

# High Dimensional Data Classification

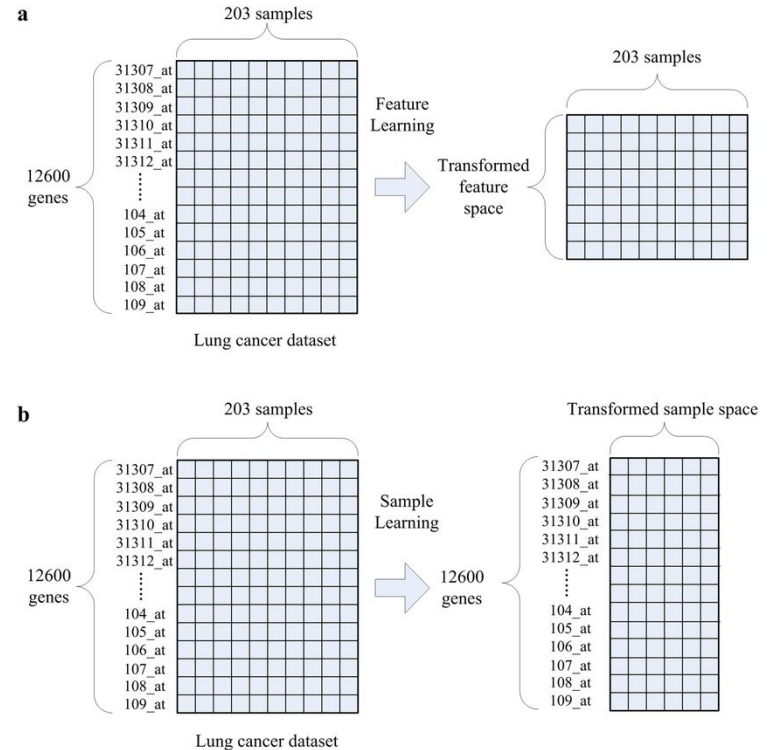
Mentee: Elvin Liu  
Mentor: Zhaoxing Wu

# Overview

1. **Introduction**
2. **Background** (Fisher's Linear Discriminant Analysis)
3. **Solution** (Penalized Discriminant Analysis Projection Pursuit)
4. **Analysis**

# Premise and Motivation

- Classification is predicting labels from a dataset's features
- Prediction algorithms rely on sufficiently *large sample sizes* ( $n$ ) to train such **features** ( $p$ )

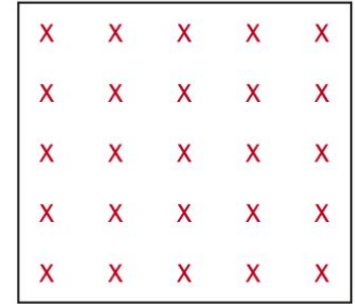


# Curse of Dimensionality

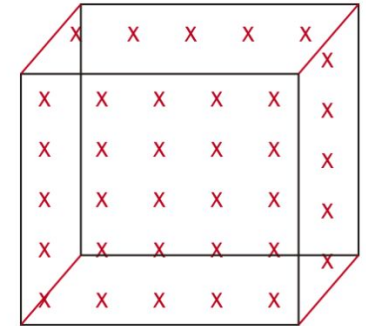
Accuracies of classification algorithms tend to dip in high dimensions due to the **curse of dimensionality**



*A one-dimensional features space with five data points*



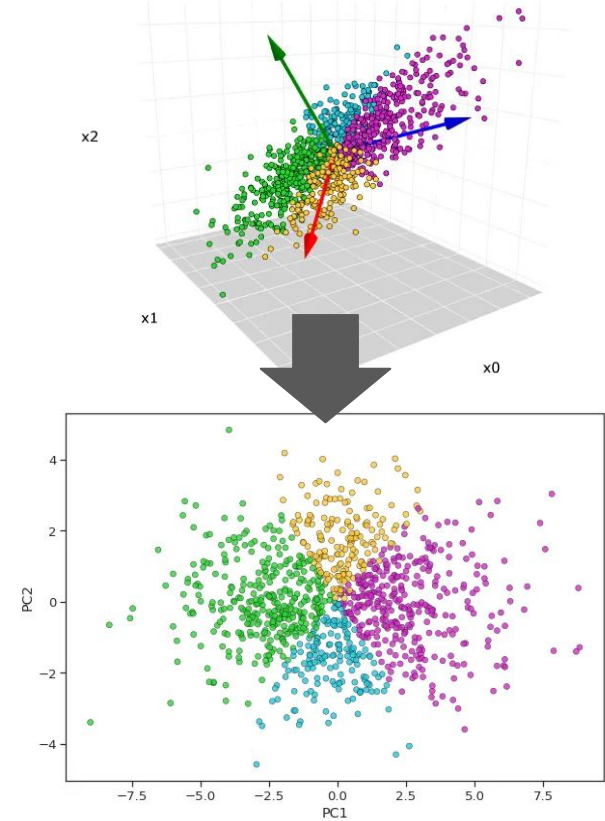
*A two-dimensional features space with 25 data points*



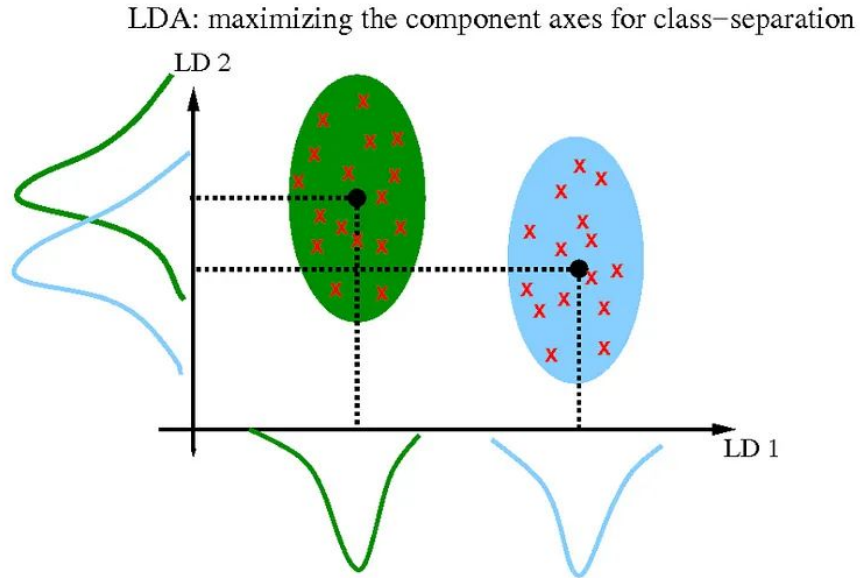
*A three-dimensional features space with 125 data points*

# Projection Pursuit

- Seek interesting *low-dimensional* projections



# Fisher's Linear Discriminant Analysis (LDA)



- Supervised dimensionality reduction
- Reduce dimensions but preserve features relevant for class discrimination

# Between-Class and Within-Class Scatter Matrices

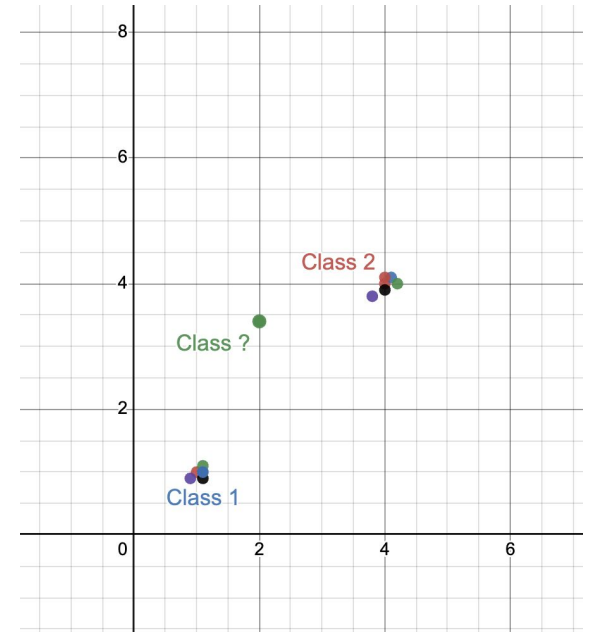
1. The **between-class** scatter matrix  $\mathbf{S}_B$  is computed by the following equation,

$$\mathbf{S}_B = \sum_{i=1}^c N_i (\mathbf{m}_i - \mathbf{m})(\mathbf{m}_i - \mathbf{m})^T$$

where  $\mathbf{m}$  is the overall mean, and  $\mathbf{m}_i$  and  $N_i$  are the sample mean and sizes of the respective classes.

# Fisher's LDA

Intuitively, makes sense to *maximize between-class* scatter matrix and *minimize within-class* scatter matrix.





# Fisher's LDA

$$\mathbf{Q}\mathbf{v} = \lambda\mathbf{v}$$

where...

$$\mathbf{Q} = \mathbf{S}_w^{-1}\mathbf{S}_B$$

$\mathbf{v}$  = eigenvector

$\lambda$  = eigenvalue

*Eigenvectors* of largest eigenvalues *maximize*  
**between-class/within-class variance** most

$k$  most important eigenvectors of  $\mathbf{S}_w^{-1}\mathbf{S}_B$  are **linear discriminant function**

Projected data trims least important features

$$I_{\text{LDA}}(\mathbf{A}) = \begin{cases} 1 - \frac{|\mathbf{A}^T\mathbf{S}_w\mathbf{A}|}{|\mathbf{A}^T(\mathbf{S}_w + \mathbf{S}_B)\mathbf{A}|}, & \text{for } |\mathbf{A}^T(\mathbf{S}_w + \mathbf{S}_B)\mathbf{A}| \neq 0, \\ 0, & \text{for } |\mathbf{A}^T(\mathbf{S}_w + \mathbf{S}_B)\mathbf{A}| = 0, \end{cases}$$

# Penalized Discriminant Analysis

$n < p$  leads to data piling issues in LDA

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# PDA PP-Index

Use  $\tilde{\Sigma}(\lambda) = (1 - \lambda)\hat{\Sigma} + \lambda \cdot \text{diag}(\hat{\Sigma})$  to estimate the variance-covariance matrix

$\Sigma(\text{hat})$  = maximum likelihood estimator (MLE) of  $\Sigma$

Using standardized data vectors, the above equation turns to

$\tilde{\mathbf{R}}(\lambda) = (1 - \lambda)\hat{\mathbf{R}} + \lambda\mathbf{I}$ , where

$\mathbf{R}(\text{hat})$  = MLE of correlation matrix

$\mathbf{I}$  = identity matrix

# PDA PP-Index

$$\boldsymbol{\Sigma}^B = \sum_{i=1}^g n_i (\bar{\mathbf{X}}_{i.}^* - \bar{\mathbf{X}}_{..}^*) (\bar{\mathbf{X}}_{i.}^* - \bar{\mathbf{X}}_{..}^*)^T,$$

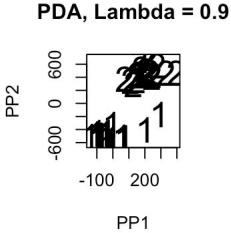
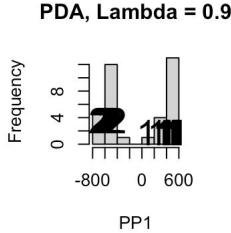
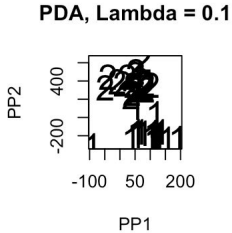
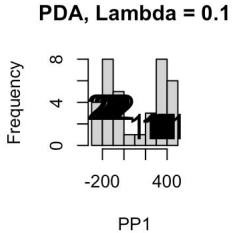
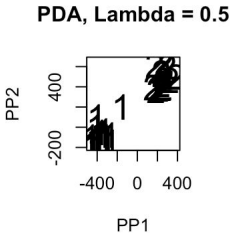
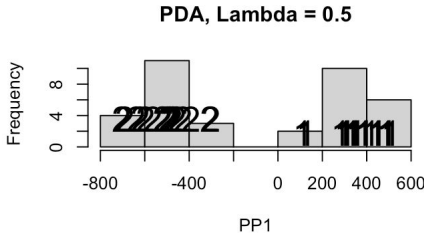
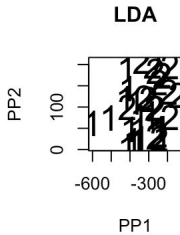
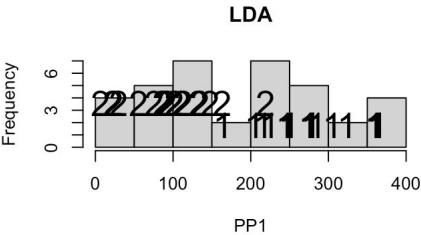
$$\boldsymbol{\Sigma}^S = \sum_{i=1}^g \sum_{j=1}^{n_i} (\mathbf{X}_{ij}^* - \bar{\mathbf{X}}_{i.}^*) (\mathbf{X}_{ij}^* - \bar{\mathbf{X}}_{i.}^*)^T$$

$\mathbf{X}_{i.}^*$  =  $i$ -th group mean of the standardized data and

$\mathbf{X}_{..}^* = 0$  = total mean of the standardized data

$$I_{\text{PDA}}(\mathbf{A}, \lambda) = 1 - \frac{|\mathbf{A}^T \{(1 - \lambda) \boldsymbol{\Sigma}^S + n\lambda \mathbf{I}_p\} \mathbf{A}|}{|\mathbf{A}^T \{(1 - \lambda) (\boldsymbol{\Sigma}^B + \boldsymbol{\Sigma}^S) + n\lambda \mathbf{I}_p\} \mathbf{A}|}$$

# Example Projections



Histogram on the left is 1-D projection  
Scatter plot on the right is 2-D projection

# Sample Data Background

## Sample:

- 18 malignant cancer tumors paired
- 18 normal tissue from the *same patient*

## Features:

- 3200 full-length human cDNA
- 3400 expressed sequence tags

**Classifier:** Malignant Tumor | Normal Tissue

## Features (≈6600)

	D00003	D00015	D00102	D00137	D00173	D00265	D00306	D00...
Description	"Human liver cytochrome P-450 mRNA, complete cds"	"Human prion protein mRNA, human PrP 27-30 mRNA, complete cds"	"Human lymphoxin (LT) mRNA, complete cds"	"Human class I alcohol dehydrogenase 1 mRNA, complete cds"	"Human class I alcohol dehydrogenase 2 mRNA, complete cds"	"Human class I alcohol dehydrogenase 3 mRNA, complete cds"	"Human class I alcohol dehydrogenase 4 mRNA, complete cds"	"Human class I alcohol dehydrogenase 5 mRNA, complete cds"
Tumor 27	1.9902240632390829	26.370468837917851	4.6686788790820941	17.912016569151746	17.912016569151746	17.912016569151746	17.912016569151746	17.912016569151746
Tumor 29	7.173473209273732	12.507594313603112	2.4971831973351564	12.691529524097275	12.691529524097275	12.691529524097275	12.691529524097275	12.691529524097275
Tumor 34	0.65853450319171225	12.84142281223839	0.47362627449372235	10.865819302663253	10.865819302663253	10.865819302663253	10.865819302663253	10.865819302663253
Tumor 28	-2.7763564697932877	9.0231585268281833	9.5920166575686583	28.4576538153812	28.4576538153812	28.4576538153812	28.4576538153812	28.4576538153812
Tumor 35	0.44465402930747431	1.62970144070940724	-5.2614759984570361	5.623877704513404	5.623877704513404	5.623877704513404	5.623877704513404	5.623877704513404
Tumor 8	10.222020982249887	9.8812869495082243	2.9894510975425206	63.035796057207627	63.035796057207627	63.035796057207627	63.035796057207627	63.035796057207627
Tumor 3	14.886598402409456	20.24577382727686	-5.4481527946289319	26.200413188240642	26.200413188240642	26.200413188240642	26.200413188240642	26.200413188240642
Tumor 9	-2.0161903166423043	17.473649410905171	-1.8416276062139911	135.75681465395556	135.75681465395556	135.75681465395556	135.75681465395556	135.75681465395556
Tumor 4	36.299670587041831	21.231882796194277	-3.4559535817835747	26.026178911463955	26.026178911463955	26.026178911463955	26.026178911463955	26.026178911463955
Tumor 32	-1.3219976812463907	17.18596985620308	6.5885311040226977	41.86325990613571	41.86325990613571	41.86325990613571	41.86325990613571	41.86325990613571
Tumor 39	-3.9677947110620218	14.87923016648258	-7.8834956694158214	7.604939862868874	7.604939862868874	7.604939862868874	7.604939862868874	7.604939862868874
Tumor 10	0.53250744003636341	19.7027575181345449	-7.0823789745956756	19.7027575181345449	19.7027575181345449	19.7027575181345449	19.7027575181345449	19.7027575181345449
Tumor 33	2.6193733526487497	5.2387467052974994	3.9744120856425567	36.671226937082494	36.671226937082494	36.671226937082494	36.671226937082494	36.671226937082494
Tumor 5	38.74942272244642	31.506540011077423	-8.9153033817698581	14.485765522334448	14.485765522334448	14.485765522334448	14.485765522334448	14.485765522334448
Tumor 11	8.0498667406096516	3.7566044789511706	3.3611582782056133	13.953102350390063	13.953102350390063	13.953102350390063	13.953102350390063	13.953102350390063
Tumor 6	4.740003032078058	18.43345124720002	-4.4576461325075227	15.53676605121344	15.53676605121344	15.53676605121344	15.53676605121344	15.53676605121344
Tumor 12	1.4133376204569557	52.293491956907367	0	13.191151124264918	13.191151124264918	13.191151124264918	13.191151124264918	13.191151124264918
Tumor 40	-0.480389763115507256	28.823385789340353	-0.92846552930720204	16.33251942792865	16.33251942792865	16.33251942792865	16.33251942792865	16.33251942792865
Normal 27	5.9930998	54.4827251	-1.9744580	70.827426	70.827426	70.827426	70.827426	70.827426
Normal 29	0.7385694	50.2227205	1.1974120	116.5093260	116.5093260	116.5093260	116.5093260	116.5093260
Normal 34	0.7437448	44.8726007	0.7795597	118.0075025	118.0075025	118.0075025	118.0075025	118.0075025
Normal 28	6.5490816	31.7113426	-3.2807549	118.5728464	118.5728464	118.5728464	118.5728464	118.5728464
Normal 35	8.8752411	14.5807532	-1.2928787	104.6010558	104.6010558	104.6010558	104.6010558	104.6010558
Normal 8	7.0757083	15.920438	-0.9075868	41.8646077	41.8646077	41.8646077	41.8646077	41.8646077
Normal 3	36.2621814	65.8639622	-15.5396633	100.6460545	100.6460545	100.6460545	100.6460545	100.6460545
Normal 9	3.6570486	28.249789	2.2941931	81.1864784	81.1864784	81.1864784	81.1864784	81.1864784
Normal 4	625.7826412	23.6396864	1.2261492	47.2793727	47.2793727	47.2793727	47.2793727	47.2793727
Normal 32	0.3125257	79.3815404	-11.3866482	137.5113298	137.5113298	137.5113298	137.5113298	137.5113298

Samples (36)

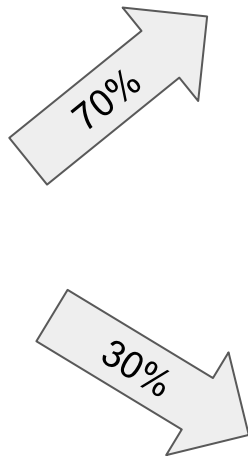
# Training/Testing Split

Let's split *training/testing* in a 70:30 ratio

**Original dataset:**

**36** samples

**18** normal tissue/**18** tumors



**Training dataset:**

**25** samples

**13** normal tissue/**12** tumors

**Testing dataset:**

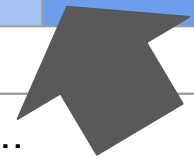
**11** samples

**5** normal tissue/**6** tumors

# Predictions

	Feature 1	Feature 2	Feature 3	...
Tumor $\mu$	2	3	4	...
Normal $\mu$	7	8	9	...

	Feature 1	Feature 2	Feature 3	...
Tumor 1...	1	6	10	...
Tumor 2...	2	7	11	...
Tumor x...	...	...	...	...
Normal 1...	5	5	7	...
Normal 2...	6	6	8	...
Normal y...	...	...	...	...





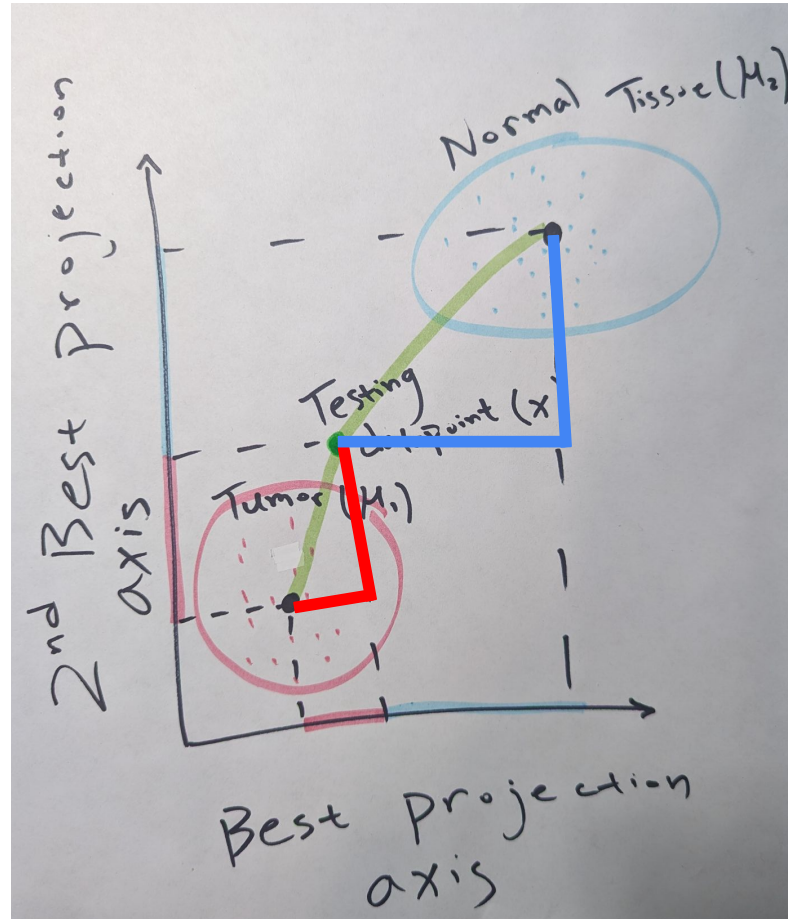
# Predictions

	Feature 1	Feature 2	Feature 3	...
Test Datapoint	3	4	5	...

	Feature 1	Feature 2	Feature 3	...
Tumor $\mu$	2	3	4	...
Normal $\mu$	7	8	9	...

	Feature 1	Feature 2	Feature 3	...
(Test Datapoint - Normal $\mu$ ) <sup>2</sup>	$(2 - 7)^2$	$(3 - 8)^2$	$(4 - 9)^2$	...
(Test Datapoint - Tumor $\mu$ ) <sup>2</sup>	$(3 - 2)^2$	$(4 - 3)^2$	$(5 - 4)^2$	...

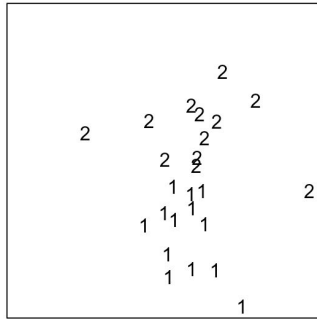
# Predictions



Testing datapoint is classified as **Tumor** since its distance to the **Tumor mean** is *smaller* than to **Normal Tissue's mean**

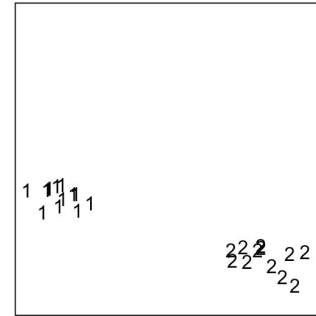
# Prediction Results

2-Dimensional LDA  
projection of testing data



[1] 0.8181818

2-Dimensional PDA ( $\lambda = 0.5$ )  
projection of testing data



[1] 0.9090909

# Support Vector Machines

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Call:  
svm(formula = classifier ~ ., data = cc

Parameters:  
SVM-Type: C-classification  
SVM-Kernel: radial  
cost: 1

Number of Support Vectors: 25

	Predicted	
Actual 0	1	3
1	0	6

*e1071* package

**2/5** normal tissues *correctly* classified

**3/5** normal tissues *incorrectly* classified as tumors

**6/6** tumors *correctly* classified

**Accuracy:  $(2 + 6)/(5 + 6) = 8/11 \approx 72.73\%$**

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