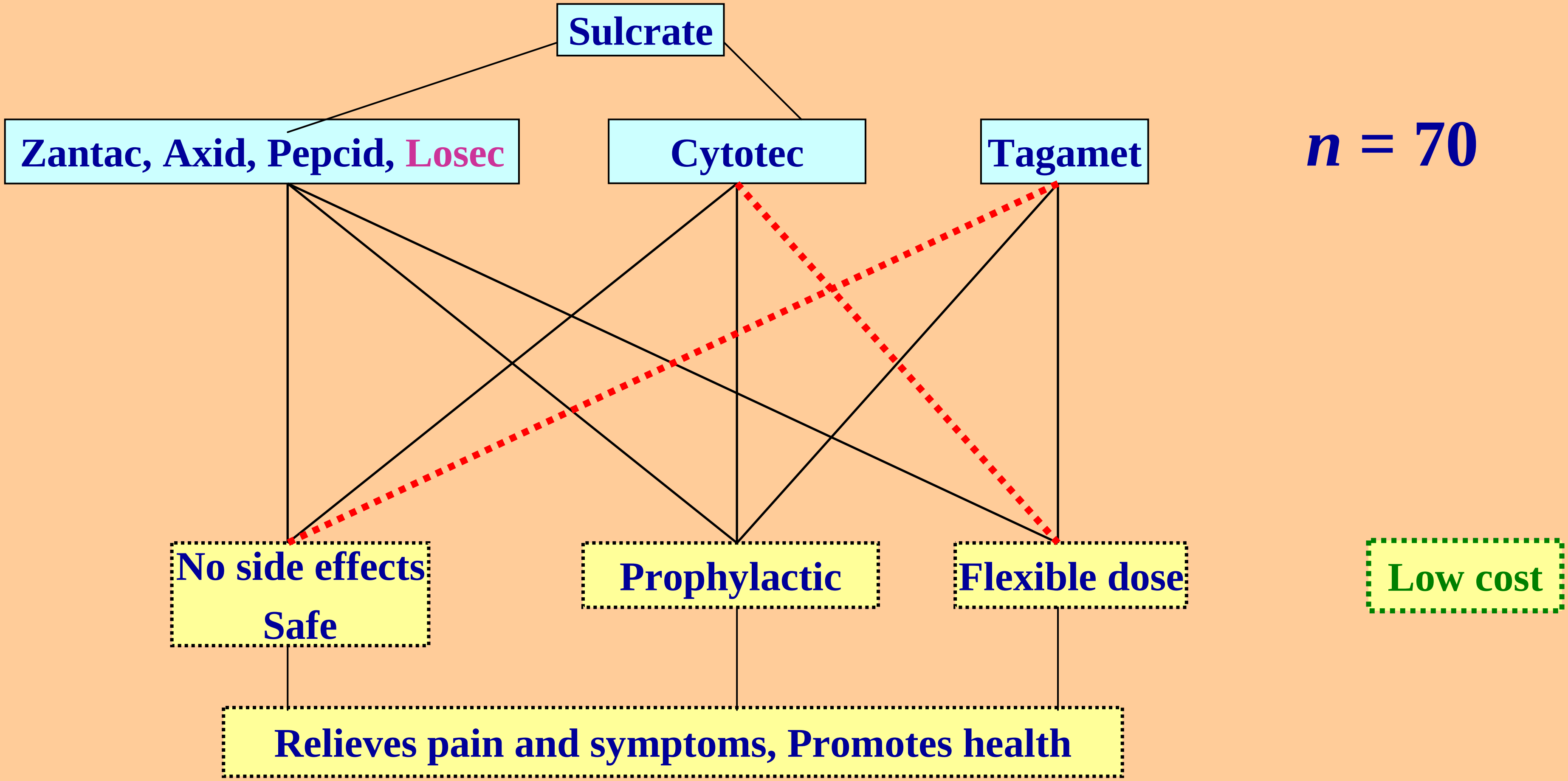
Doctor Type 2



Doctor Type 3

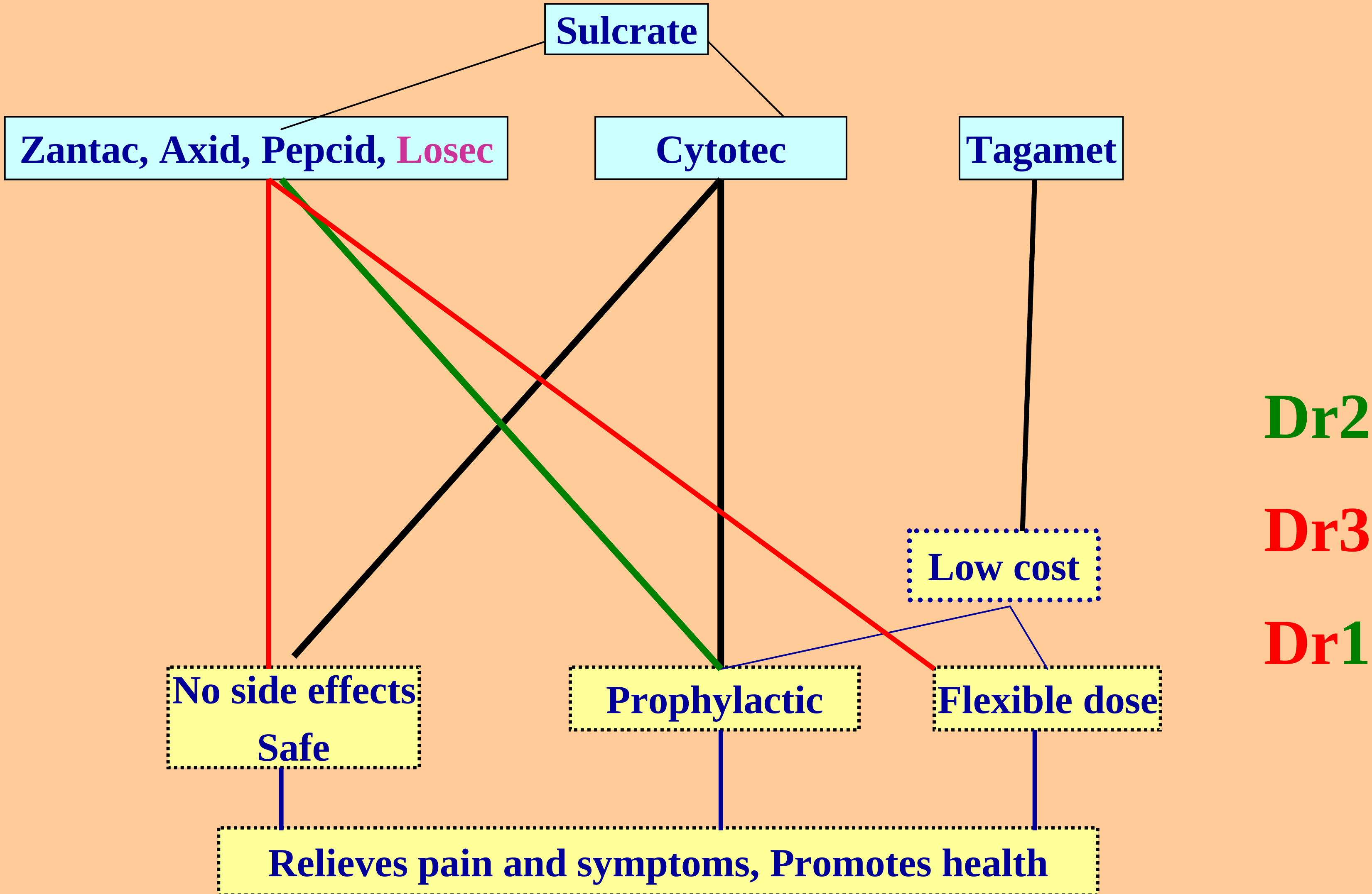


Doctor Type 1



A

Doctor Types



A

Characterisation of Doctor Types

Brand Name	Dr 2 (*n*=69)	Dr 3 (*n*=98)	Dr 1 (*n*=70)
Zantac	a0, a1	a0, ,a2, a3	a0, a1, a2, a3
Axid	a0, a1	a0, ,a2, a3	a0, a1, a2, a3
Pepcid	a0, a1	a0, ,a2, a3	a0, a1, a2, a3
Losec	a0, a1	a0, ,a2, a3	a0, a1, a2, a3
Cytotec	a0, a1	a0, a1, ,a3	a0, a1, XX,a3
Sulcrate	a0, a1	a0, a1, a2, a3	a0, a1, a2, a3
Tagamet	a0, a1, a2	a0, ,a2	a0, a1, a2,XX

- a0={Relieves Pain, Relieves Symptoms, Promotes Healing}
- a1={Prophylactic}, a2={Flexible Dosage}, a3={No Side Effects, Safe}
- Doctor Type 4 has no links; Low Cost has no links

Further Considerations

- No information on Low Cost (more complex HiClas models can model a separate component for Low Cost)
- Tagamet is relatively inexpensive, while the others are not
- Don’t the doctors see this?
- HiClas3 suggest they do not.

Proportions of Ones across Doctors

	Tagamet	Zantac	PepCid	Axid	Losec	Sulcrate	Cytotec
RelievePain	.8	.9	.8	.7	.8	.7	.5
RelieveSymptoms	.9	.9	.8	.8	.9	.7	.6
PromotesHealth	.7	.8	.7	.7	.8	.7	.6
NoSideEffect	.3	.7	.6	.6	.4	.8	.4
RelativeSafe	.2	.6	.5	.5	.4	.7	.4
FlexbileDose	.7	.7	.5	.4	.3	.4	.3
Prophylactic	.4	.5	.4	.3	.2	.6	.7
LowCost	.7	.2	.2	.2	.0	.3	.1

Further Considerations

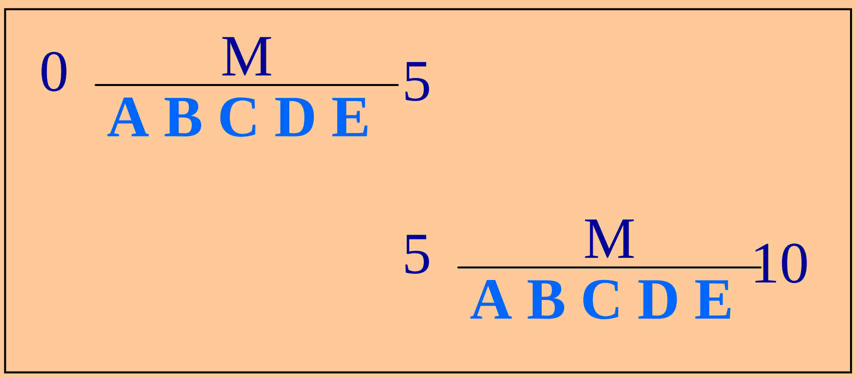
- **Surprise**
  Tagamet is the only relatively inexpensive brand
- **Possible reason:**
  Doctors from all groups say Tagamet is not expensive.
  Thus unrelated to the present groups.
- **Possible solution:**
  More groups for attributes
  (we are working on this)
- **Question**
  Other variability not present in HiClas solution?

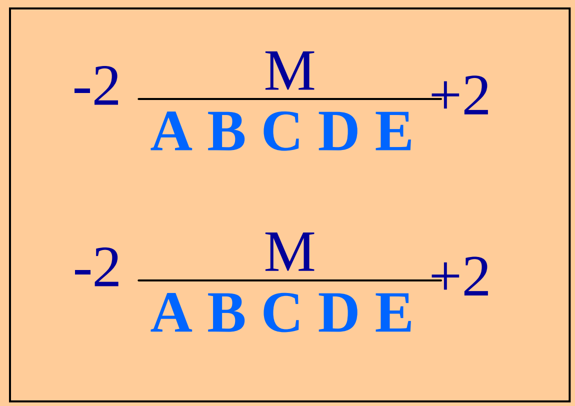
Further Analyses

- Treat the binary data as numerical and analyse with Tucker3.
- Handle the data such that emphasis is on:
  - relative differences between brands
  - relative differences between attributes.

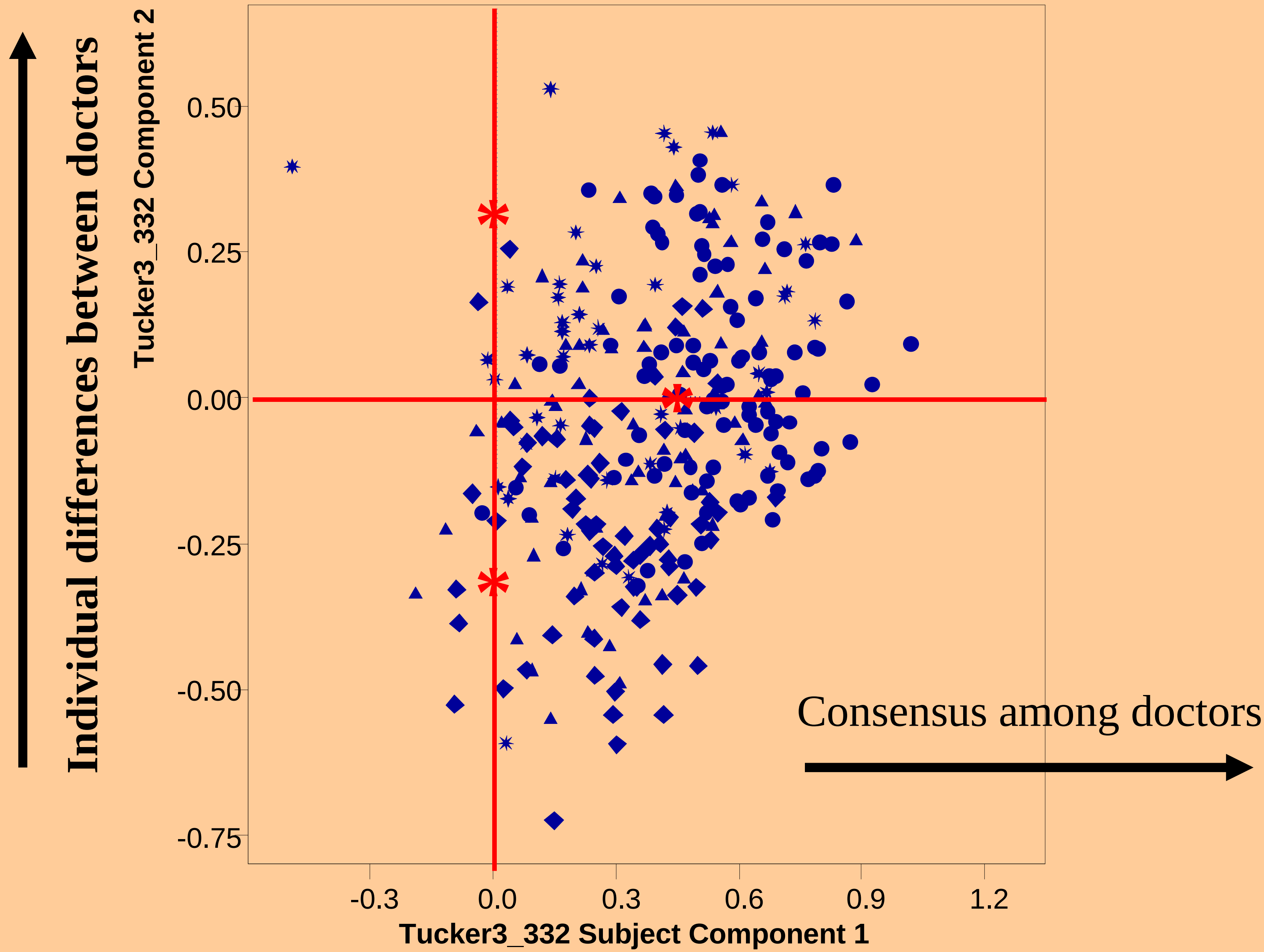
Three-Mode Component Analysis

- **Concentrate on consensus and individual differences between doctors in the relationships between brands and attributes.**
- **Absolute differences between brand and between attributes are ignored.**



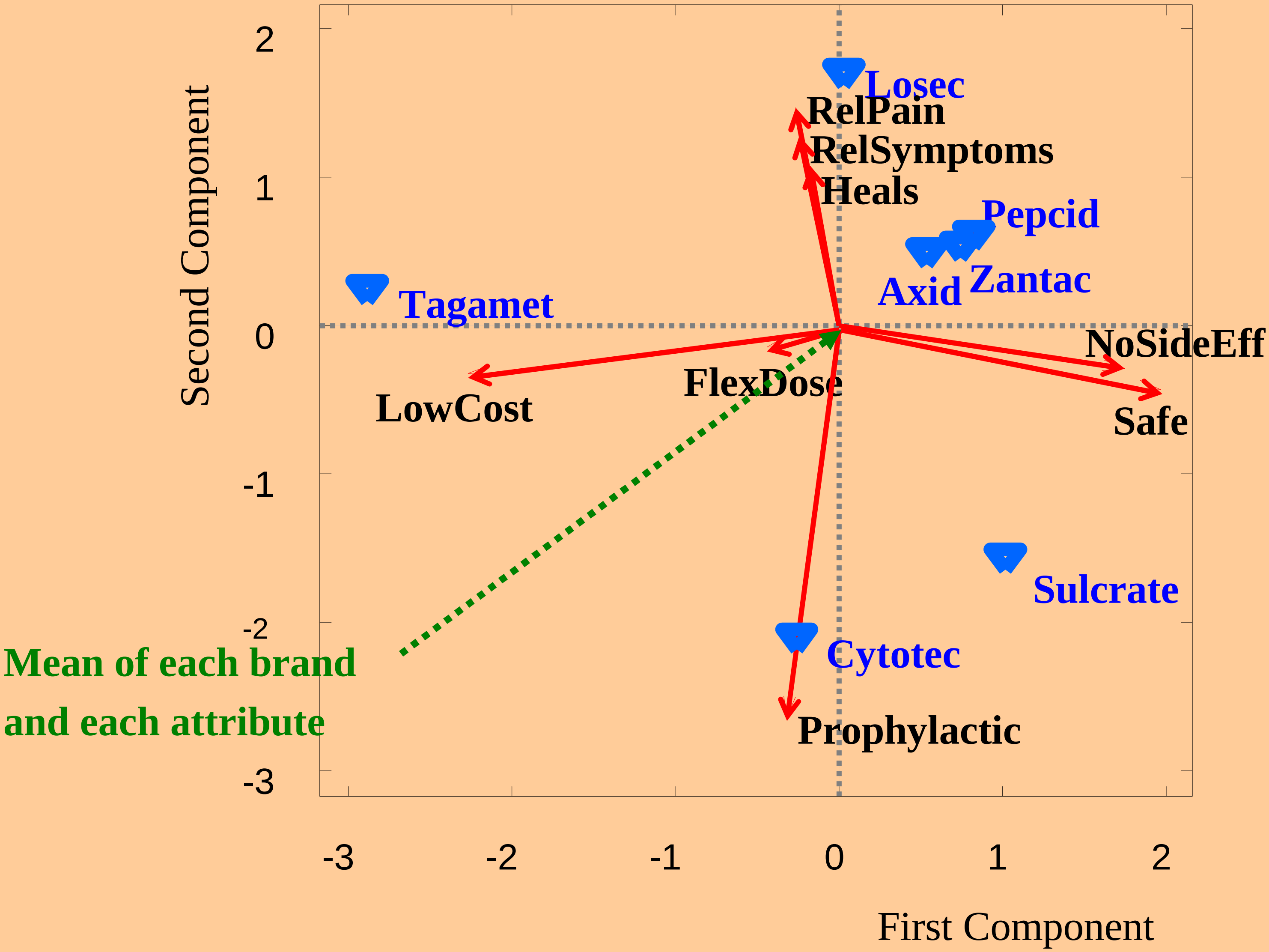


Component Scores



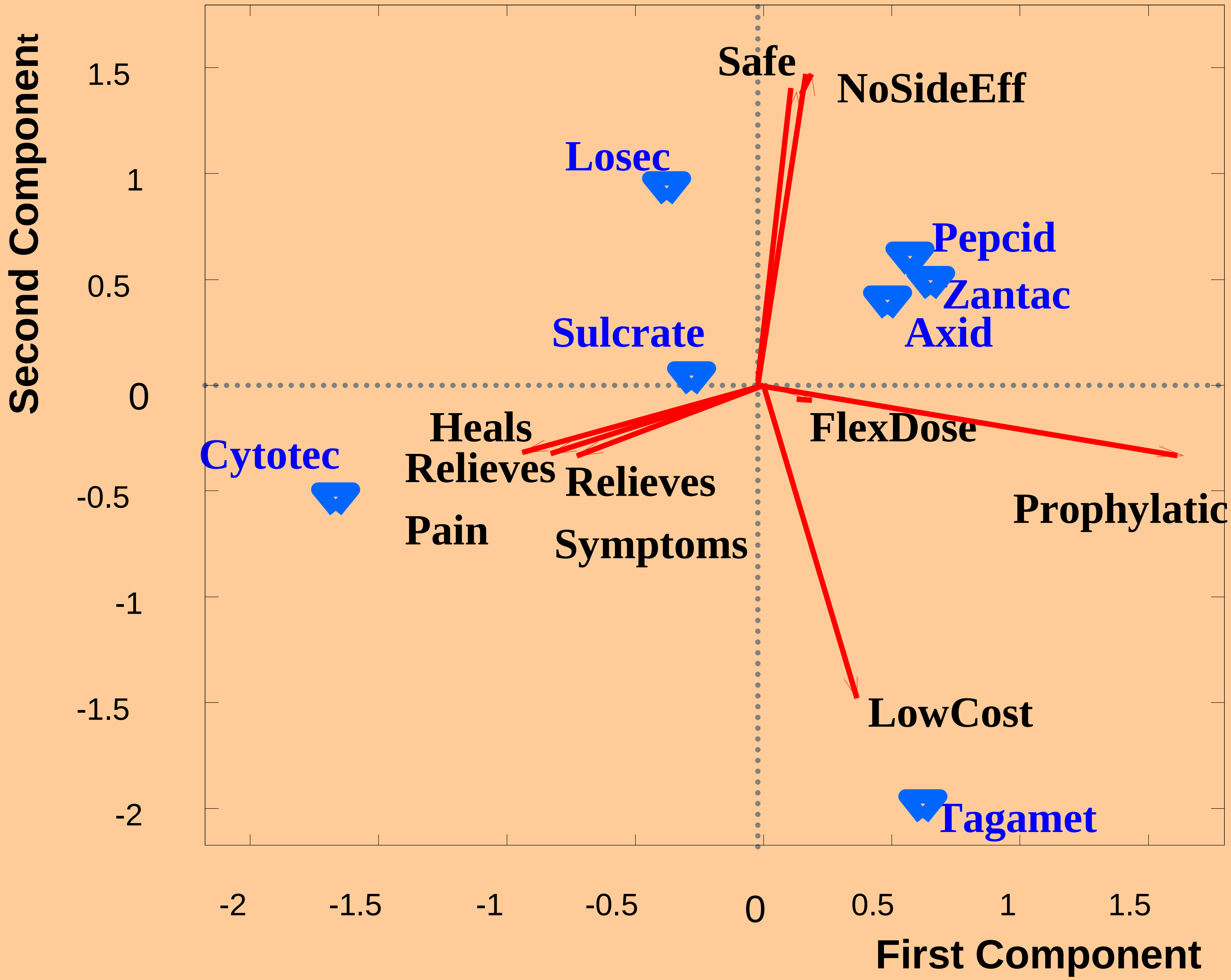
Joint Biplot

(Consensus among doctors - Mean)



Joint Biplot

(Individual differences between doctors - Deviations from mean)



Conclusions - 1

HiClas model

- **Given the data are binary, the binary hierarchical classes model is an obvious analysis method and has a relatively straightforward interpretation.**
- **Effective graphics to display results**
- **Many components might be necessary to model all systematic variability present.**

Conclusions - 2

Tucker3 model

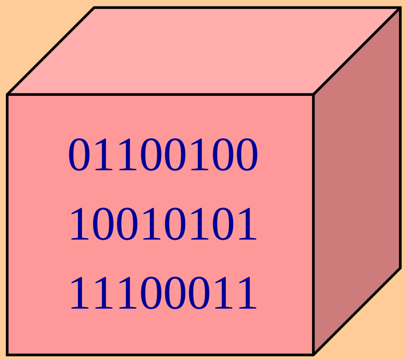
- **By using a numerical model variance can be portrayed in a different and also insightful manner**
- **Differential weighting may simplify model description**
- **Enlightning graphics are available (joint biplots), but it requires some training to understand them**

Conclusions - 3

Substantive conclusions concern the perceptual mappings of the brands with respect to the attributes as seen by the doctors.

The main patterns have been discussed during the presentation and will not be repeated.

Thank You.



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Tucker3 Model in Matrix Notation

$$\mathbf{X} = \mathbf{A}\mathbf{G}\,(\mathbf{B}' \otimes \mathbf{C}') + \varepsilon$$

A, (I × P) loadings matrix for ***brands***

B, (J × Q) loadings matrix for ***attributes***

C, (K × R) loadings matrix for ***subjects***

$\underline{\mathbf{G}}$, (P × Q × R) core array with **links** between the components

PARAFAC/CANDECOMP Model:

$$\hat{x}_{ijk} = m_{ijk} = \sum_{s=1}^{S} g_{sss} a_{is} b_{js} c_{ks}$$

m_{ijk} is the **model matrix** or **structural image**

A is the ($I \times S$) loadings matrix for ***brands***

B is the ($J \times S$) loadings matrix for ***attributes***

C is the ($K \times S$) loadings matrix for ***subjects***

G is the ($S \times S \times S$) superdiagonal core array
exclusive **links** between the components s of the three modes

- (Harshman 1970, 1976; Harshman and Lundy 1984, 1994; Carroll and Chang 1970)
- Based on the principle of Parallel Proportional Profiles (Cattell 1944).

Three-Mode Components Analysis: Model Comparison

MODELS	NUMBER OF COMPONENTS A	B	C	STANDARDIZED SS	Number of Param.	St.Fit/#Param (x1000)
TUCKALS2	3	3	---	.49	2754	.19
TUCKALS2	2	3	---	.40	1723	.23
TUCKALS3	3	3	5	.40	1462	.27
TUCKALS2	2	2	---	.31	1154	.27
TUCKALS3	2	2	4	.31	1154	.27
TUCKALS3	2	3	4	.35	1165	.30
TUCKALS3	3	3	4	.37	1179	.37
TUCKALS3	3	3	3			
TRILIN	3	3	3	.32	888	.36
TUCKALS3	2	3	3	.32	883	.36
TUCKALS3	2	2	2	.27	592	.46
TRILIN	2	2	2	.27	592	.46
TUCKALS3	2	3	2	.28	599	.47

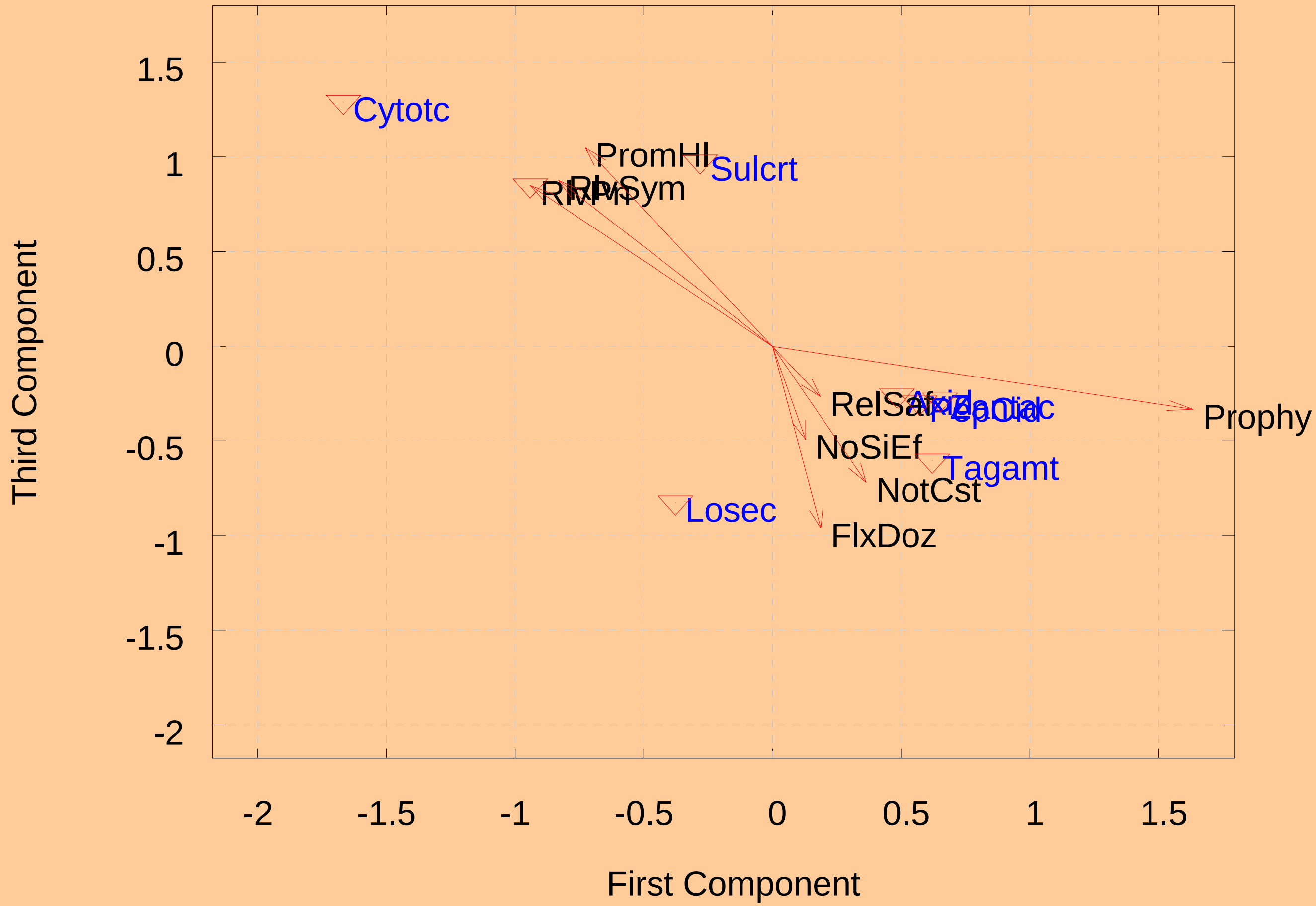
COMPUTATION OF NUMBER OF PARAMETERS:

```
A  +  B  +  C  + core  - transformational freedom
--------------------------------------------------------------
TUCKALS2:   I*P + J*Q +     + P*Q*K - P**2 - Q**2
TUCKALS3:   I*P + J*Q + K*R + P*Q*R - P**2 - Q**2 - R**2
PARAFAC :   I*S + J*S + K*S + S     - S    - S    - S
```

Varimax Rotation: Deciding On Weights

Relative Weights			Varimax Value			
A	B	C	Core	A	B	C
	unrotated		2.136	1.130	1.099	1.503
0	0	0	2.782	1.600	1.404	1.488
0.5	0.5	0.5	2.665	2.635	2.336	1.490
1.0	1.0	1.0	2.603	2.643	2.416	1.491
1.5	1.5	1.5	2.561	2.644	2.446	1.494
2.0	2.0	2.0	2.519	2.644	2.463	1.501
2.5	2.5	2.5	2.443	2.644	2.475	1.523
3.0	3.0	3.0	2.180	2.635	2.454	1.678
3.5	3.5	3.5	2.134	2.637	2.465	1.679
4.0	4.0	4.0	2.099	2.638	2.473	1.679
4.5	4.5	4.5	2.071	2.640	2.478	1.679
5.0	5.0	5.0	2.049	2.640	2.482	1.680
5.5	5.5	5.5	2.030	2.641	2.484	1.680
100	100	100	1.895	2.644	2.470	1.681
1000	1000	1000	1.843	2.644	2.498	1.681
10000	10000	10000	1.842	2.644	2.498	1.681
0.5	0.5	3.0	2.629	2.641	2.274	1.520
0.5	1.0	3.0	2.522	2.644	2.424	1.522
1.0	1.0	3.0	2.522	2.644	2.424	1.522
1.0	1.0	3.5	2.582	2.596	2.250	1.678

Joint biplot for Brands and Attrubutes
First versus Third Component
for Second Component of Doctors



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Components for Brands and Attributes

Mode	Unrotated Components (Orthonormal)				Components After Varimax Rotation of the Core Matrix				Components After Joint Varimax Rotation of Components and the Core		
	1	2	3		1	2	3		1	2	3
Brands:											
A	.595	-.701			.836	-.385			.919	.034	
G	.098	.213			-.001	.234			-.175	.371	
D	-.609	-.385			-.390	-.606			-.220	-.414	
E	-.462	-.083			-.384	-.270			-.074	-.716	
B	.089	.304			-.048	.031			-.159	.259	
C	.105	.285			-.025	.302			-.184	.258	
F	.183	-.367			.011	.410			-.107	.209	
Attributes:											
Inexp	.481	.536	-.012		.573	-.436	-.001		.709	.100	.080
NoSiEf	-.350	-.222	.127		-.361	.188	-.149		-.419	-.005	.111
Safe	-.467	-.251	.229		-.461	.225	-.266		-.535	-.001	.218
Prophy	-.490	.575	-.421		-.424	-.736	.160		-.006	.863	-.064
RelPain	.291	-.302	-.122		.194	.301	.249		.050	-.327	-.284
FlexDo	.130	.195	.762		.302	.036	-.737		.177	-.261	.732
RelSym	.245	-.278	-.267		.130	.234	.371		.037	-.224	-.397
Heals	.160	-.253	-.296		.048	.188	.373		-.013	-.145	-.395

Core Array

	Unrotated				Varimax Rotation of the Core Only				Joint Varimax Rotation of the Components and the Core		
Components for Brands:	Components for Attributes										
Frontal Slice 1:											
	1	2	3		1	2	3		1	2	3
1	13.777	-2.269	2.164		14.441	.045	.550		14. 105	-1.235	.610
2	-3.628	-10.714	.950		.202	10.959	.562		.592	-9.748	.563
Frontal Slice 2:											
	1	2	3		1	2	3		1	2	3
1	-2.081	5.647	3.469		-.672	4.805	2.312		-.048	2.372	-.804
2	-5.500	-.754	4.409		4.306	1.911	7.113		-2.241	7.680	7.997

Assessment of Goodness of Model Fit:

- Kroonenberg and De Leeuw (1980), and Kroonenberg (1983) show that

$$SS(Residual) = SS\ (Total) - SS(Fit)$$

$$SS\ Accounted\ For = SS(Fit)\ /\ SS\ (Total)$$

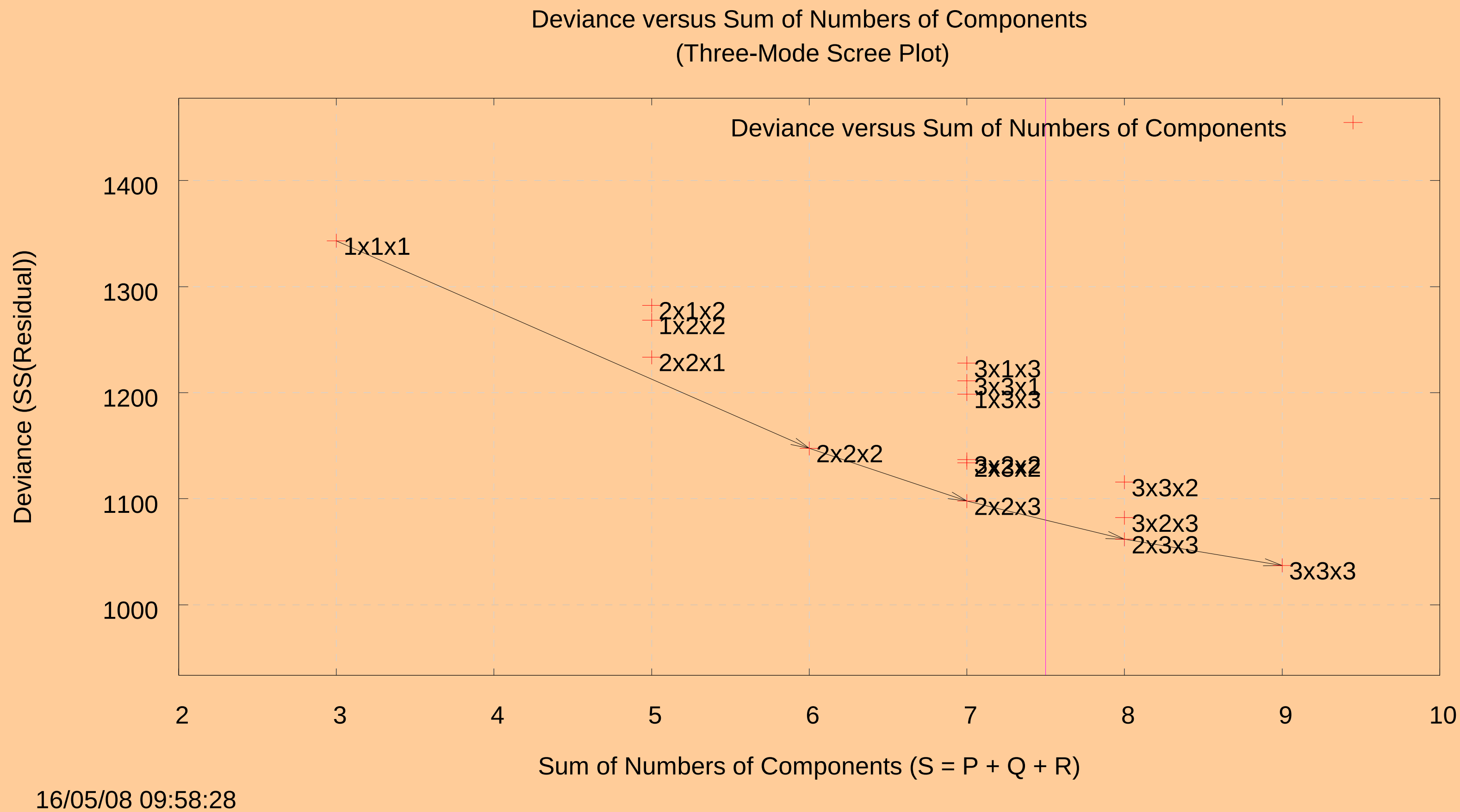
- Also, as it has been shown by Ten Berge, De Leeuw, and Kroonenberg (1987), when the ALS algorithm has converged,

$$SS\ (Residual_m) = SS\ (Total_m) - SS(Fit_m)$$

where *m* stands for any level of any mode of the data matrix.

- Using the last relationship, the relative fit of individual levels of a mode can be established. Also, whether a given level fits the model well or badly can be determined.

Model selection Tucker3 model



Tucker 3 Solutions

	Raw SS	Standardized SS
SS(Total)	1564.857	1.0000
A.EST.SS(Fit)	885.938	.5661
B.EST.SS(Fit)	1008.107	.6442
C.EST.SS(Fit)	465.270	.2973
SS(Fit)	430.970	.2754
SS(Residual)	1133.887	.7246

DF = **Number of data points** (minus loss of information due to preprocessing or missing data) **minus** the **number of independent parameters**

Number of independent parameters =
$(I*P) + (J*Q) + (K*R) + (P*Q*R) - P**2 - Q**2 - R**2$

with I, J, K the numbers of levels of 1st, 2nd, and 3rd modes, respectively,

and P, Q, R the numbers of components of 1st, 2nd, and 3rd modes, respectively.

Relating Subject Components to External Variables

- Y: Number of years of experience as a medical doctor (standardized)
- X_1 : First component score for "subjects" mode,
- X_2: Second component score for "subjects" mode,

- Linear Model: $Y = X_1 B_1 + X_2 B_2$
- Estimates: B_1= -1.054 , std. error = 0.997, t= 1.058, p-value=0.29
- B_2 = 1.350, std. error = 0.997, t =1.345, p-value=0.18
- R^2=0.01, F-value=1.477, df=(2, 282), p-value=0.23.
- Conclusion: Subject components are not related to number of years of experience as a medical doctor.

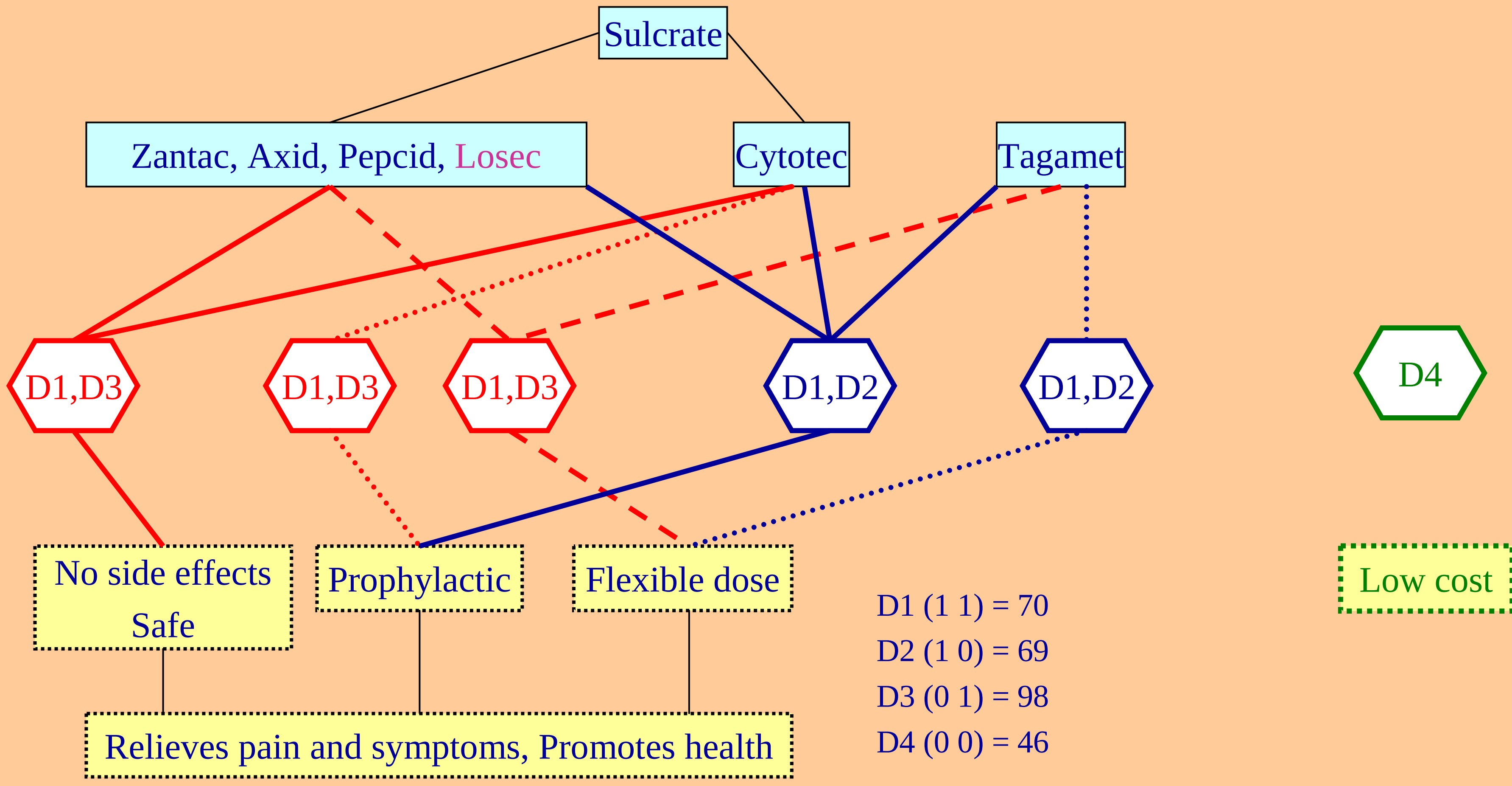
Relating Residuals to External Variables:

- Y: Number of years of experience as a medical doctor (standardized)
- X: Sum of squares of residuals for each subject

- Linear Regression: Y = B X

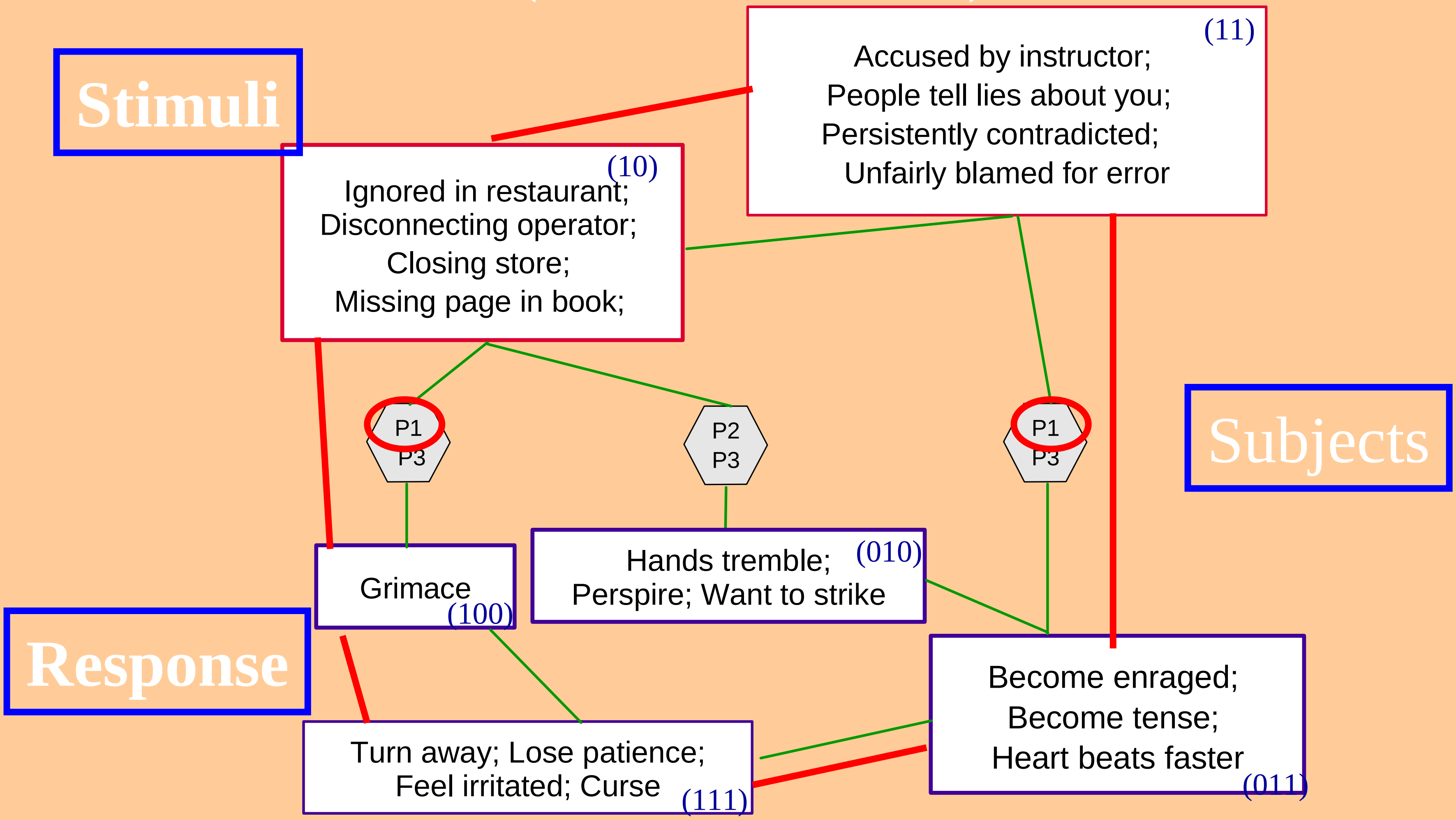
- Estimated B = - 0.006, R^2= 0.0007, F-value = 0.212, d.f. = (1, 282)
- p-value = 0.646
- Conclusion : Residuals are not related to number of years of experience.

Result HiClas3-model (2D×3A×3B)



HICLAS3: Example

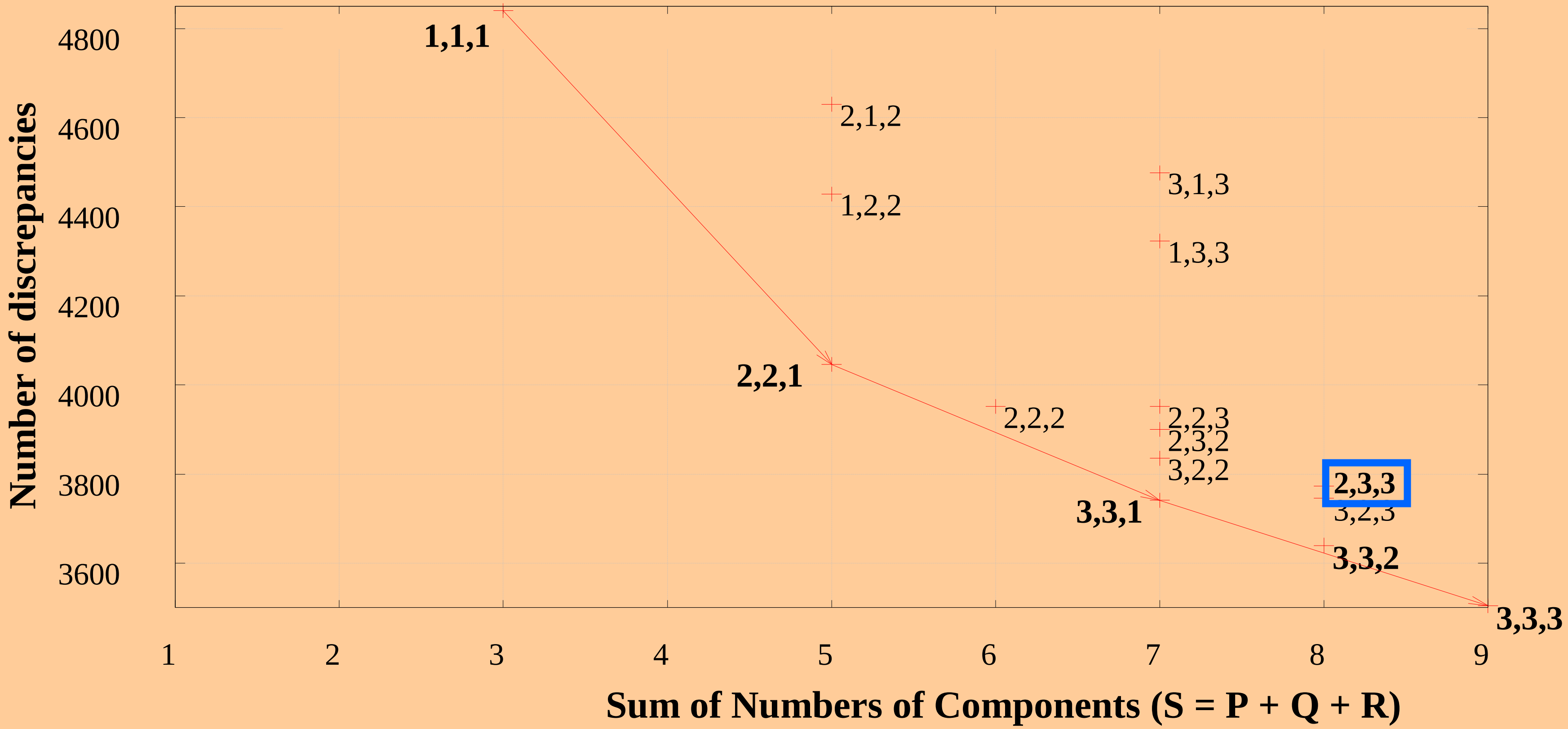
(Tucker3-HICLAS)



Based on example Leuven group

HiClas3 – Three-mode scree plot

Doctors × Attributes × Brands

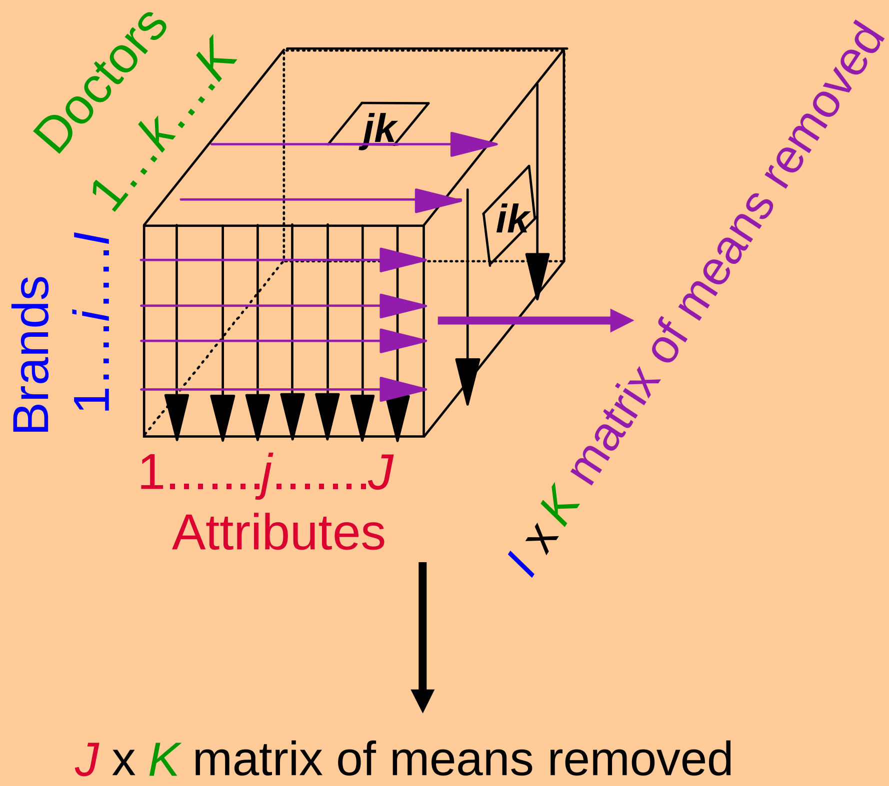


**

Preprocessing: Double Centring

(in three-mode component analysis)

- **Double centring**:
  doctors may not use the attrubutes uniformly across the brands and across the attributes.
- **Double centring:**
  Scores in deviations from
  brand means $\bar{x}_{i.k}$
  attribute means. $\bar{x}_{.jk}$
  Origin = zero point for both brands and attributes of each subject's scores



$$x^{*}_{ijk} = x_{ijk} - \bar{x}_{.jk} - \bar{x}_{i.k} + \bar{x}_{..k}$$

Preprocessing: Double centring

Three-way factorial design without replacement (1 observation per cell):

Dependent variable: Brand possesses attribute (score = 1)

$$x_{ijk} = m + a_i + b_j + c_k + ac_{ik} + bc_{jk} + ab_{ij} + abc_{ijk}$$

After centring:

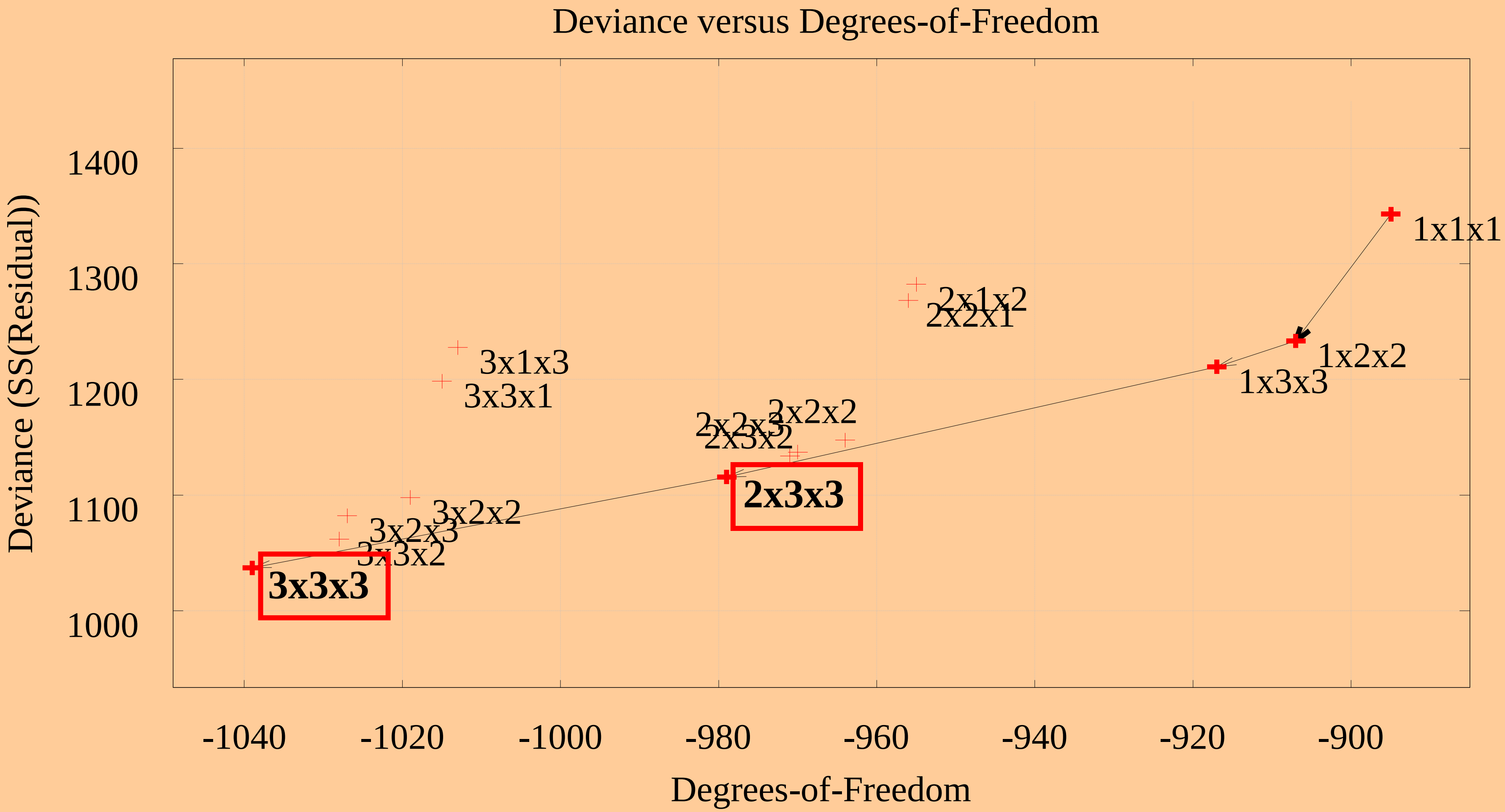
$$x_{ijk} = \cancel{m} + \cancel{a_i} + \cancel{b_j} + \cancel{c_k} + \cancel{ac_{ik}} + \cancel{bc_{jk}} + ab_{ij} + abc_{ijk}$$

Analysed with Three-mode PCA

ab_{ij} = **consensus** of doctors about attributes of brands

abc_{ijk} = **differences** between doctors about attributes of brands

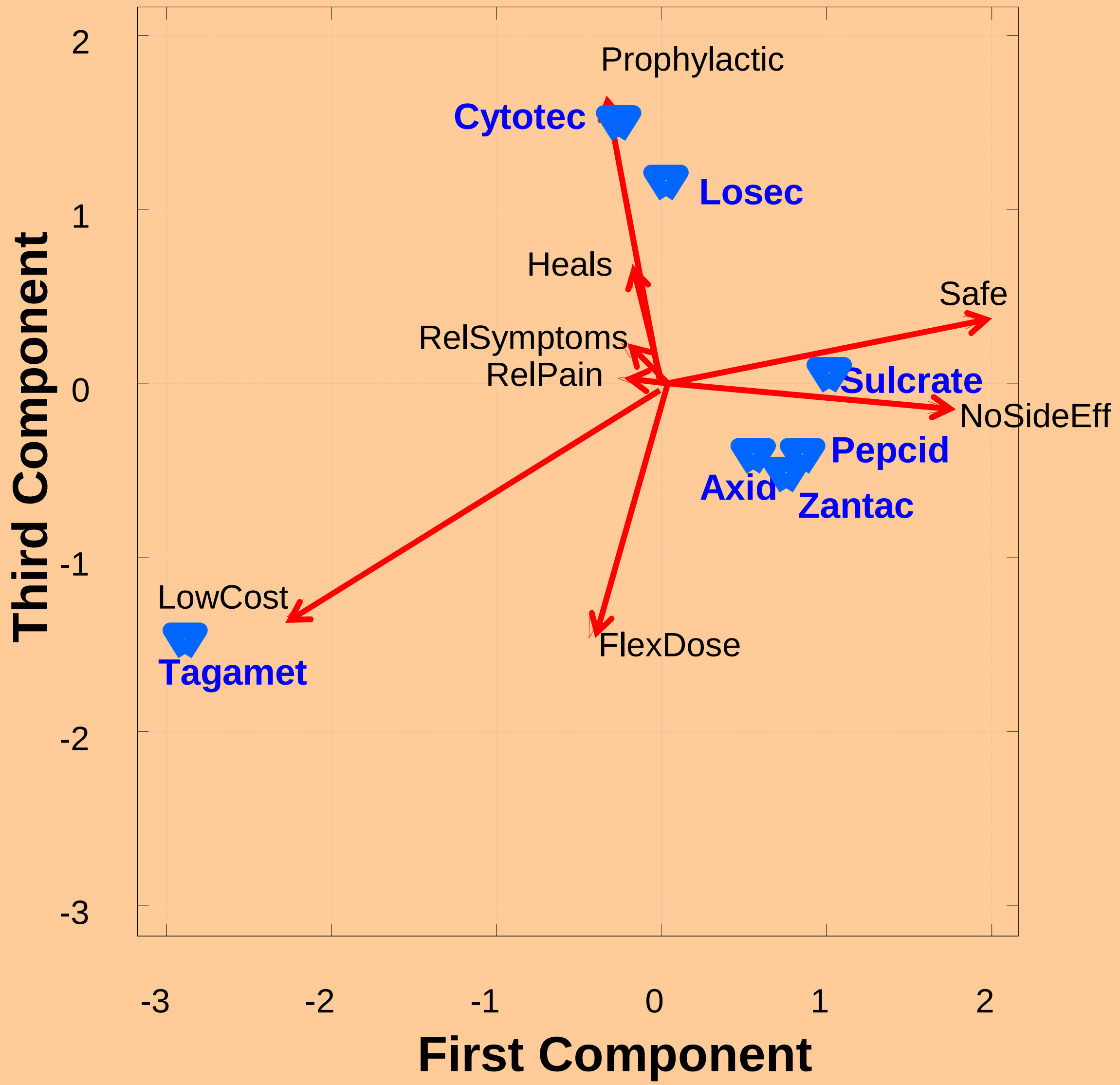
Model selection Tucker3 model



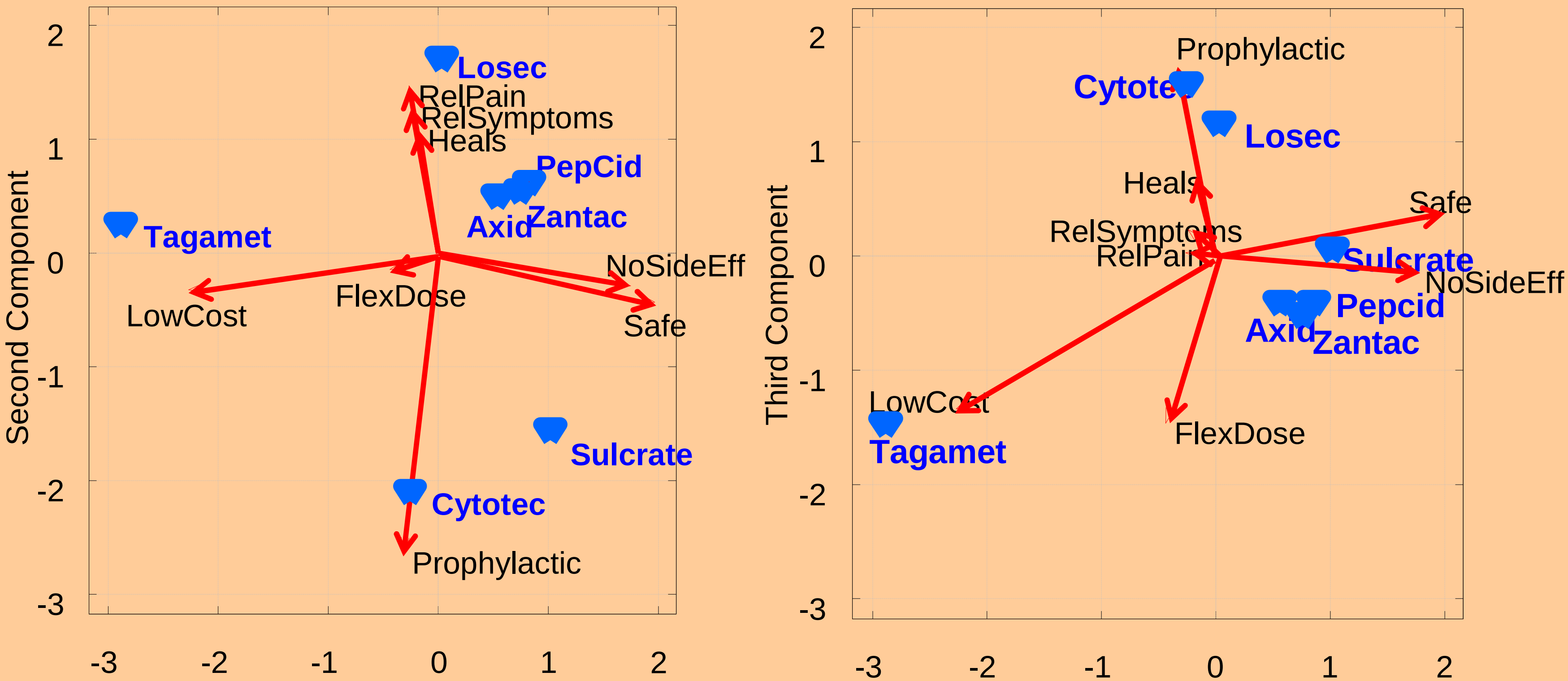
Model complexity: (**Docs = 2; Attr = 3; Brands = 3**) or (**Docs = 3; Attr = 3; Brands = 3**)

Joint biplot

(Consensus)



Joint biplot (Consensus)



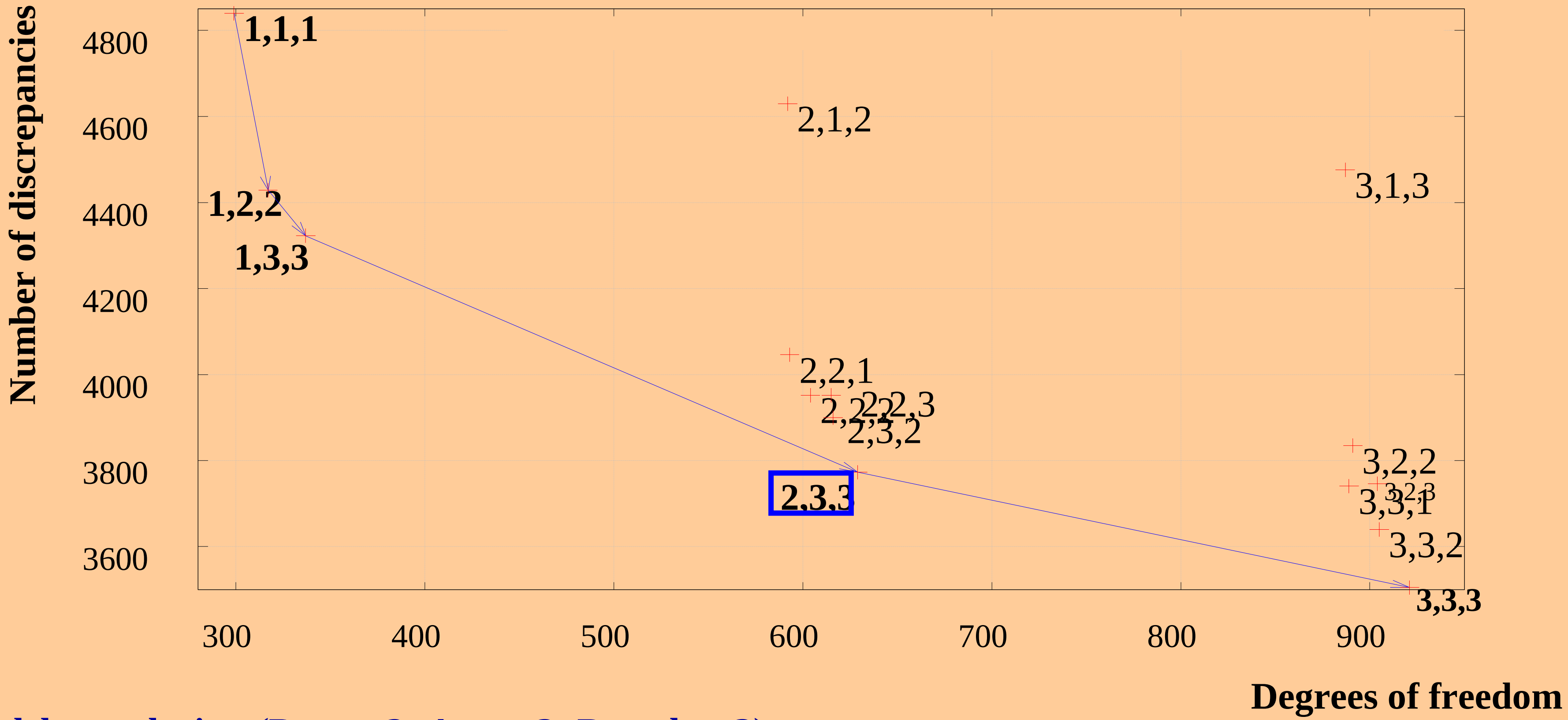
Conclusions

Where to go from here

- Irregular patterns in some doctors combined with low number of ones were excluded from the HiClas analysis while these doctors were scattered all over the plot of the doctors' components.
  Thus Tucker analysis picked up some information which was not available to the HiClas analysis. Similarly for the LowCost attribute.
- Is the numerical information such as the variance somewhere to be found in the HiClas results and if so can it be used?
- Construct exactly fitting hierarchical classes models and run a Tucker3 analysis on them.
- Construct doctors/attributes/brands artificially according to a specific pattern and include them in the analysis to facilitate interpretation.
- Sort out the mathematics of the comparison between models.

HiClas3 – Three-Mode Deviance Plot

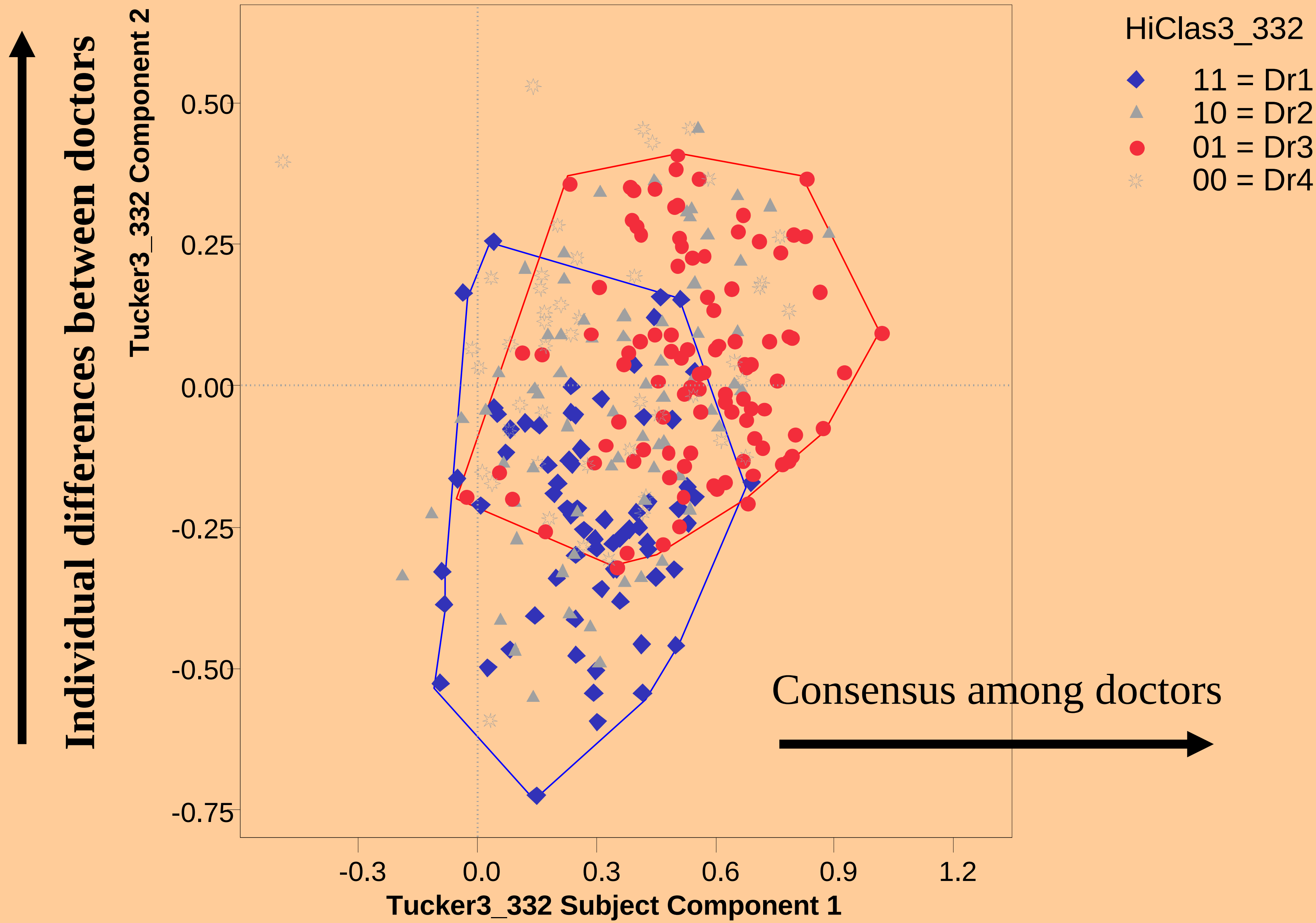
Doctors × Attributes × Brands



Model complexity: (**Docs = 2; Attr = 3; Brands = 3**) or
(**Docs = 3; Attr = 3; Brands = 3**)

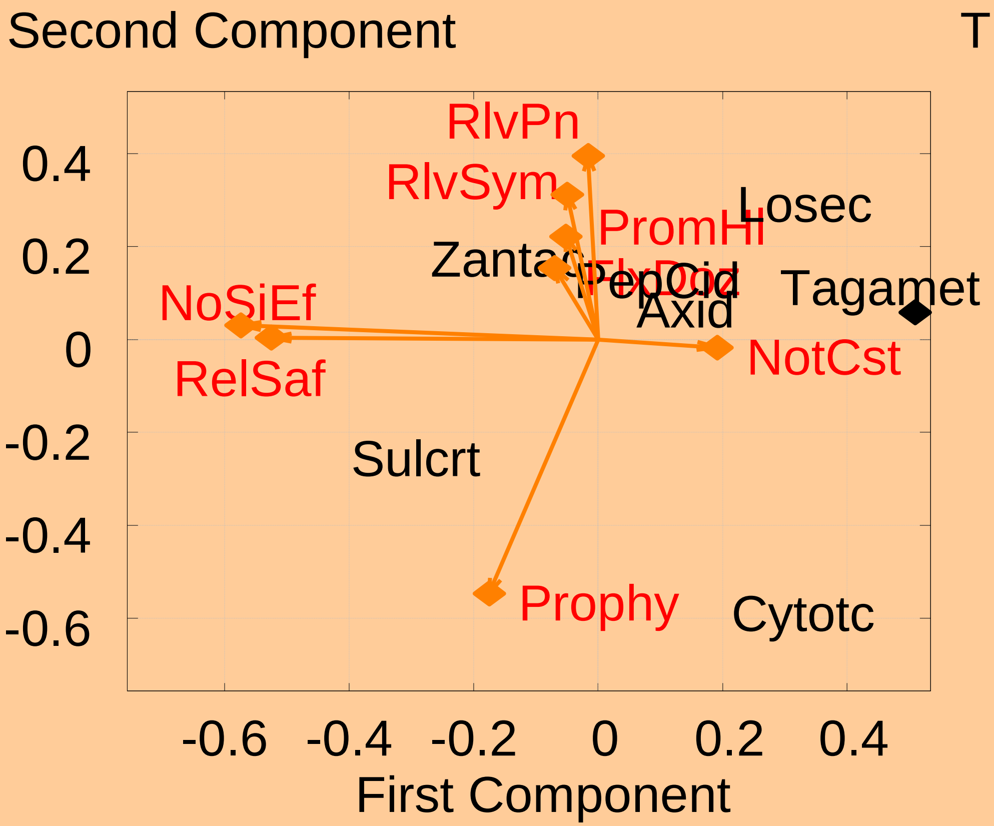
**

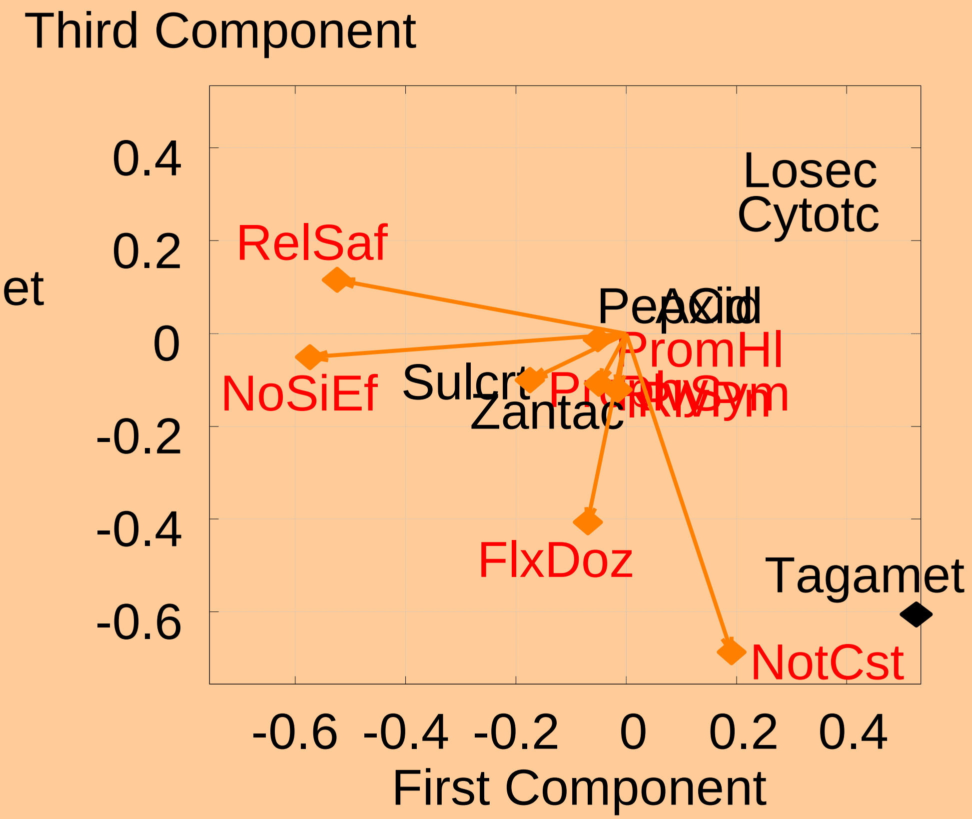
Component Scores



Gastro –SVD-Biplot

(means across doctors - attributes centred)





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