# Pee Stain Pathology

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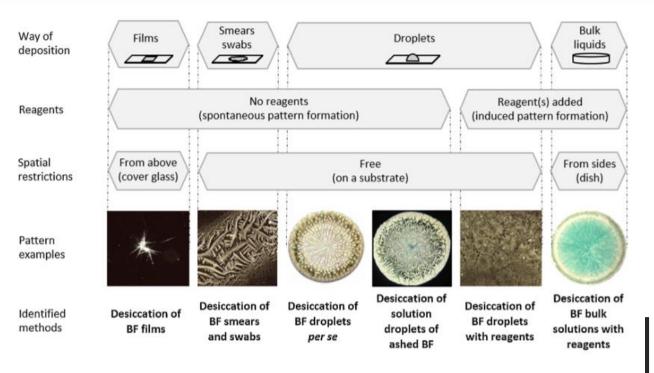


## Desiccation Pattern Diagnostics

Dried droplets of various body fluids used as diagnostic tool for many diseases

Most use visual inspection for classification

ML classification have been applied to blood diagnosis, not much for urine.

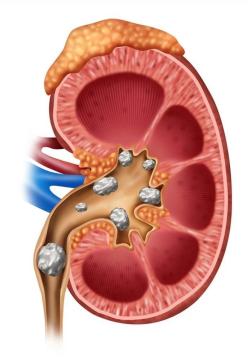


<u>Diagnostic tests based on pattern formation in drying body fluids – A mapping review | Elsevier Enhanced Reader</u>

## Urological diseases

Diseases in urinary tract can alter composition of urine

- Kidney stones contain CaC<sub>2</sub>O<sub>4</sub>
- Kidney failure, cystitis, pregnancy issues release albumins



#### **Project Aims**

Test & compare different image classification models to be used for urological diagnostics.

Models used to detect high concentrations of disease biomarkers in dried samples of artificial urine.

Biomarkers used in study:

- Calcium oxalate  $CaC_2O_4$
- Ovalbumin

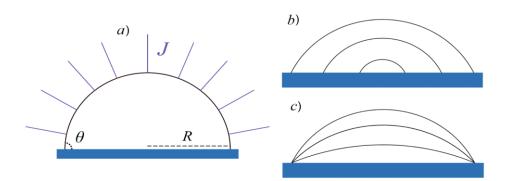
$$Ca^{2+}\begin{bmatrix} O & O \\ C & C \end{bmatrix}^{2-}$$

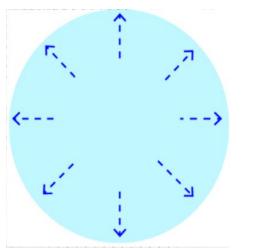
## Physics of Drying Droplets

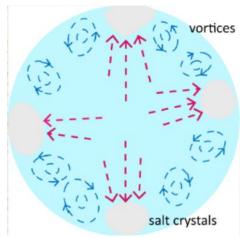
Diffusion limited model

Modes of evaporation

Capillary and crystallisation driven internal flows







<u>Dynamics of droplet drying -Crystallization-Driven Flows within</u> <u>Evaporating Aqueous Saline Droplets |</u>

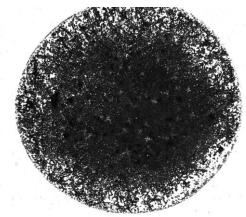
## Desiccation patterns

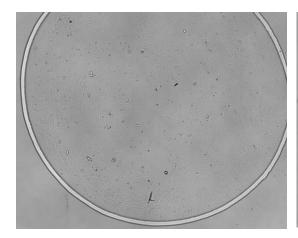
Capillary flow advect and deposit particles to the drop perimeter, coffee ring effect.

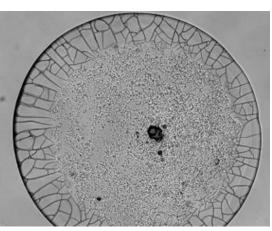
#### Key patterns:

- Crystallisation of salts
- Cracking of protein gels







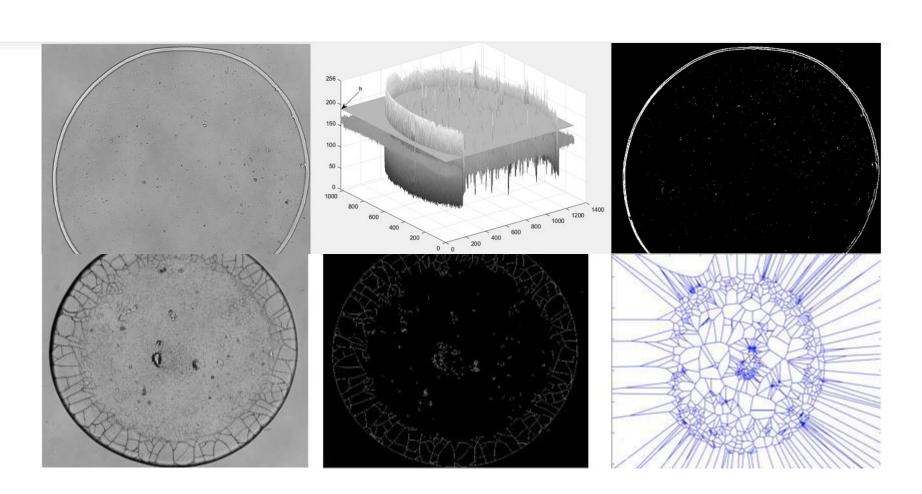


## Image Processing

Raw image

Minkowski analysis

Voronoi analysis



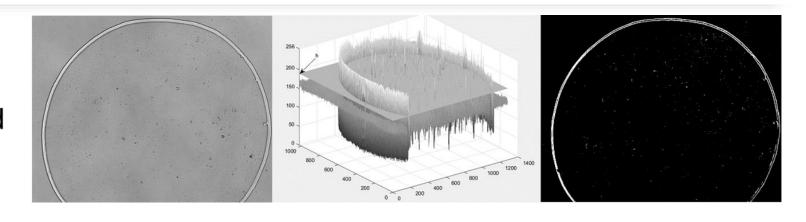
## Minkowski Analysis

Minkowski functionals:  $A, P, \chi$ 

Scan image binarise threshold

Marching matrix calculation of functionals

Functionals normalised then concatenated to a "Minkowski signature"



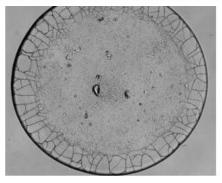
$$Q_1 = \begin{pmatrix} 1 & 0 \\ 0 & 0 \end{pmatrix} \quad Q_2 = \begin{pmatrix} 1 & 0 \\ 1 & 0 \end{pmatrix} \quad Q_3 = \begin{pmatrix} 1 & 1 \\ 1 & 0 \end{pmatrix}$$
$$Q_4 = \begin{pmatrix} 1 & 1 \\ 1 & 1 \end{pmatrix} \quad Q_D = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$$

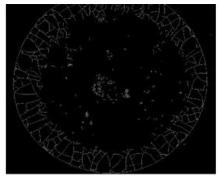
## Voronoi Analysis

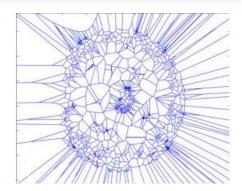
Extract crack skeleton, find branch points, seed Voronoi mosaic

Parameters extracted from Voronoi mosaic:

- Number of nodes
- Number of vertices
- Angular defect
- Isoperimetric ratio



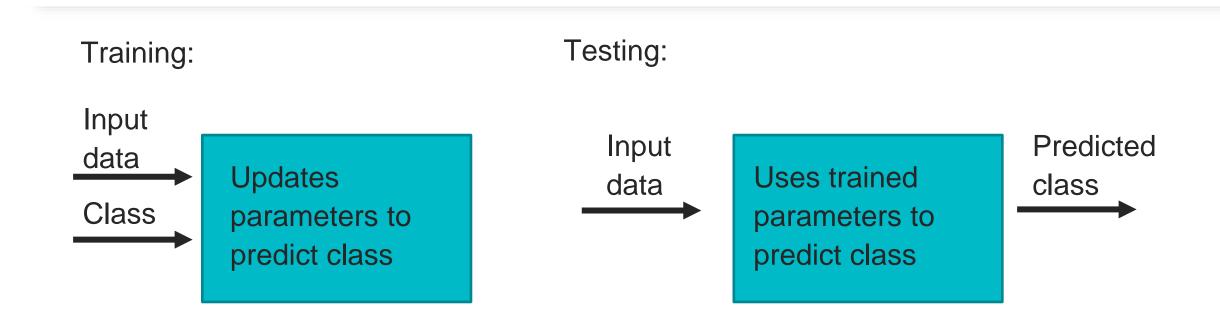




$$D = \frac{1}{\sum_{i}^{v} |\theta_{i} - \frac{(v-2)\pi}{v}| + 1}$$

$$\lambda = rac{4\pi A}{L^2}$$

## Machine learning



#### Metrics

Accuracy 
$$A = \frac{TP + TN}{TP + TN + FP + FN}$$

Precision 
$$P = \frac{TP}{TP + FP}$$

Recall 
$$R = \frac{TP}{TP + FN}$$

Total population: TP+FN+FP+TN		Predicted class	
		High conc	Low
Actual class	High conc	TP	FN
	Low	FP	TN

## Machine Learning Models

Neural networks vs non-neural networks

Raw image data vs image mined data

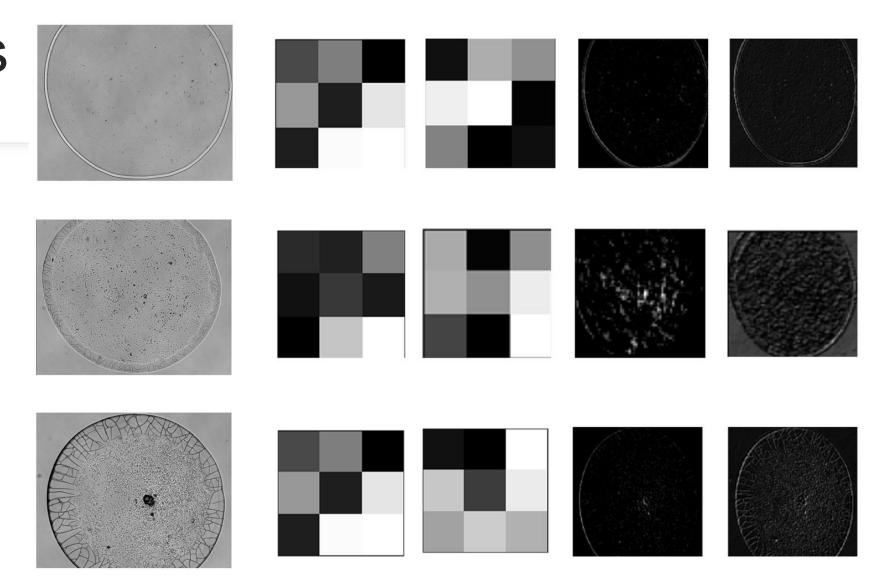
#### **Neural Networks**

- CNN
- Raw NN
- Voronoi NN
- Minkowski NN

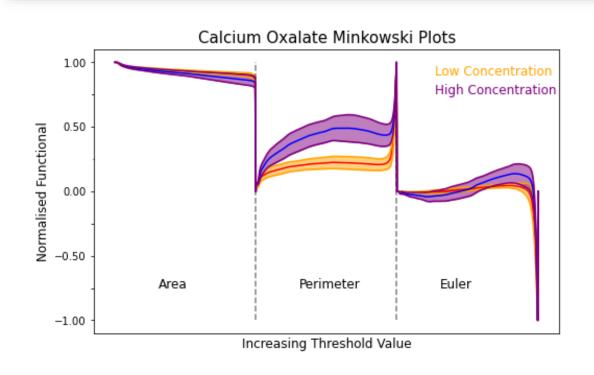
#### Non-NN

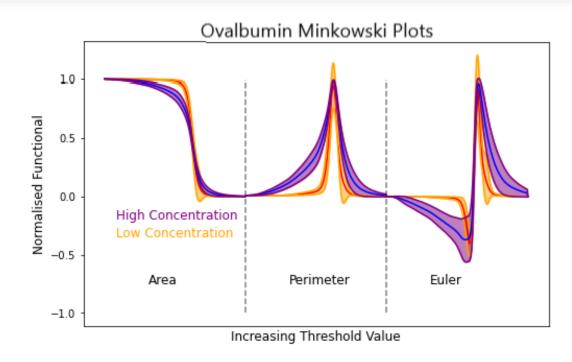
- Voronoi logistic regression
- Voronoi k-nearest neighbours

#### **CNN** Results

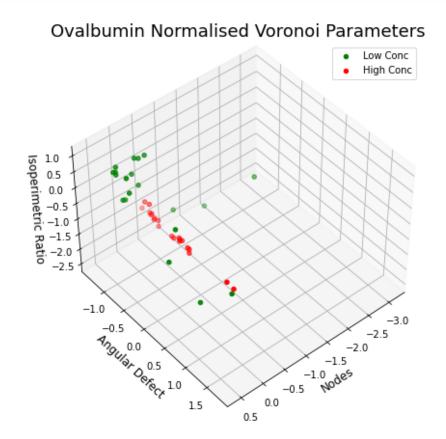


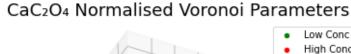
## Minkowski Analysis Results

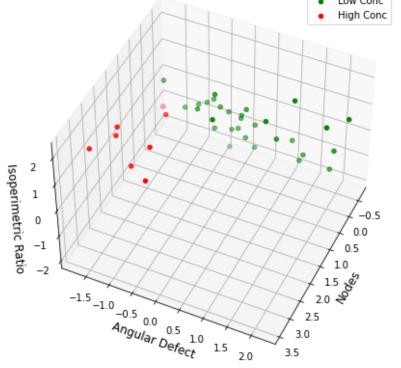




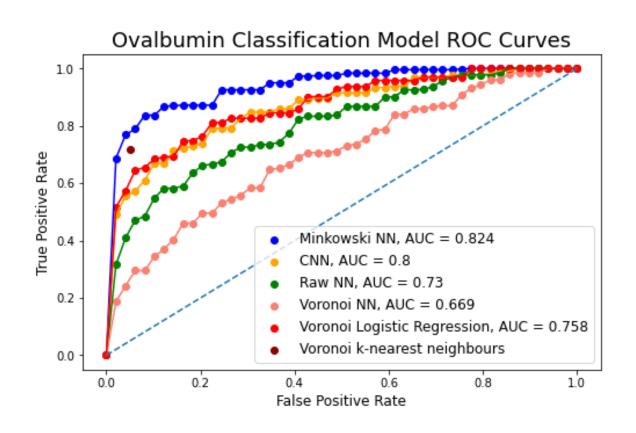
#### Voronoi Parameters Results

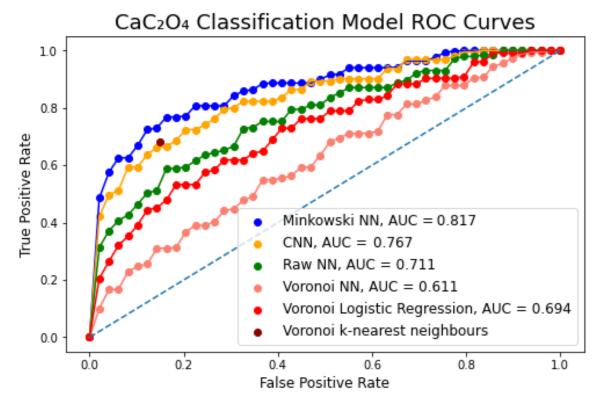






## Model Comparison





#### Calcium oxalate results

Model	Accuracy	Precision	Recall
NN	0.697	0.692	0.728
CNN	0.755	0.824	0.724
Minkowski NN	0.799	0.855	0.768
Voronoi log reg	0.451	0.723	0.412
Voronoi NN	0.391	0.660	0.311
K means	0.563	0.853	0.540

#### Ovalbumin results

Model	Accuracy	Precision	Recall
NN	0.709	0.855	0.662
CNN	0.783	0.769	0.792
Minkowski NN	0.873	0.879	0.868
Voronoi log reg	0.521	0.785	0.812
Voronoi NN	0.521	0.652	0.647
K means	0.671	0.829	0.623

#### Discussion

- Model urine
- Tweaking within models, vary architectures
- Overfitting issues

#### Conclusions

- Neural networks outperformed non neural networks
- Minkowski analysis was optimal, closely followed by CNN
- Models performed better at protein detection than salt detection