TEXTURE ANALYSIS

BRAIN Glioblastomas

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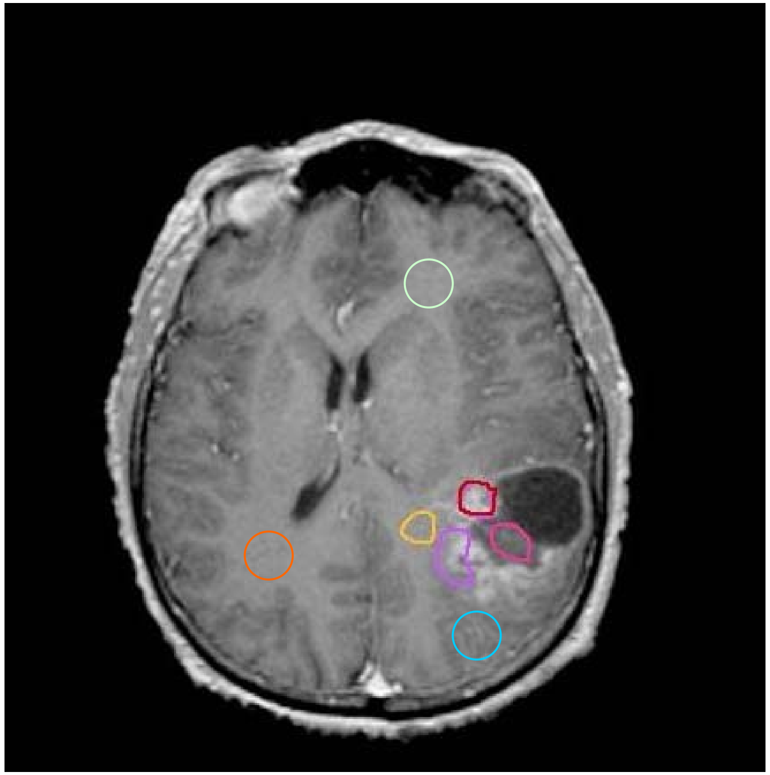
COST B21 - Slovenia, Bled ***March 2007, 29th-31st***

BRAIN: Glioblastomas

- Tumor Heterogeneity and Margin



🟥 Necrosis

🟥 Tumor

🟪 Margin (interface between the tumor and the parenchyma)

🟦 Oedema

🟨 Peritumoral White Matter

🟩 Normal region in the cerebral hemisphere with tumor

🟧 Normal region in the contralateral hemisphere

Objectives

Characterization of intra and extra-tumoral regions of Brain Glioblastomas

- Necrosis / Tumor / Oedema / White Matter (Macroscopic Normal tissue)

- Tumor vs Necrosis
- Tumor vs Oedema
- Tumor vs WM

- Peri-tumoral WM / Homo-lateral WM / Contra-lateral WM
- Peri-tumoral WM vs WM (HL + CL)

Method & Data

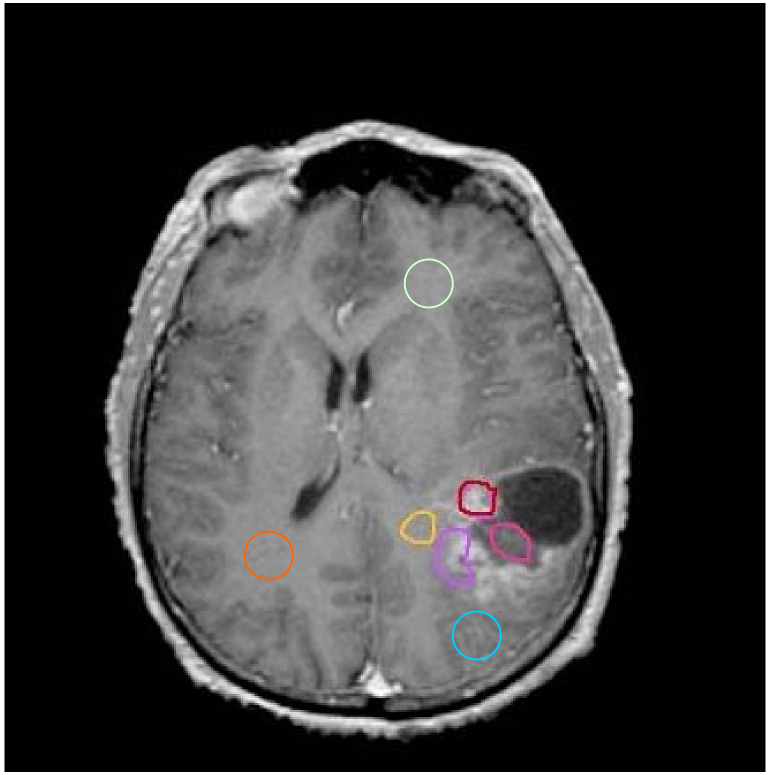
- Texture Analysis on MR Images of Brain Glioblastomas
  - MaZda software - version 4.5
  - 2D TA

- Database
  - 3T MRI from Rennes University Hospital
  - 10 patients
  - 3D T1w
  - 2 series of images for each patient (before and after injection)

- Regions of interest (ROIs)
  - 5 selected slices from non-injected series per patient
  - ROIs drawn on each slice : **necrosis**, **tumor**, **oedema**, **peritumoral white matter** (WM), **far homolateral** WM, **contralateral** WM
  - ROIs size : >100 pixels

BRAIN: Glioblastomas

- Necrosis vs Tumor vs Oedema vs WM



🟥 Necrosis

🟥 Tumor

🟪 Margin (interface between the tumor and the parenchyma)

🟦 Oedema

Extratumoral White Matter

🟨 Peritumoral White Matter

🟩 Normal region in the hemisphere with tumor

🟧 Normal region in the contralateral hemisphere

Necrosis / Tumor / Oedema / WM

- Dataset : 300 data

Misclassified (%)				
	Fisher	POE+ACC	MI	MI+PA+F
Raw+kNN	43	42	45	38
LDA+kNN	21	21	25	10
PCA+kNN	43	48	48	43

Tab1 - Standardization of feature vector: NO

Misclassified (%)				
	Fisher	POE+ACC	MI	MI+PA+F
Raw+kNN	7	11	7	7
LDA+kNN	16	12	24	10
PCA+kNN	8	11	7	7

Tab2 - Standardization of feature vector: YES

- Method of features selection :
  - None better than another (among Fisher, PA or MI)
- Standardization of feature vector
  - gives much better classification with Raw+kNN and PCA+kNN
  - has no such influence with LDA+kNN
- MI+PA+F / LDA returns the best classification results (with F score rather high compared to other methods)

Necrosis / Tumor / Oedema / WM

Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Dataset	Train	Test	Train	Test	Train	Test	Train	Test
NDA-3	4	14	3	17	19	32	0	23
NDA-4	2	14	3	19	4	21	0	25

- Dataset : 300 data
  - Training set : 180 data
  - Test set : 120 data
- Trials with NDA
  - NDA-3 : with 3 neurons in the 1st hidden layer
  - NDA-4: with 4 neurons in the 1st hidden layer

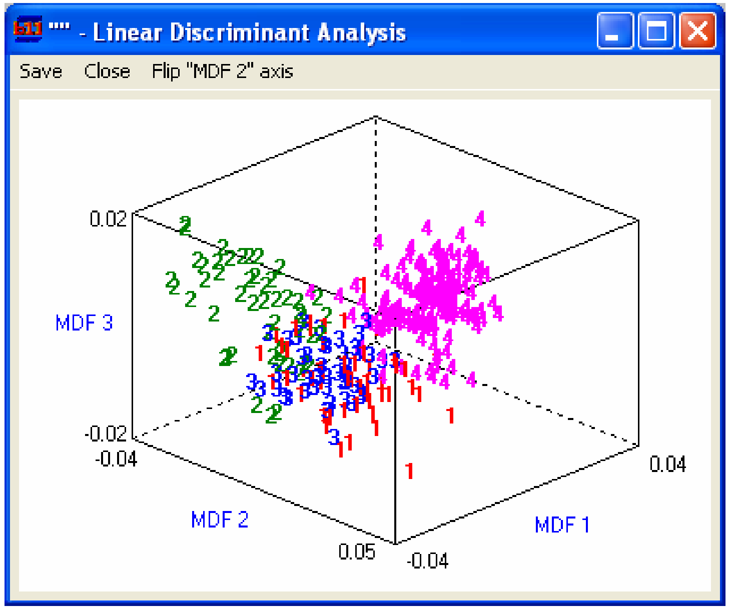
- NDA results not much better than LDA
- Data put as training data set or test data set need to be discussed
  - No randomization here

Necrosis(1) / Tumor(2) / Oedema(3) / WM(4)

MI+PA+F

*features
1 Perc.10%
2 Perc.01%
3 Mean
4 Perc.50%
5 Perc.90%
6 Perc.99%
7 WavEnLL_s-2
8 S(2,0)Entropy
9 135dr_RLNonUni
10 Horzl_RLNonUni
11 S(5,0)DifEntrp
12 S(4,-4)SumAverg
13 S(5,5)Contrast
14 GrNonZeros
15 Teta3
16 WavEnLL_s-1
17 S(1,1)SumOfSqs
18 Skewness
19 S(4,4)InvDfMom
20 Sigma
21 Vertl_RLNonUni
22 45dgr_RLNonUni
23 Variance
24 S(1,0)Correlat
25 S(1,0)Contrast
26 WavEnHH_s-1
27 S(1,0)SumAverg
28 S(1,0)DifVarnc
29 S(2,0)SumAverg
30 S(1,0)InvDfMom

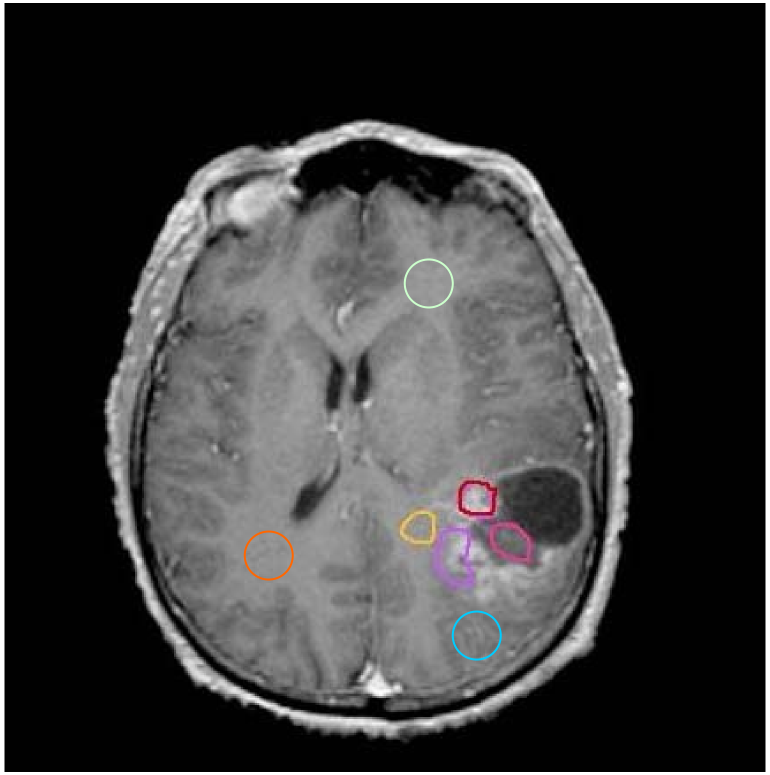
MI+PA+F/LDA



- Ability of TA with proper method to highlight tumor heterogeneities

BRAIN: Glioblastomas

- Necrosis vs Tumor

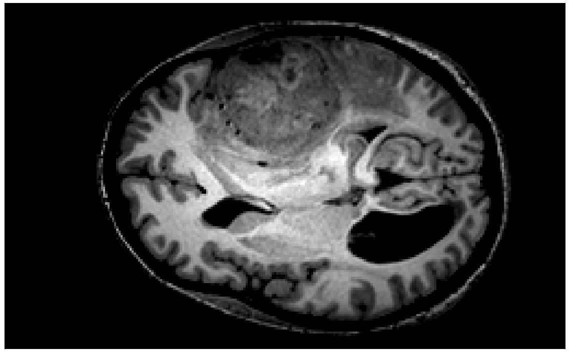


- 🟥 Necrosis
- 🟥 Tumor
- 🟪 Margin (interface between the tumor and the parenchyma)
- 🟦 Oedema
- 🟨 Peritumoral White Matter
- 🟩 Normal region in the cerebral hemisphere with tumor
- 🟧 Normal region in the contralateral hemisphere

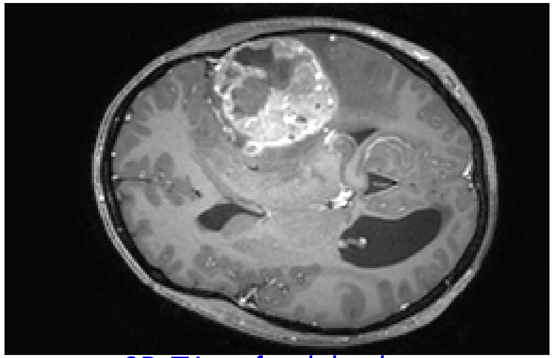
Necrosis vs Tumor

- Differentiation between necrosis and tumoral tissue highlighted with injection of contrast agent
- Observations: irregularities of necrosis

BOC

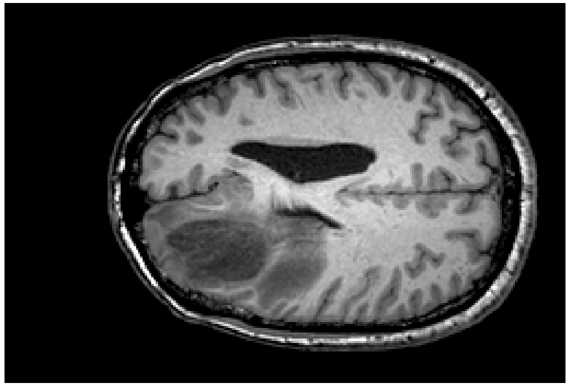


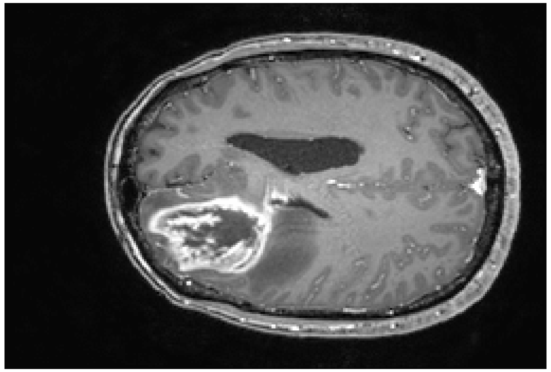
3D T1w before injection



3D T1w after injection

BOU





<u>Question</u> :

Could we discriminate necrosis from tumor tissue, on non-injected MR images, using MRI-TA method?

Necrosis vs Tumor

Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Standardization	No	Yes	No	Yes	No	Yes	No	Yes
Raw+kNN	28	19	33	12	28	7	28	7
LDA+kNN	27	21	21	21	31	31	10	10
PCA+kNN	28	21	33	13	28	8	28	8

- Dataset : 100 data
- Features selected with Fisher, PA, MI and MI+PA+F
  - COM parameters
- Standardization of feature vector
  - gives better classification with Raw+kNN and PCA+kNN
  - has no influence with LDA+kNN

- Dataset : 100 data
  - Training set : 60 data
  - Test set : 40 data
- Trials with NDA
  - NDA-1 : with 1 neuron in the 1st hidden layer
  - NDA-2: with 2 neurons in the 1st hidden layer

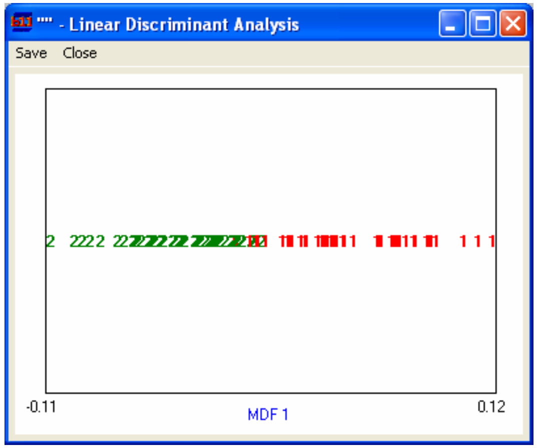
Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Dataset	Train	Test	Train	Test	Train	Test	Train	Test
NDA-1	10	28	10	15	12	28	0	13
NDA-2	10	23	0	18	12	28	0	8

Necrosis (1) / Tumor (2)

MI+PA+F

1 WavEnLL_s-2
2 S(0,1)DifEntrp
3 S(5,0)SumEntrp
4 S(3,3)SumEntrp
5 S(1,0)Entropy
6 S(1,0)DifEntrp
7 S(2,2)SumEntrp
8 WavEnLL_s-1
9 S(2,0)Entropy
10 Perc.10%
11 S(4,-4)SumAverg
12 S(0,5)DifVarnc
13 S(5,-5)AngScMom
14 Perc.01%
15 S(4,4)InvDfMom
16 S(5,5)AngScMom
17 S(0,3)AngScMom
18 S(0,5)AngScMom
19 S(1,-1)SumOfSqs
20 S(0,5)SumEntrp
21 S(1,0)SumAverg
22 S(1,1)SumAverg
23 WavEnHH_s-1
24 S(4,-4)SumOfSqs
25 S(0,5)SumOfSqs
26 S(0,5)SumVarnc
27 S(5,-5)SumVarnc
28 S(0,4)SumVarnc
29 S(0,4)SumOfSqs
30 S(3,-3)DifEntrp

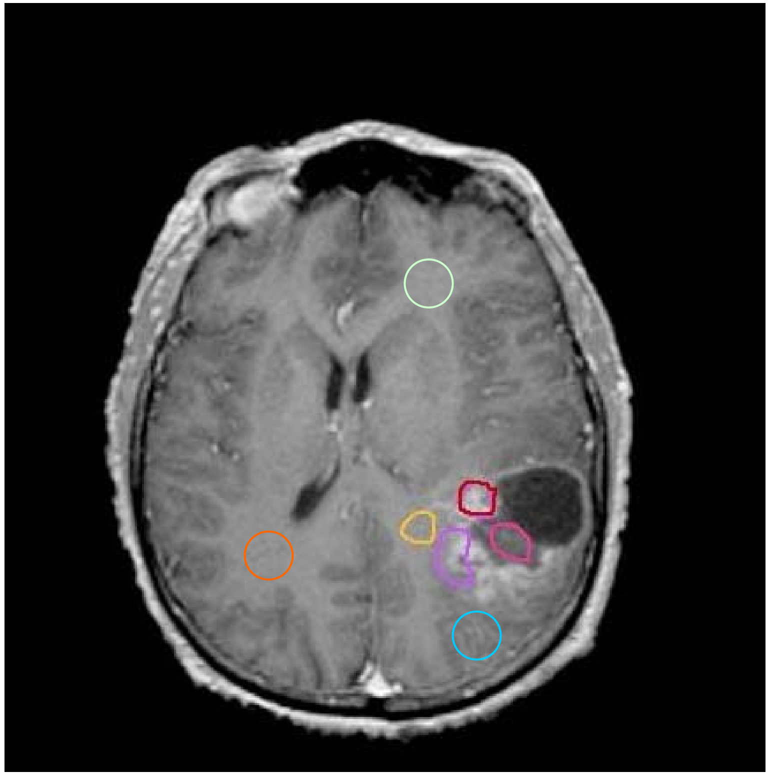
MI+PA+F/LDA



- With MI+PA+F/LDA : 10% misclassified (F score=8)
- Overlapping between regions
  - Due to irregularities of necrosis
  - Tumoral cells in necrosis regions?

BRAIN: Glioblastomas

- Tumor vs Oedema



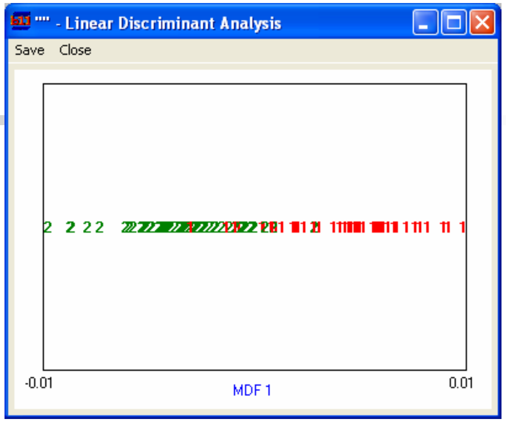
- 🟥 Necrosis
- 🟥 Tumor
- 🟪 Margin (interface between the tumor and the parenchyma)
- 🟦 Oedema
- 🟨 Peritumoral White Matter
- 🟩 Normal region in the cerebral hemisphere with tumor
- 🟧 Normal region in the contralateral hemisphere

Tumor(1) / Oedema(2)

Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Standardization	No	Yes	No	Yes	No	Yes	No	Yes
Raw+kNN	38	18	26	11	25	8	31	11
LDA+kNN	23	23	18	18	17	17	12	12
PCA+kNN	39	18	39	11	39	6	39	13

- Dataset : 100 data
- Fisher coefficient F:
  - Raw+kNN : between 0,8 and 1,4
  - LDA+kNN : between 3,4 and 8
  - PCA+kNN: between 0,8 and 1,2

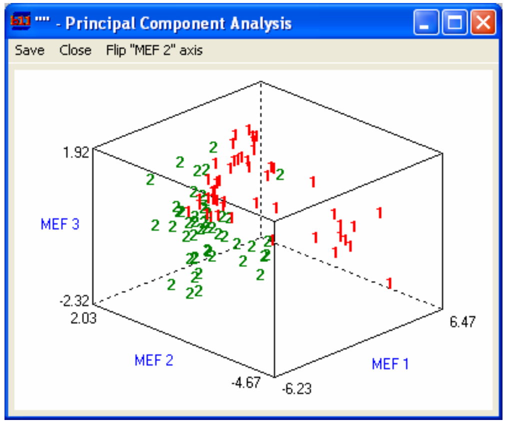
- Better classification with MI/PA method
  - However, F score is higher with LDA method
  - Results more reliable with LDA?



MI+PA+F/LDA

Misclassified : 12%

Fisher coefficient = 8



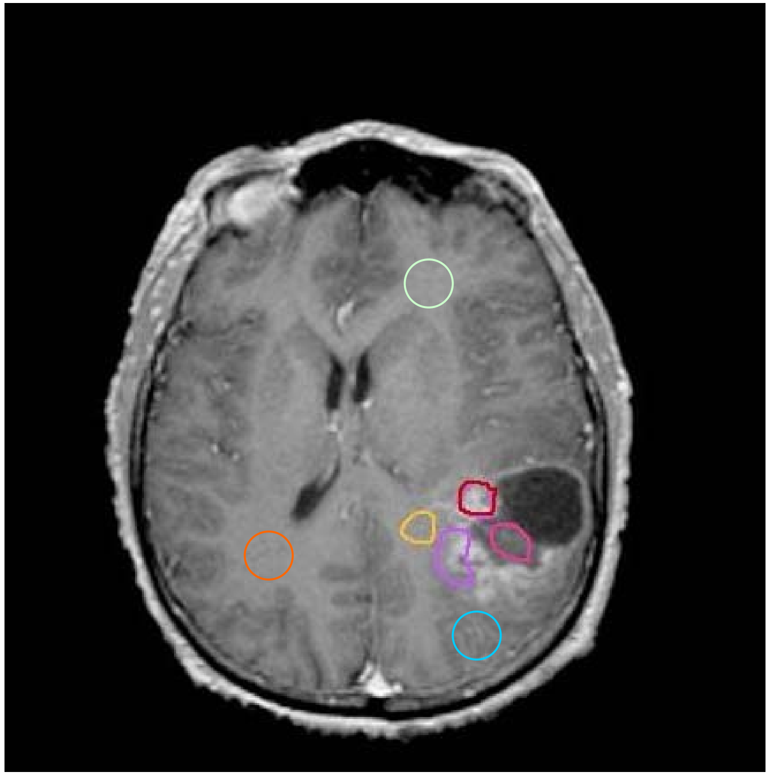
MI/PCA

Misclassified : 6%

Fisher coefficient = 1,2

BRAIN: Glioblastomas

- Tumor vs Extratumoral White Matter



🟥 Necrosis

🟥 Tumor

🟪 Margin (interface between the tumor and the parenchyma)

🟦 Oedema

	Extratumoral White Matter
🟨	Peritumoral White Matter
🟩	Normal region in the hemisphere with tumor
🟧	Normal region in the contralateral hemisphere

Tumor / WM

Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Standardization	No	Yes	No	Yes	No	Yes	No	Yes
Raw+kNN	1	1	8	1	0	1	3	1
LDA+kNN	3	3	5	5	1	1	0	0
PCA+kNN	1	1	28	1	1	1	2	1

- Dataset : 200 data (50 ZT, 150 WM)
- WM includes PT, HL and CL ROIs
- Fisher coefficient F:
  - Raw+kNN : between 1,5 and 4
  - LDA+kNN : between 16 and 62
  - PCA+kNN: between 1,5 and 4

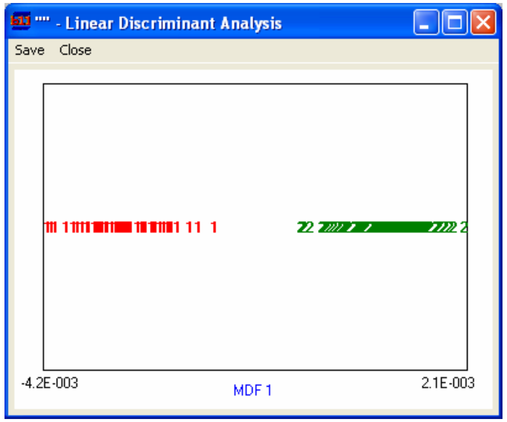
- Dataset : 200 data
  - Training set : 120 data
  - Test set : 80 data
- Trials with NDA
  - NDA-1 : with 1 neuron in the 1st hidden layer
  - NDA-2: with 2 neurons in the 1st hidden layer

Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Dataset	Train	Test	Train	Test	Train	Test	Train	Test
NDA-1	0	3	0	10	8	9	0	5
NDA-2	0	1	0	4	0	1	0	1

Tumor(1) / WM(2)

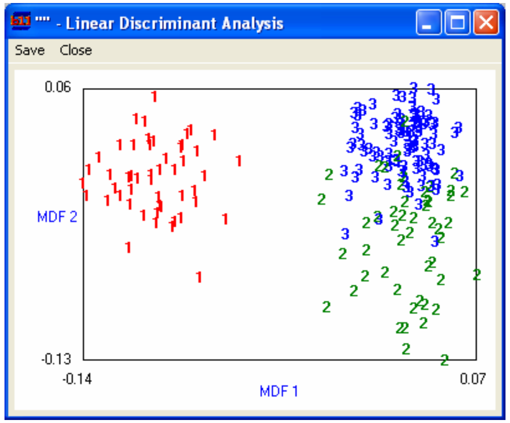
MI+PA+F/LDA

(1) Tumor
(2) White Matter WM (PT+HL+CL)



MI+PA+F/LDA

(1) Tumor
(2) Peritumoral White Matter
(3) White Matter WM (HL+CL)

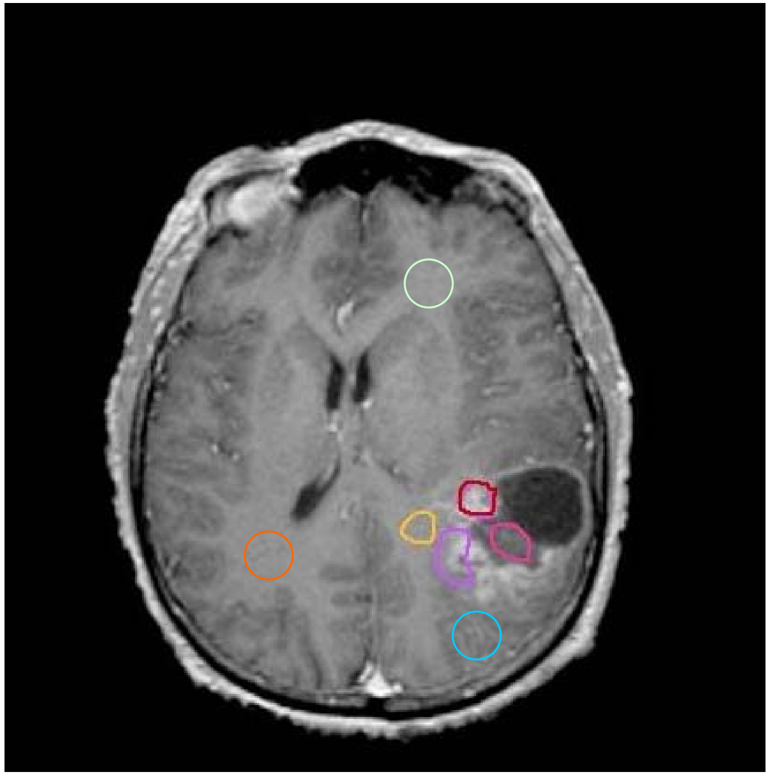


MI+PA+F

*features
1 Perc.01%
2 Perc.10%
3 Perc.50%
4 Mean
5 Horzl_RLNonUni
6 S(1,0)Entropy
7 135dr_RLNonUni
8 Vertl_RLNonUni
9 45dgr_RLNonUni
10 Perc.90%
11 135dr_GLevNonU
12 Sigma
13 S(0,1)AngScMom
14 S(5,5)AngScMom
15 S(4,4)AngScMom
16 Perc.99%
17 45dgr_GLevNonU
18 Teta1
19 S(5,5)SumOfSqs
20 S(1,0)AngScMom
21 S(0,1)Entropy
22 S(1,-1)Entropy
23 S(2,0)Entropy
24 S(1,1)Entropy
25 S(0,2)Entropy
26 Variance
27 S(3,0)Entropy
28 S(2,-2)Entropy
29 S(4,0)Entropy
30 S(2,2)Entropy

BRAIN: Glioblastomas

- Peritumoral WM vs Far extratumoral WM



🟥 Necrosis

🟥 Tumor

🟪 Margin (interface between the tumor and the parenchyma)

🟦 Oedema

🟨 Peritumoral White Matter

Far Extratumoral White Matter

🟩 Normal region in the cerebral hemisphere with tumor

🟧 Normal region in the contralateral hemisphere

Peri-tumoral WM / Far extra-tumoral WM

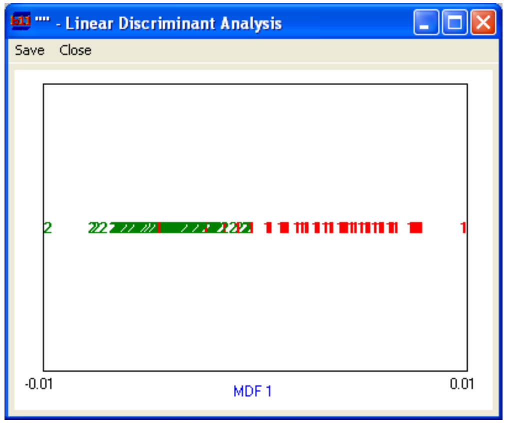
Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Standardization	No	Yes	No	Yes	No	Yes	No	Yes
Raw+kNN	39	23	34	23	29	22	30	16
LDA+kNN	17	17	21	21	25	25	5	5
PCA+kNN	39	21	35	23	29	23	34	17

- Dataset : 150 data (50 PT, 100 Far-WM)
- Far WM includes HL and CL ROIs
- Fisher coefficient F:
  - Raw+kNN : between 0,2 and 1,1
  - LDA+kNN : between 3,5 and 12,7
  - PCA+kNN: between 0,2 and 1,1

MI+PA+F

*features

1 S(2,0)SumEntrp
2 S(1,-1)SumAverg
3 S(2,0)SumAverg
4 S(1,0)SumAverg
5 S(5,0)Entropy
6 S(4,0)SumEntrp
7 S(5,-5)DifEntrp
8 S(5,0)AngScMom
9 Teta2
10 S(4,-4)SumEntrp
11 S(5,-5)Contrast
12 S(2,-2)SumAverg
13 S(5,0)DifVarnc
14 S(1,0)InvDfMom
15 S(5,5)AngScMom
16 S(1,1)InvDfMom
17 S(0,3)SumOfSqs
18 GrNonZeros
19 S(2,2)SumAverg
20 S(5,0)SumEntrp
21 Variance
22 S(5,-5)Entropy
23 S(5,-5)SumEntrp
24 S(4,-4)Entropy
25 S(4,0)Entropy
26 S(5,0)Correlat
27 Teta4
28 S(3,-3)Entropy
29 S(4,-4)AngScMom
30 S(3,0)Entropy



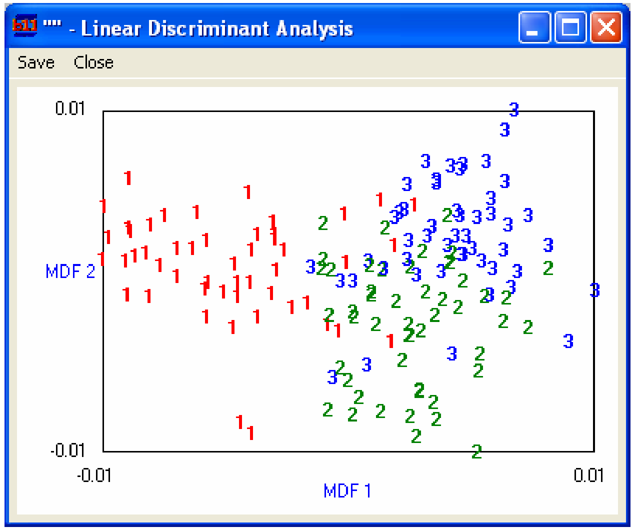
MI+PA+F/LDA

PT-WM(1) / HL-WM(2) / CL-WM(3)

- Dataset : 150 data

Misclassified (%)								
	Fisher		PA		MI		MI+PA+F	
Standardization	No	Yes	No	Yes	No	Yes	No	Yes
Raw+kNN	52	36	59	50	53	41	69	37
LDA+kNN	46	46	47	43	40	43	27	26
PCA+kNN	46	37	59	50	53	42	67	37

MI+PA+F/LDA



- *Most of misclassified data are between far-homolateral and contralateral WM*
  - *Overlapping of homolateral and contralateral WM regions*

- *Peritumoral White Matter (1), rather well-differentiated from far extratumoral (Homolateral and Contralateral) White Matter*

Synthesis of results

	MI+PA+F/ LDA method	
Classes	% of misclassified data	Comments / Hypothesis
Necrosis / Tumor / Oedema / WM	10%	Highlight heterogeneities of brain glioblastoma
Tumor vs Necrosis	10%	Potential tumoral cells in necrosis?
Tumor vs Oedema	12%	Potential tumoral cells in oedema?
Tumor vs WM	0%	Strong discrimination
Peritumoral WM / Far extratumoral WM	5%	Moderate differentiation
Peritumoral WM / HL-WM / CL-WM	26%	Overclass : HL-WM and CL-WM data are similar

Conclusion

- Methods
  - The best classification is obtained with MI+PA+F / LDA methods
  - Most selected parameters from Cooccurrence Matrix
  - Fisher coefficient
    - very low (between 0 and 2) with other methods (Raw, PCA)
    - the highest with analysis performed by LDA
  - Standardization of feature vector
    - gives better classification with Raw+kNN and PCA+kNN
    - has no influence with LDA+kNN

- Results
  - on 2D-TA (MaZda), gives rather good or expected results, with a proper method
  - *Question : What do misclassified data actually correspond to ?*
    - *the choice of analysis and classification methods,*
    - *or does it really have biological significance ?*

- Perspectives
  - Comparison between 2D-TA and 3D-TA
  - Correlation with biological data (*Grand-Ouest Glioma Project, France*)