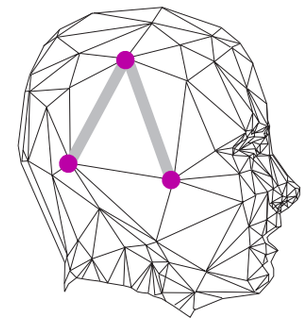
GOBIERNO DE ESPAÑA
MINISTERIO DE ECONOMIA Y COMPETITIVIDAD
UNIÓN EUROPEA
Fondo Europeo de Desarrollo Regional
"Una manera de hacer Europa"
TIN2013-46638-C3-3-P



S.I.M.D.
Sistemas Inteligentes y Minería de Datos

Applications

4th February 2016

Javier Cózar and José Miguel Puerta

University of Castilla-La Mancha, Albacete

Index

- Introduction
- Localization of GFP proteine
- Gold particle detection and quantization
- Predicción reingreso COPD
- H.264/HEVC Video Transcoder
- Scene Classification from images by means of Bayesian Networks and using contextual information

Introduction

- We will describe five collaborations which end up with four software tools in the scope of medicine among others applications
  - Localization of GFP protein
  - Gold particle detection and quantization
  - Predicción reingreso COPD
  - H.264/HEVC Video Transcoder
  - Scene Classification from images by means of Bayesian Networks and using contextual information.
- This tools has been successfully used by their respective collaborators

Index

- Introduction
- Localization of GFP proteine
- Gold particle detection and quantization

Automatic localization of chimeric GFP protein

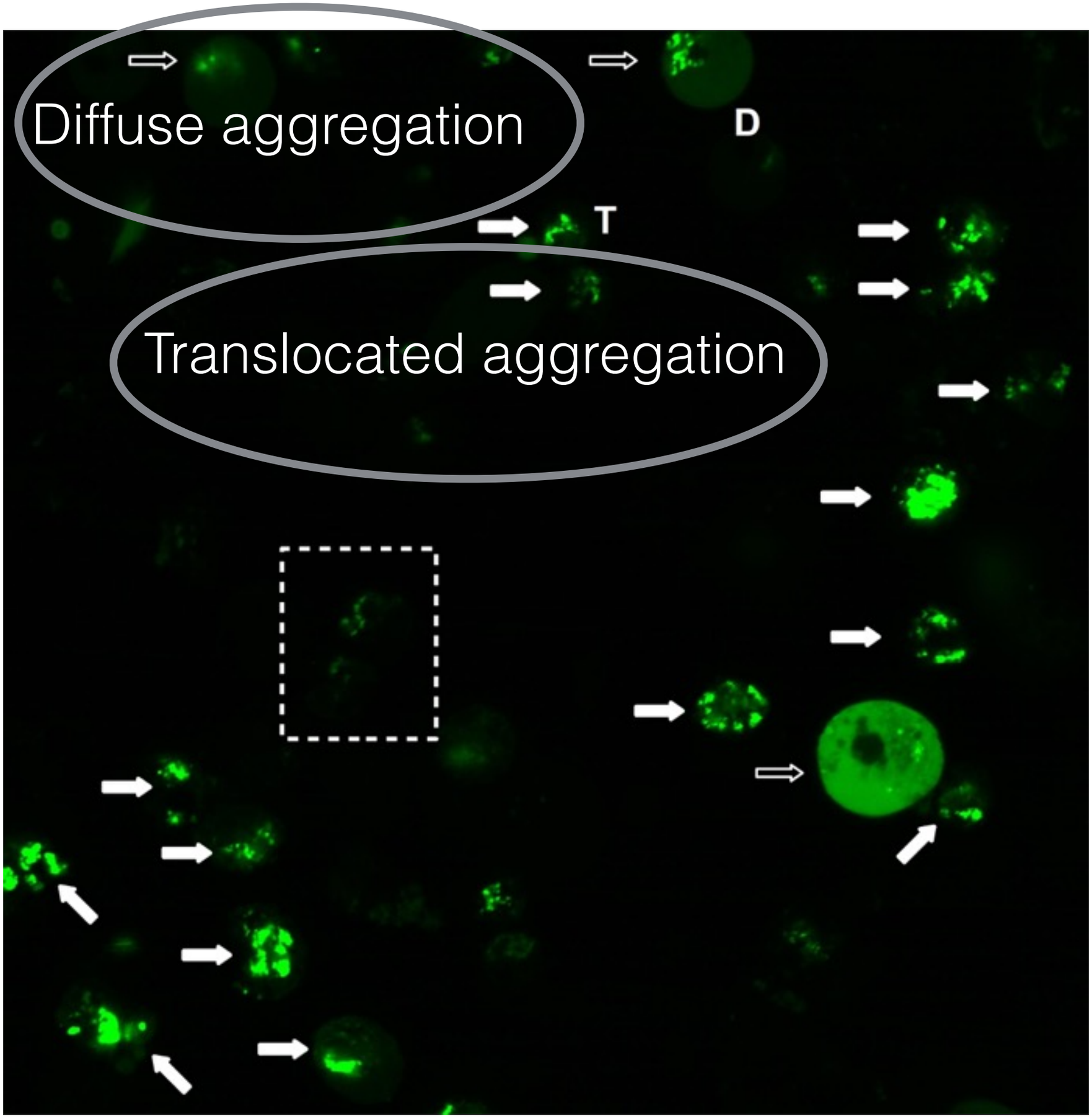
- It is a collaboration with the **Neuropharmacology group** of the faculty of Medicine and the **Unit of Neuropsychopharmacology** of the Faculty of Pharmacy, both in Albacete, Spain

- The objetive is to detect the subcellular trafficking of a GFP protein, which is involved in different tasks

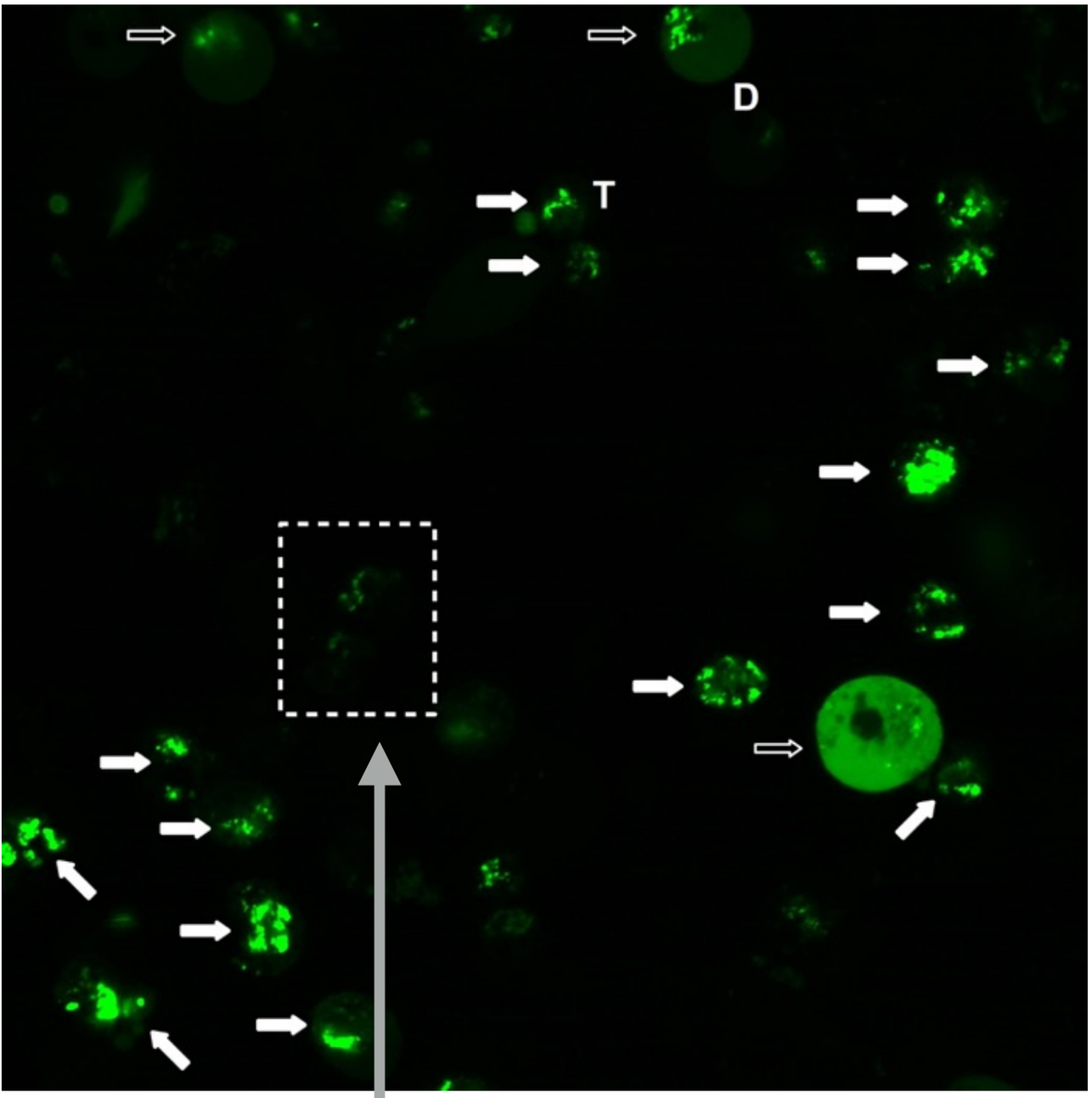
- They marked the GFP protein to appear fluorescent green on the image taken by the microscope

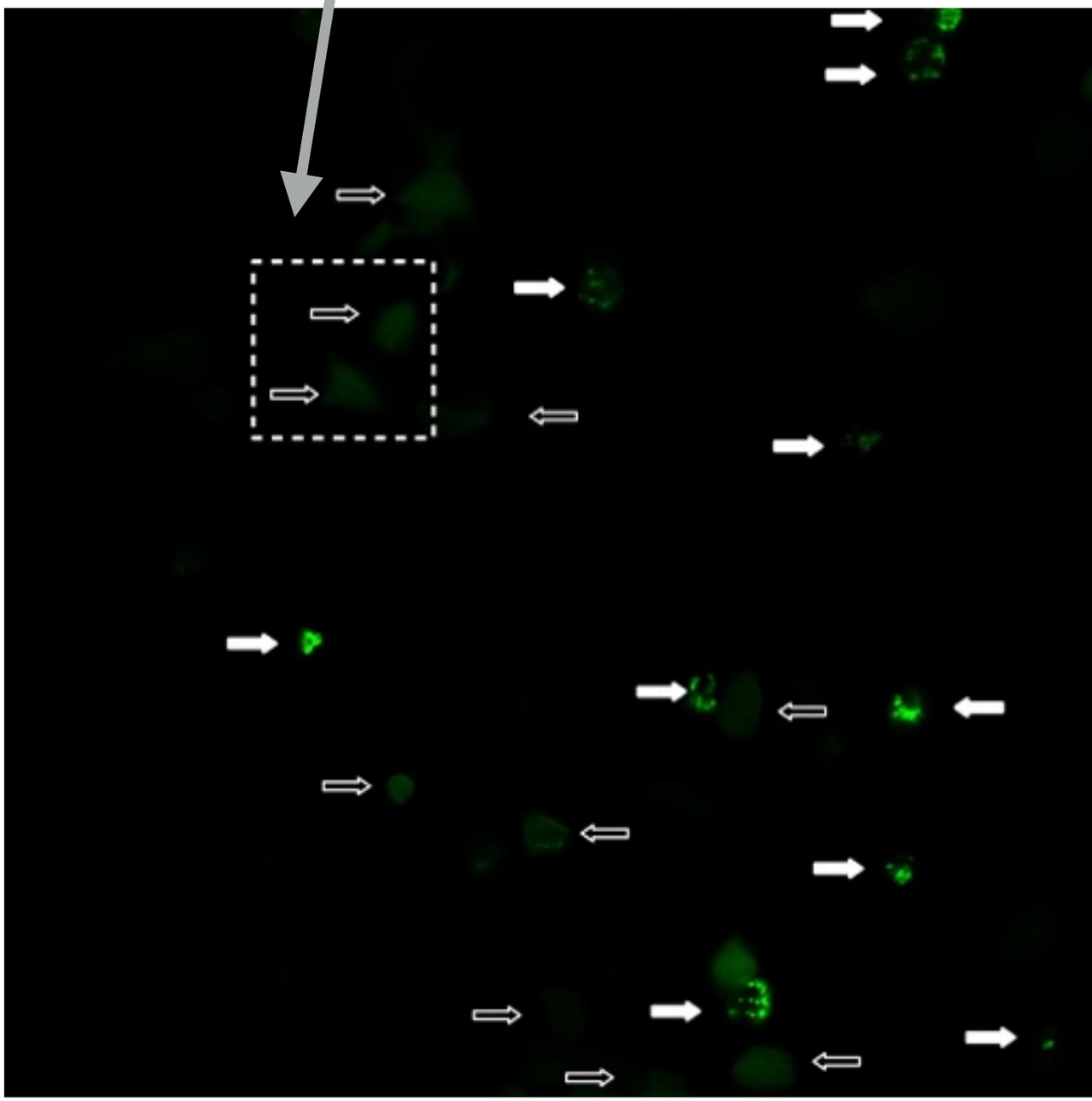
- ✗ They require experimented stuff and, even so, the interpretation of the images is very subjective

  - ✓ The software does the required tasks, being objetive and consistent (same input ⟶ same output)


Diffuse aggregation
D
T
Translocated aggregation

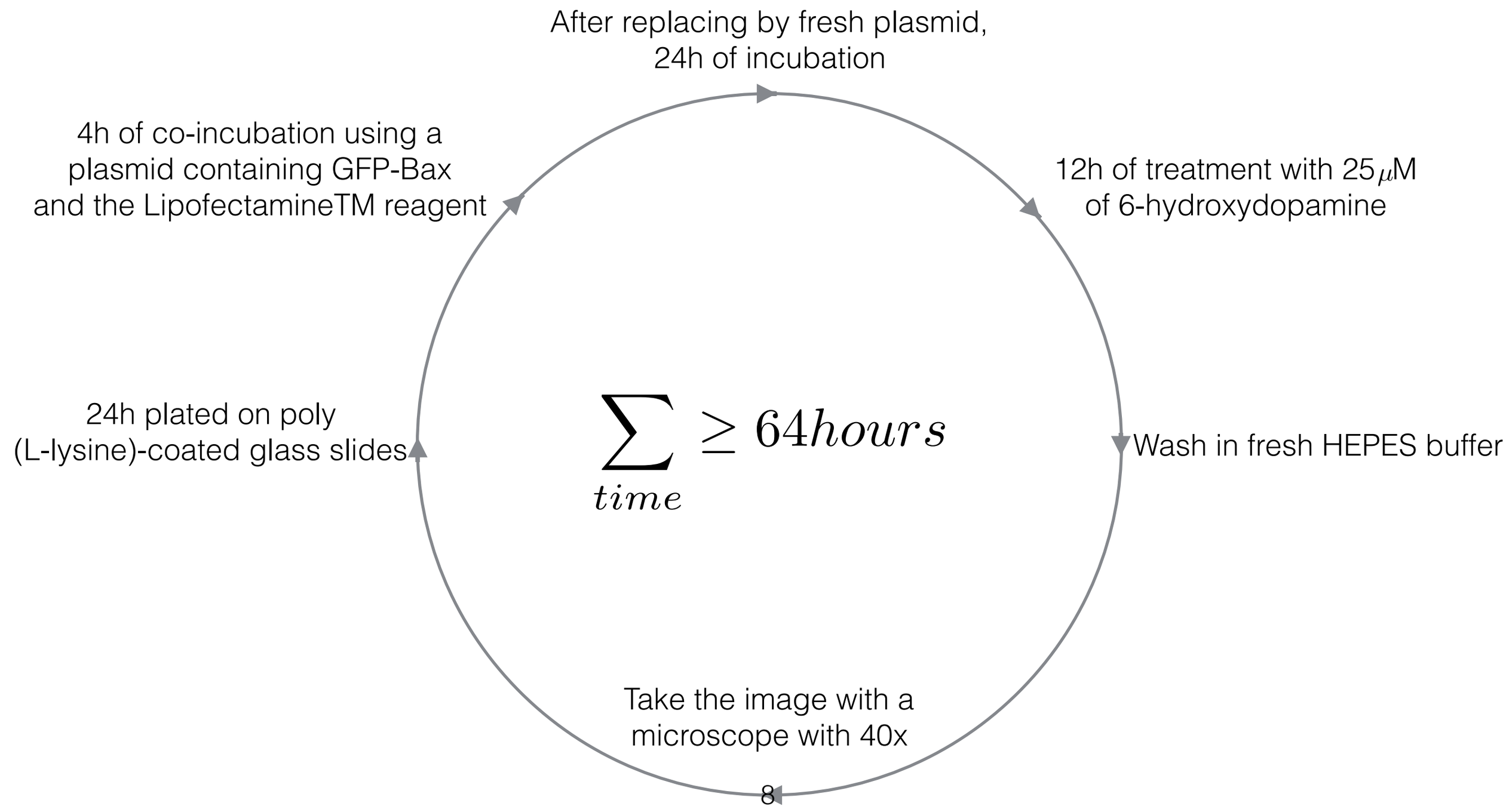
Objects considered transfected cells



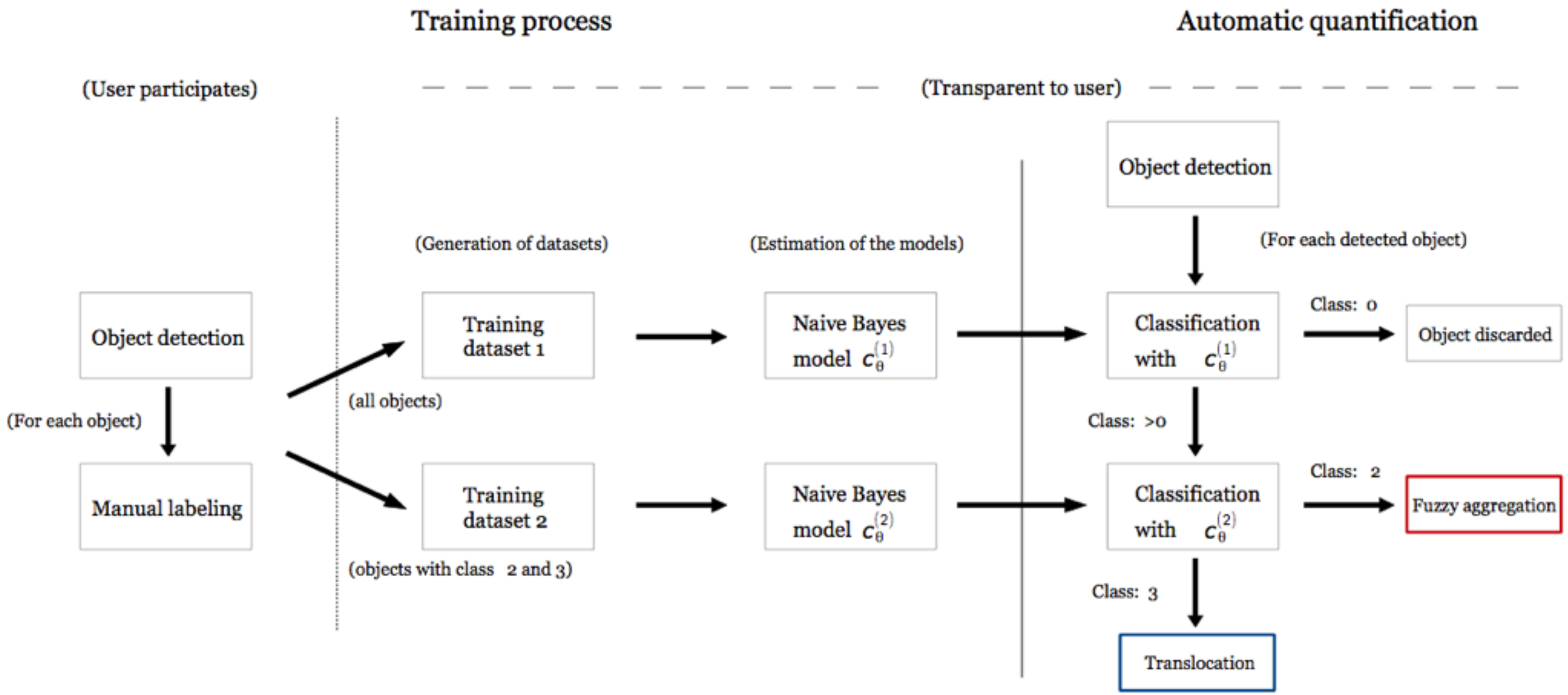


Object discarded by the expert

Protein tagging process



Classification workflow



Object detection

Parameters:

lowerBackGroundThreshold: Background threshold (intensity of color). Default Value = 8.

minCellSize: Minimum size of a cell (number of pixels). Default Value = 200.

smallCellMaxSize: Maximum size of a "small" cell (number of pixels). Default Value = 4000.

minCumSize: Minimum size of an accumulation of cells (number of pixels). Default Value = 1500.

upperBackgroundThreshold: Upper background threshold (intensity of color). Default Value = 15.

aggregationThreshold: Threshold which denotes an aggregation (intensity of color). Default Value = 40.

maxNumCellsCum: Maximum number of cells in an accumulation. Default Value = 2.

Procedure:

step 1) The image is segmented into a set of objects, being an object a set of connected pixels such that the intensity of their color is over *lowerBackGroundThrehold*. All objects with occupy a number of pixels smaller than *minCellSize* are considered noise, and therefore discarded.

step 2) Those objects with size (number of pixels) smaller than *smallCellMaxSize* are discarded, unless a number of pixels over *minCellSize* corresponds to a potential aggregation of protein, i.e., the intensity of their color is over *aggregationThreshold*.

step 3) All objects whose size (number of pixels) is smaller than *minCumSize* are considered as a potential cell.

step 4) The remaining objects (those greater than *minCumsize*) may be an accumulation of cells, and are processed individually:

step 4.a) The own object is segmented in different sub-objects such that their colour is over *upperBackgroundThreshold*.

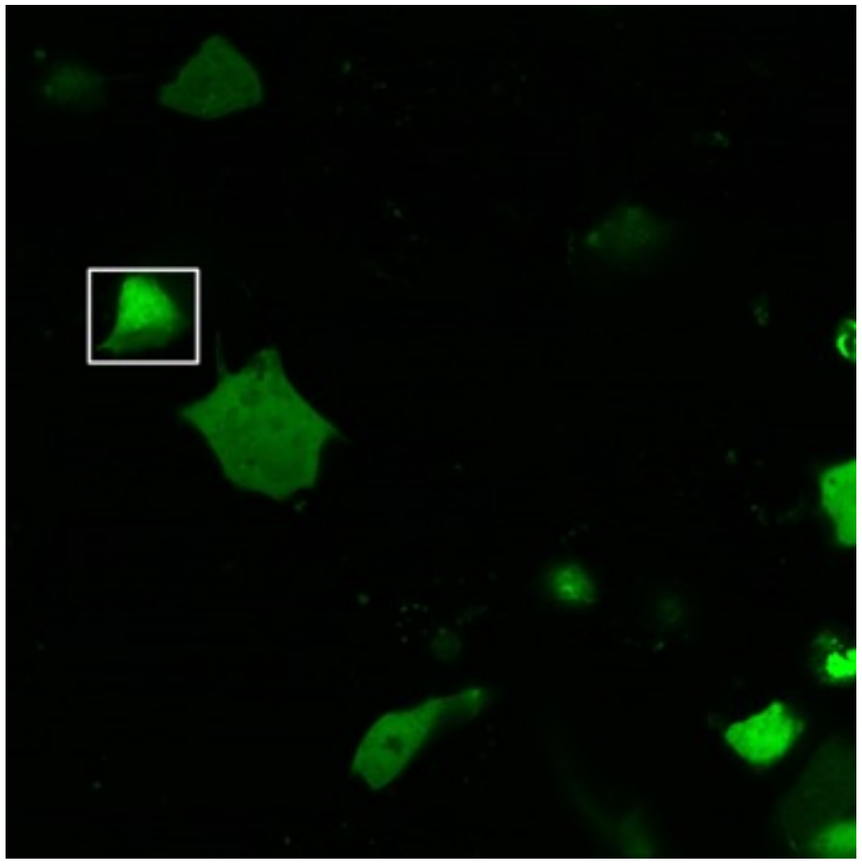
step 4.b) All sub-objects with a size (number of pixels) smaller than *minCellSize* are removed.

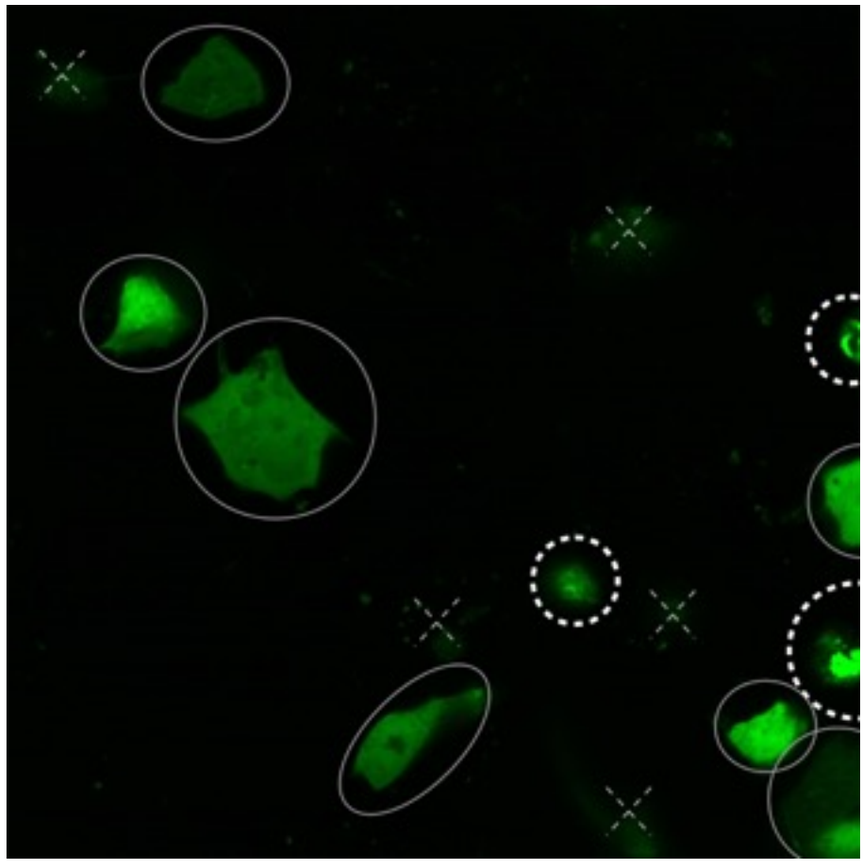
step 4.c) If there is no sub-objects left, the whole object is considered as a potential (dark) cell.

step 4.d) If there is only one part left, the whole object is considered as a potential cell.

step 4.e) If there are several sub-objects, the bigger ones are considered potential cells. The parameter *maxNumCellsCum* determines the maximum number of cells that can appear in an accumulation.

Object detection





```
Which class is the object?

     [ ]: Discarded
     [2]: Cell (Diffuse aggregation)
     [3]: Cell (Translocated aggregation)

Input: 2
```

```
Image1.jpg: (15 objects detected)

Transfected Cells: 10

     Diffuse aggregation: 7
     Translocated aggregation: 3
```

Naive Bayes: Parameter estimation

- We use two Naive Bayes models
- $C_\theta^{(1)}$ is used to classify if an object (labelling process assisted) is a transfected cell or not
- $C_\theta^{(2)}$ is used to classify if a transfected cell presents a translocation of the protein or not

Naive Bayes: Parameter estimation

Feature name	Description
X_1	Size of the object/cell (Number of pixels)
X_2	Number of pixels over the upper background colour threshold
X_3	Proportion of pixels over the upper background colour threshold
X_4	Number of pixels over the aggregation colour threshold
X_5	Proportion of pixels over the aggregation colour threshold
X_6	Length of the major axis in the ellipse which surrounds the object/cell
X_7	Length of the minor axis in the ellipse which surrounds the object/cell
X_8	Average color of the object/cell
X_9	Number of pixels (in the whole image) over the upper background colour threshold
X_{10}	Proportion of pixels (in the whole image) over the upper background colour threshold
X_{11}	Number of pixels (in the whole image) over the aggregation colour threshold
X_{12}	Proportion of pixels (in the whole image) over the aggregation colour threshold
X_{13}	Average color of the image
X_{14}	Proportion of pixels of the object over the upper background colour threshold in relation with the same proportion for the whole image (X_3/X_{10})
X_{15}	Proportion of pixels of the object over the aggregation colour threshold in relation with the same proportion for the whole image (X_4/X_{12})
X_{16}	Average color of the object in relation with the average color of the image (X_8/X_{13})
$X_{17}, \ldots, X_{272}$	Histogram (relative frequencies) obtained from the image of the object. Each image is transformed to gray scale, and each pixel takes a value between 0 and 255. Each one of these features contains the proportion of pixels with the corresponding value (from X_{17}, which corresponds to 0, to X_{272} which corresponds to 255).
Y	{ $k = 0$: Discarded Object, $k = 2$: Cell with diffuse aggregation, $k = 3$: Cell with translocated aggregation }

Naive Bayes model $C_\theta^{(1)}$: Parameter estimation

- Features from X_1 to X_{16}

- Estimation of the parameters of the distribution (Gaussian)

Naive Bayes model $C_\theta^{(2)}$: Parameter estimation

- The whole set of features

- Estimation of the parameters of the distribution (Gaussian)

Automatic localization of chimeric GFP protein

$C_\theta^{(1)}$

Total	True Condition +	True Condition -
Predicted condition +	58	1
Predicted condition -	3	22

$$Accuracy = \frac{58+22}{58+22+3+1} = 0.9524 \quad Precision = \frac{58}{58+1} = 0.9831 \quad Recall = \frac{58}{58+3} = 0.9508$$

$C_\theta^{(1-fss)}$

Total	True Condition +	True Condition -
Predicted condition +	59	0
Predicted condition -	2	23

$$Accuracy = \frac{59+23}{59+23+2+0} = 0.9762 \quad Precision = \frac{59}{59+0} = 1.0 \quad Recall = \frac{59}{59+2} = 0.9672$$

Automatic localization of chimeric GFP protein

$C_\theta^{(2)}$

Total	True Class +	True Class -
Predicted class +	31	3
Predicted class -	1	26

$$Accuracy = \frac{31+26}{31+26+1+3} = 0,9344 \quad Precision = \frac{31}{31+3} = 0,9118 \quad Recall = \frac{31}{31+1} = 0,9688$$

$C_\theta^{(2-fss)}$

Total	True Class +	True Class -
Predicted class +	32	0
Predicted class -	0	29

$$Accuracy = \frac{32+29}{32+29} = 1,0 \qquad Precision = \frac{32}{32+0} = 1,0 \qquad Recall = \frac{32}{32+0} = 1,0$$

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- Introduction
- Proteine detection
- Gold particle detection and quantization

Gold particle detection

- It is a collaboration with the **Neurological Disabilities Research Institute (U. of CLM)**, **Pharmacology Unit (U. of Barcelona)**, **Department of Pharmacology (U. of Minnesota)**, among others.

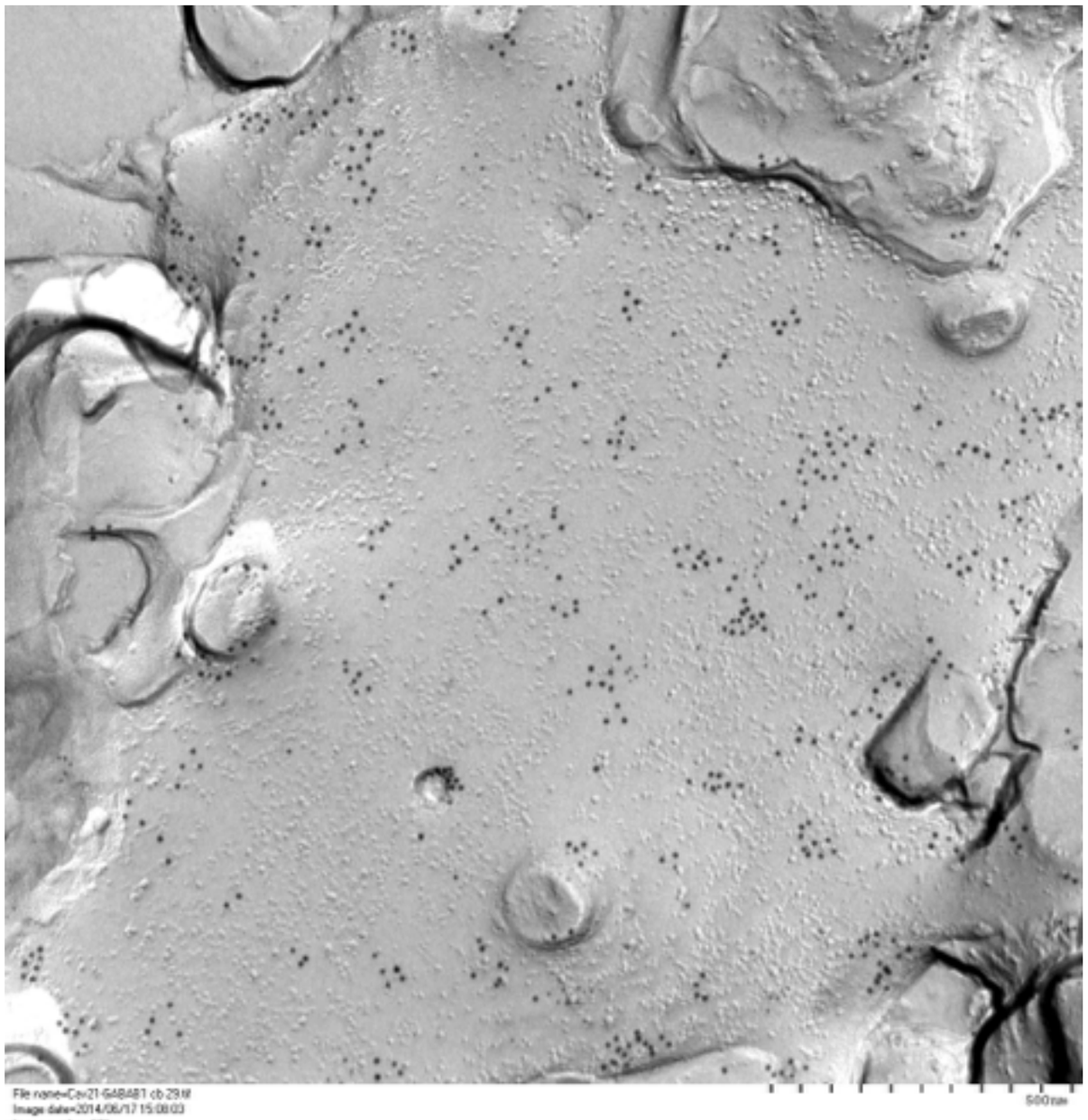
- They are interested in the localization of two types of proteins and its spatial distribution inside a neurone

- Immunogold is a technique which they use to mark those elements, each one with a different diameter of gold particle

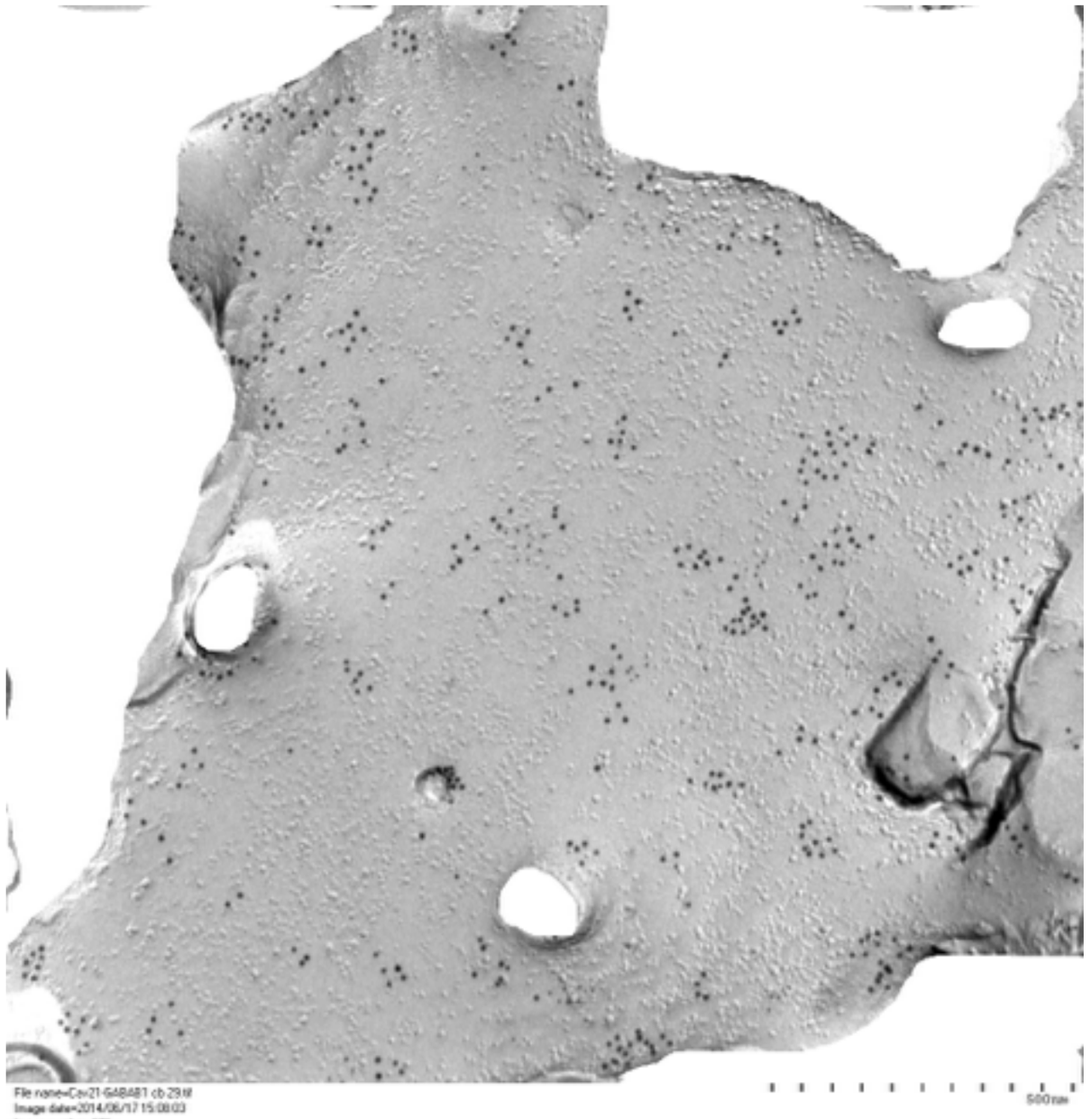
- After that, an expert detect those gold particles and he calculate a set of measurements (manual process)

- We developed a tool to detect the gold particles and to obtain those measurements automatically

Gold particle detection



File name=Cav21-GABAB1 cb 29.tif
Image date=2014/06/17 15:08:03
Image number=676
Image comment=
Calibration=1.750 nm/pixel at x 10.0k
Magnification=x10.0k
Lens mode=Zoom-1
Spot number=3
Image rotation=0°
Acc. voltage=80kV
Emission=9.6μA
Stage X=185 Y=10 Tilt angle=0.1
Azim angle=0.0



File name=Cav21-GABAB1 cb 29.tif
Image date=2014/06/17 15:08:03
Image number=676
Image comment=
Calibration=1.750 nm/pixel at x 10.0k
Magnification=x10.0k
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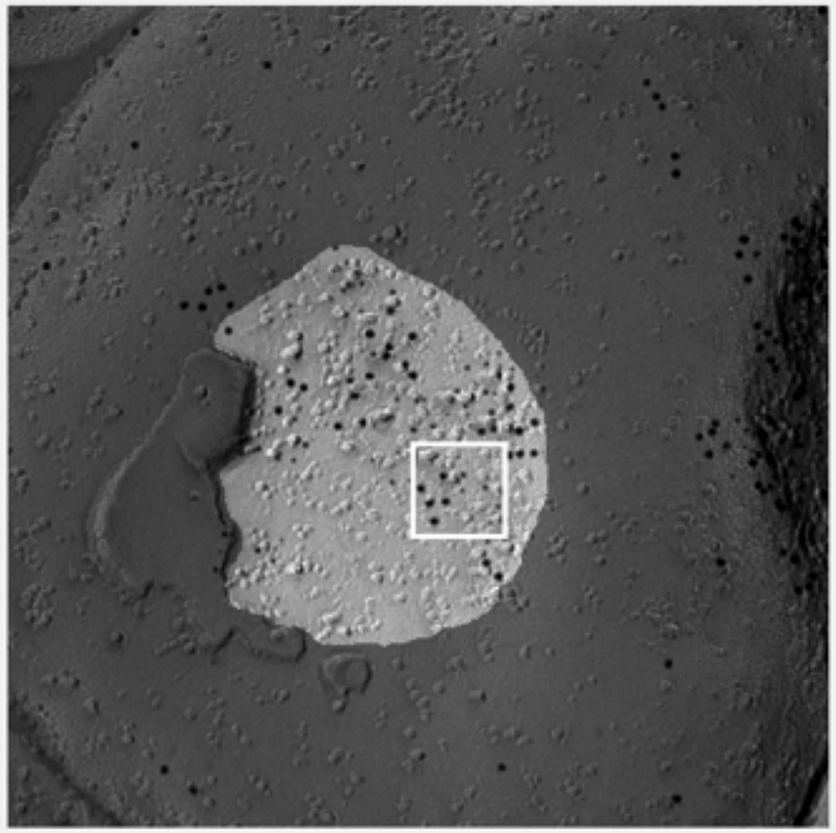
Spot number=3
Image rotation=0°
Acc. voltage=80kV
Emission=9.6μA
Stage X=185 Y=10 Tilt angle=0.1
Azim angle=0.0

Gold particle detection

- The process for detecting gold particles is guided by the tool
  - On click, it selects a area of 20 x 20 pixels and it finds the particle (circle) inside that area
    - We have to select each particle by hand but it is not need to be very precise (margin of 20 pixels)
- This is because the circle Hough Transform (used for circle detection) is very dependent of the search area and the radius of the circles to find

Figure 1

File Edit View Insert Tools Desktop Window Help



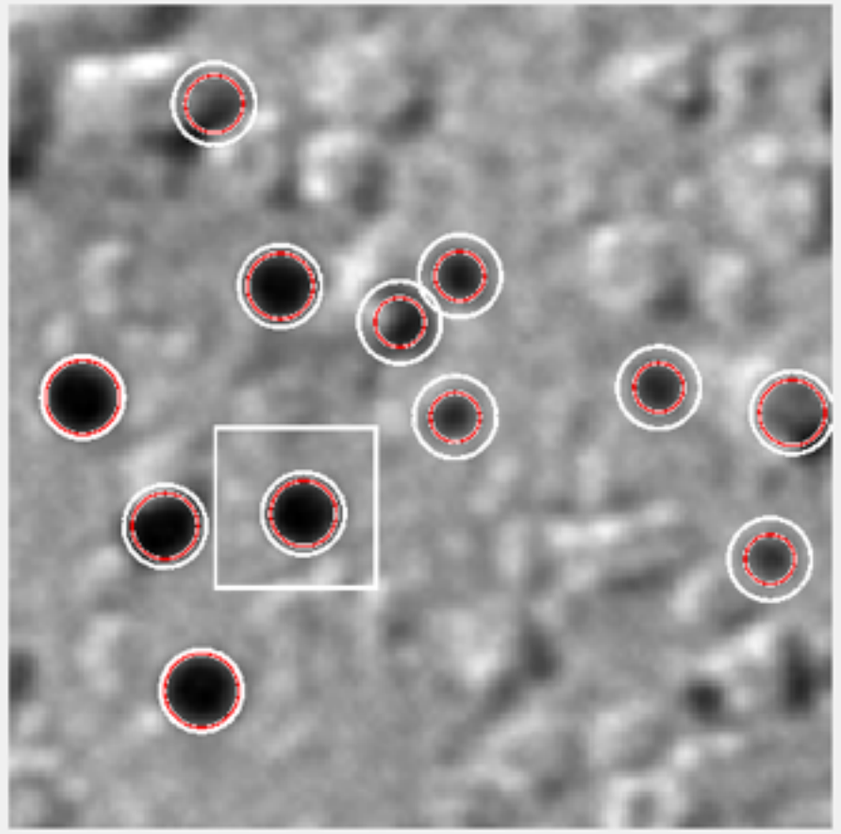
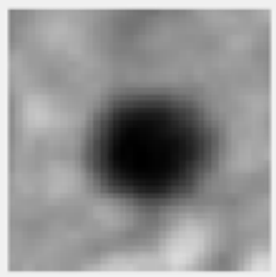
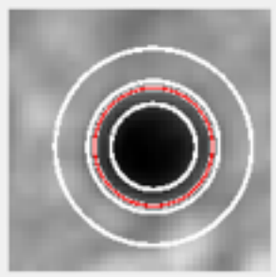


Figure 2

File Edit View Insert Tools Desktop Window Help





Select a file to view details

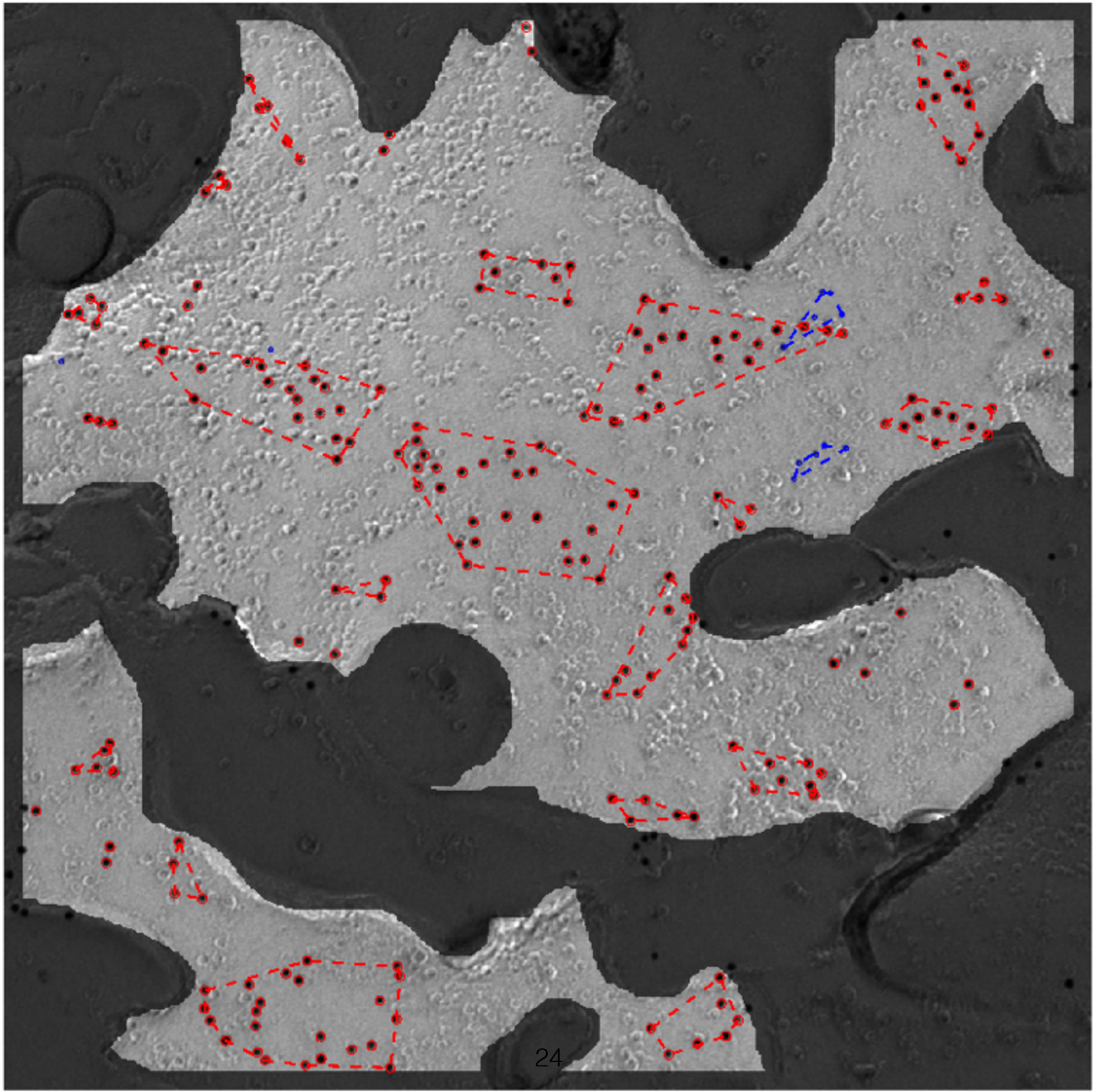
```
>> extDataFromImg('2.tif','2_mod.tif',0.875,0.5, 10, 0.95, 20, 1,
Detected radius: 4.50.

Mean image: 34973.52.
Mean dot: 14107.50.
Mean core: 8060.39.
Mean circle: 17043.10.
Mean contour: 36505.87.
```

Gold particle detection

- The particles are grouped into clusters
- We use hierarchical clustering
- The cut level (distance between clusters to join) is 2·standard deviation of this set of distances:

$$\{(\min(dist(p_1, p_2)), \forall p_2 \in P), \forall p_1 \in P\}$$



Gold particle detection

- Once we have detected the gold particles and grouped them into the clusters:
- We can easily calculate all the requested statistics (mean distance inter-cluster, intra-cluster, min distance from a 10-nm particle to a 5-nm particle, …)

Gold particle detection

- They are successfully using this tool
- They required 150h to process the whole set of images manually
- They required only 3h to process the whole set of images with this tool

Figure 1: Results visualization.

Image list file:

/home/luis/Escritorio/GPDQv0.1b/IMAGES/ir | Open File

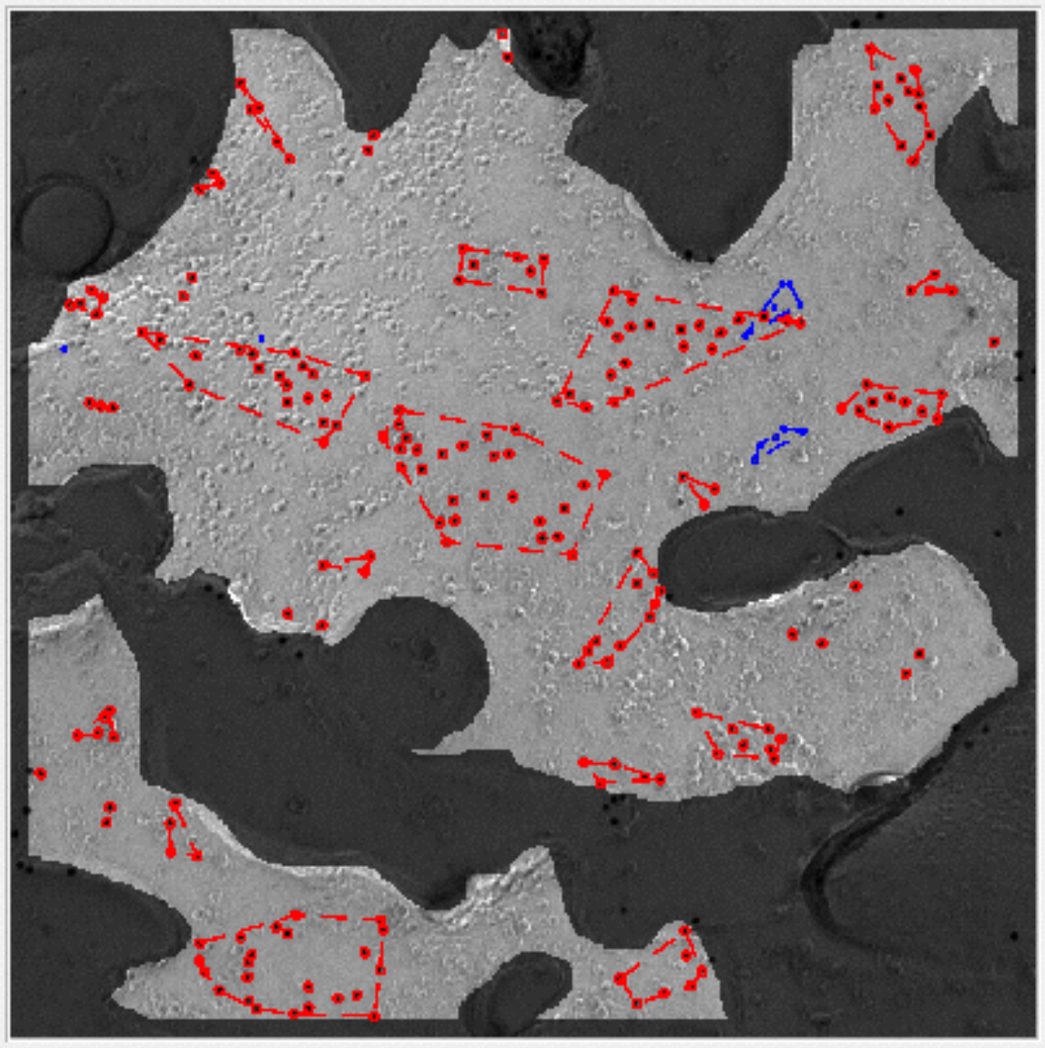
AXON/1	(AXON)
AXON/2	(AXON)
AXON/3	(AXON)
AXON/4	(AXON)
AXON/5A	(AXON)
AXON/5B	(AXON)
SPINE/1	(SPINE)
SPINE/2	(SPINE)
SPINE/3	(SPINE)
SPINE/4	(SPINE)
SPINE/6	(SPINE)
SPINE/7	(SPINE)
DENDRITE/1	(DENDRITE)
DENDRITE/2	(DENDRITE)
DENDRITE/3	(DENDRITE)
DENDRITE/4	(DENDRITE)
DENDRITE/5	(DENDRITE)
DENDRITE/6	(DENDRITE)

18 images processed (3 groups).

1728 particles counted.

2.50 Nm: 496.
5.00 Nm: 1232.

Mean/Stdv of NND (Nm): 21.03, 18.31.



☑ Particles | Export

☑ Clusters (5Nm) ☑ Clusters (10Nm) ☐ Clusters (All)

Route: /home/luis/Escritorio/GPDQv0.1b/IMAGES//DENDRITE/1.
Group: DENDRITE.
Scale: 1.1667 Nanometers / pixel.
Area of section: 0.6917 Squared micra.
Number of partiles detected: 215.

Future: Automatic detection

- We are now working on an improvement for this tool: automatic gold particle detection
- Data Set building tool

Data Set building tool

- We apply a particle detection which detect many false positives (in order to avoid false negatives)
- A manual labelling is required to build the datasets

Diameter, $\overline{\text{Color of circle}}$, $\overline{\text{Color of non-circle}}$, …			Class (No, 5nm or 10nm)
9	25	156	10nm
14	90	160	No
3	15	193	5nm
…	…	…	…

Gold particle detection

- We are now working on an improvement for this tool: automatic gold particle detection
  - Data Set building tool
  - Use of Data Mining techniques
  - Statistical study

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- Predicción reingreso COPD
- H.264/HEVC Video Transcoder
- Scene Classification from images by means of Bayesian Networks and using contextual information

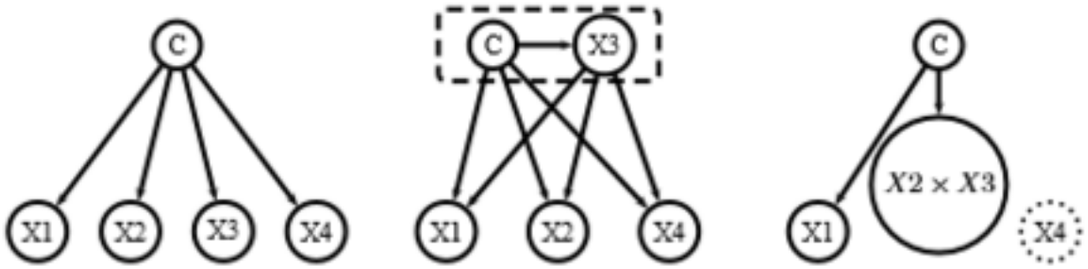
Predicción reingreso COPD hospitalario antes de 1 semana

- 156 pacientes, desbalanceada (33 vs 123)
- 8 variables descriptivas + 43 variables relativas a pruebas médicas al ingreso o durante la estancia
- La práctica médica [Jiménez, 2012] es agrupar estas 43 variables en 5 categorías

Categoría	#vars
Historia al ingreso	9
Exploración física al ingreso	7
Otras exploraciones	6
Evaluación y Tto.	7
Preparación para el alta	14

Predicción reingreso hospitalario antes de 1 semana

¿Es posible encontrar otra manera de agruparlas para incrementar wF-Measure (sin reducir F-measure[Sí] a 0)? SemiNaive bayes para seleccionar y agregar las variables (todas o según categoría).



(a) NB and wNB (b) AODE (c) Semi-NB

Aggregating variables only from the same subcategory (driven by wFalseNegativeRate)						
K	**#Atts used**	**#Atomic**	**#Joint**	**#AvgJointCard**	**wFmeasure**	**F-measure[Yes]**
2	6.79	4.14	1.25	2.13	**•0.7935**	0.0129
3	6.61	4.01	1.17	2.20	0.7806	0.0129
4	7.08	4.34	1.26	2.18	0.7613	0.0
Aggregating variables from any category (driven by wAreaUnderPRC)						
K	**#Atts used**	**#Atomic**	**#Joint**	**#AvgJointCard**	**wFmeasure**	**F-measure[Yes]**
2	11.0903	2.1226	3.2516	2.7868	0.7548	0.0452
3	11.7419	1.8968	3.3226	3.0217	0.7677	0.0258
4	9.08	2.34	2.42	2.80	0.7742	**•0.0452**

Table 3: Results of Semi-NB aggregating and selecting variables from the *Readmissions* dataset. K is the value used in the ▷ criterion. $\#Atts\ used$ is the total number of variables selected and used as atomic variables or inside joint variables. $\#Atomic$ is the number of variables finally selected and not aggregated to any variable. $\#Joint$ is the number of joint variables constructed. $\#AvgJointCard$ is the average number of variables aggregated in joint variables. Column *Driven by* is the metric used to guide the search.

Predicción reingreso hospitalario antes de 1 semana

- Mejor método: agregar variables son SNB wF-measure 0.7935, necesitando solo 7 variables de calidad asistencial
- Mejor resultado con método agregación de los médicos: usando 42 variables, Cost-sensitive A1DE. w-Fmeasure 0.7613
- Frecuencia de selección/creación de los siguientes nodos en el modelo SNB.

Variable(s)	**Frequency**	**(Sub)Group**	**Type**
Charlson index	90	Descriptive	Atomic
Arterial hypertension	75	Descriptive	Atomic
PCO_2	60	Evaluation and Treatment	Atomic
Broncho.	43	Readiness for discharge	Atomic
Edema	40	Physical exploration	Atomic
Dyspnoea	38	Admission workup	Atomic
Dyspnoea × Cause	37	Admission workup	Compound
Cause	35	Admission workup	Atomic
Skin	28	Physical exploration	Atomic
Tachypnea	25	Physical exploration	Atomic
O_2	25	Evaluation and Treatment	Atomic
Charlson index × Gender	21	Descriptive	Compound
Improv.Symp.	20	Readiness for discharge	Atomic
ChangeMedic.	18	Readiness for discharge	Atomic
Charlson index × Main diagnosis	12	Descriptive	Compound

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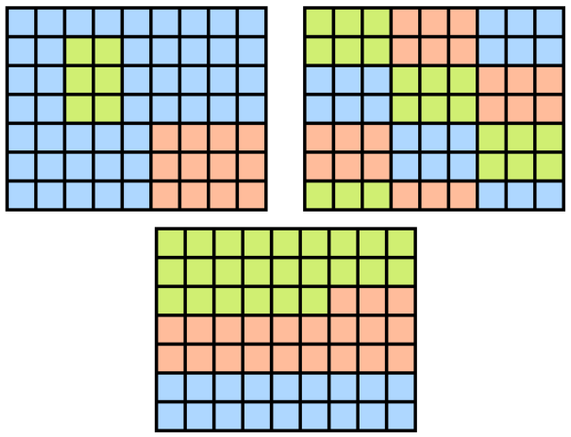
A Statistical Approach of a CTU Splitting Algorithm for an H.264/HEVC Video Transcoder

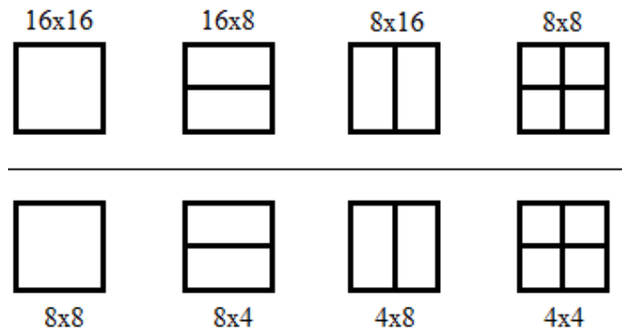
A. J. Díaz-Honrubia, J. L. Martínez, P. Cuenca,

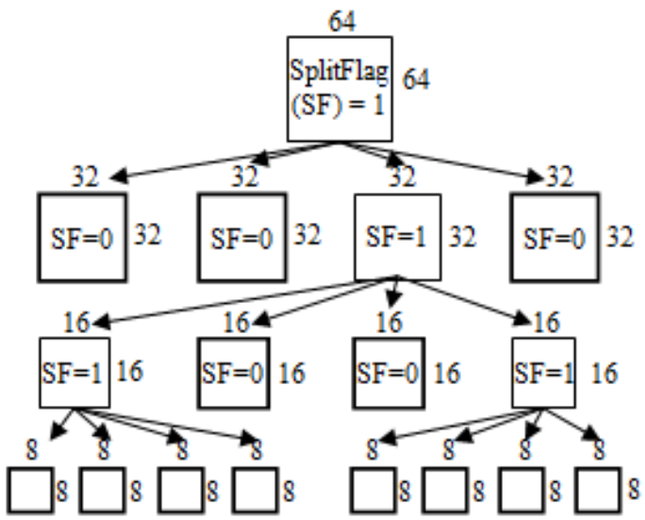
J. A. Gámez and J. M. Puerta

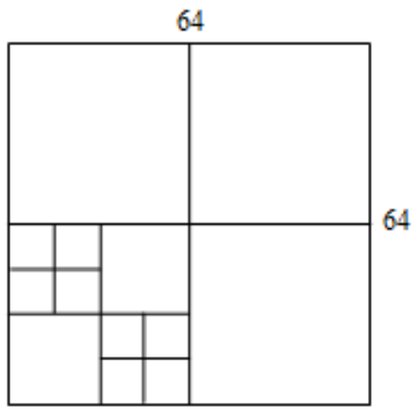
- HEVC es el sucesor de H.264/AVC.
- Existe mucho contenido multimedia elaborado para el estándar anterior.
- Se necesita pasar dicho contenido al nuevo estándar.
- Para ello se necesitan algoritmos eficientes de transcodificación.

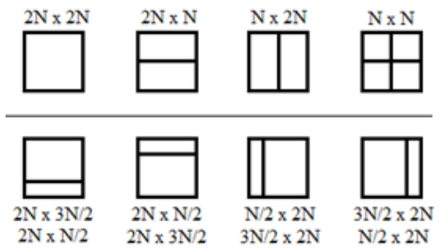
H.264/AVC HEVC



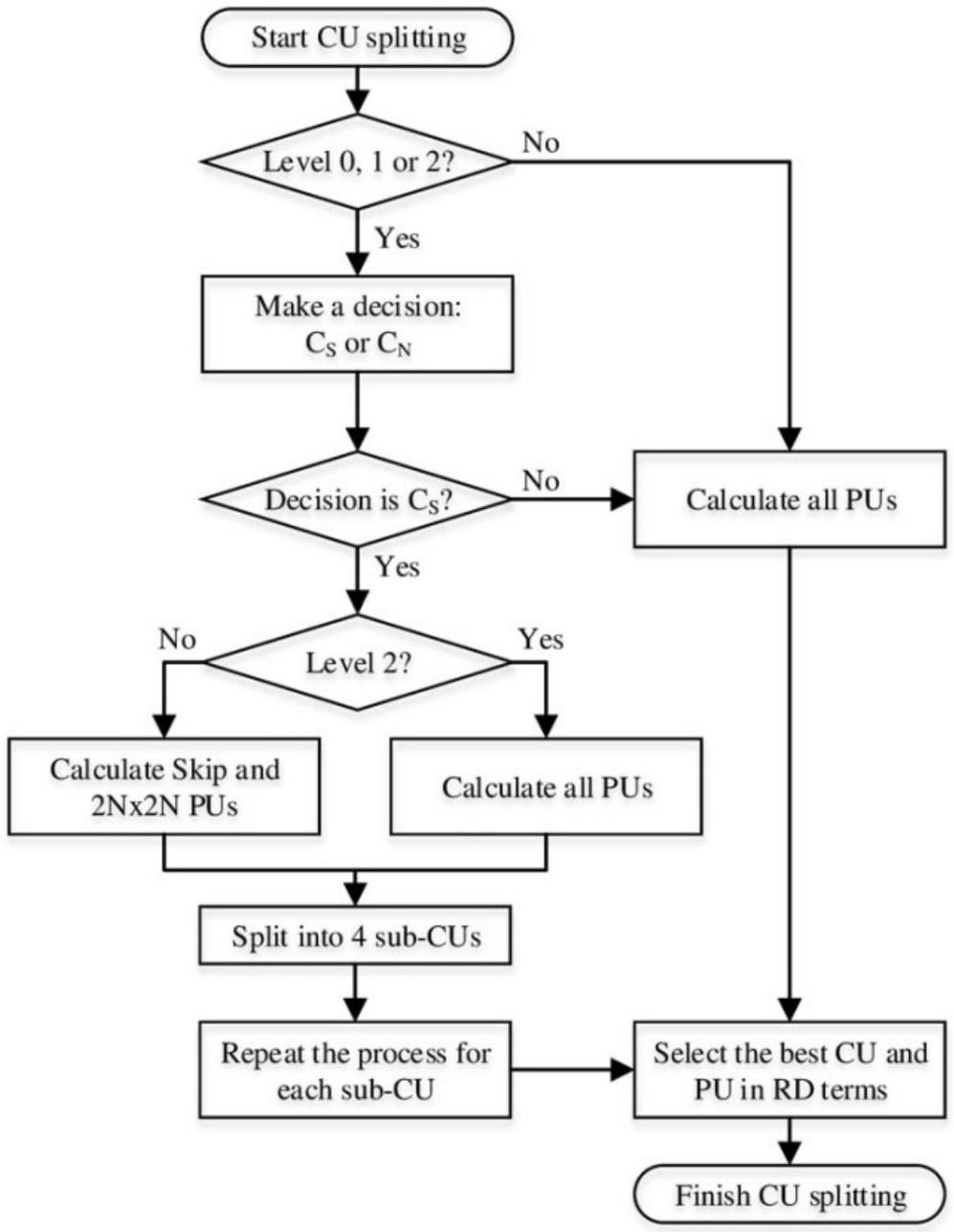






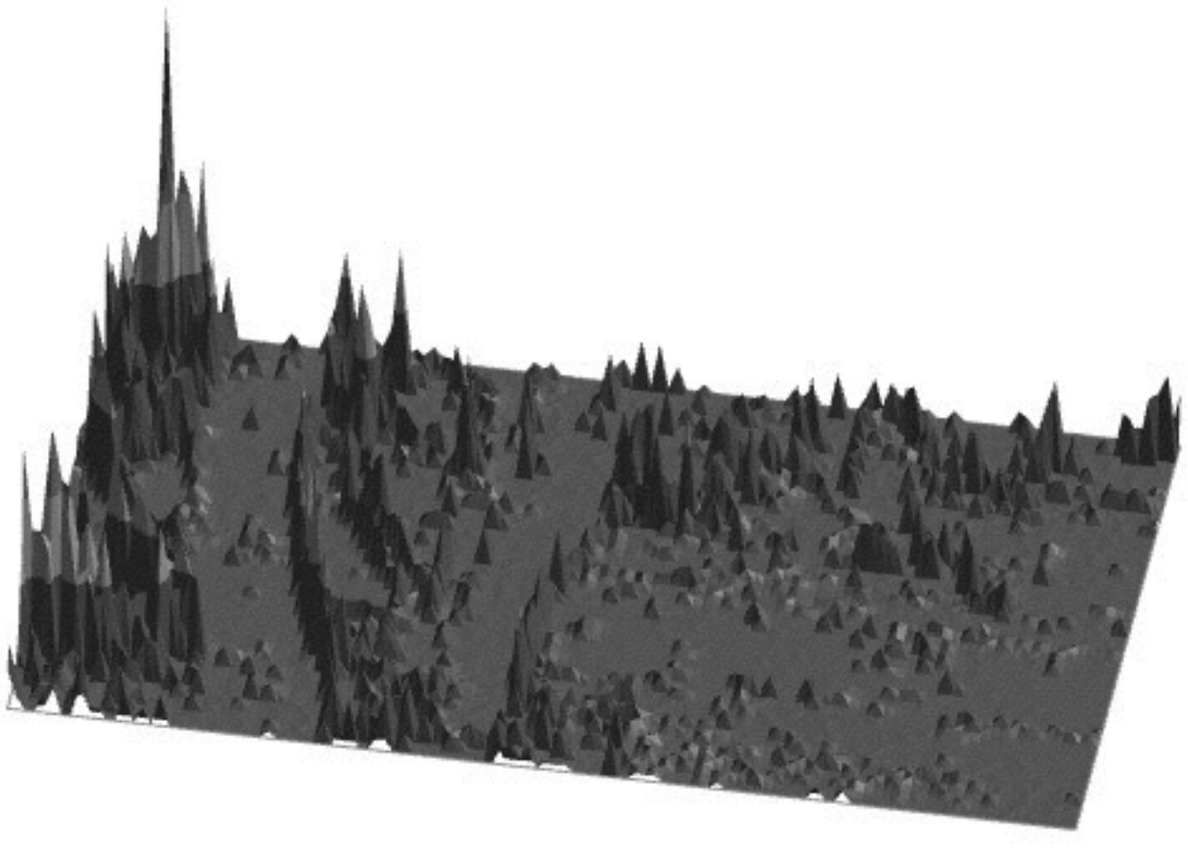


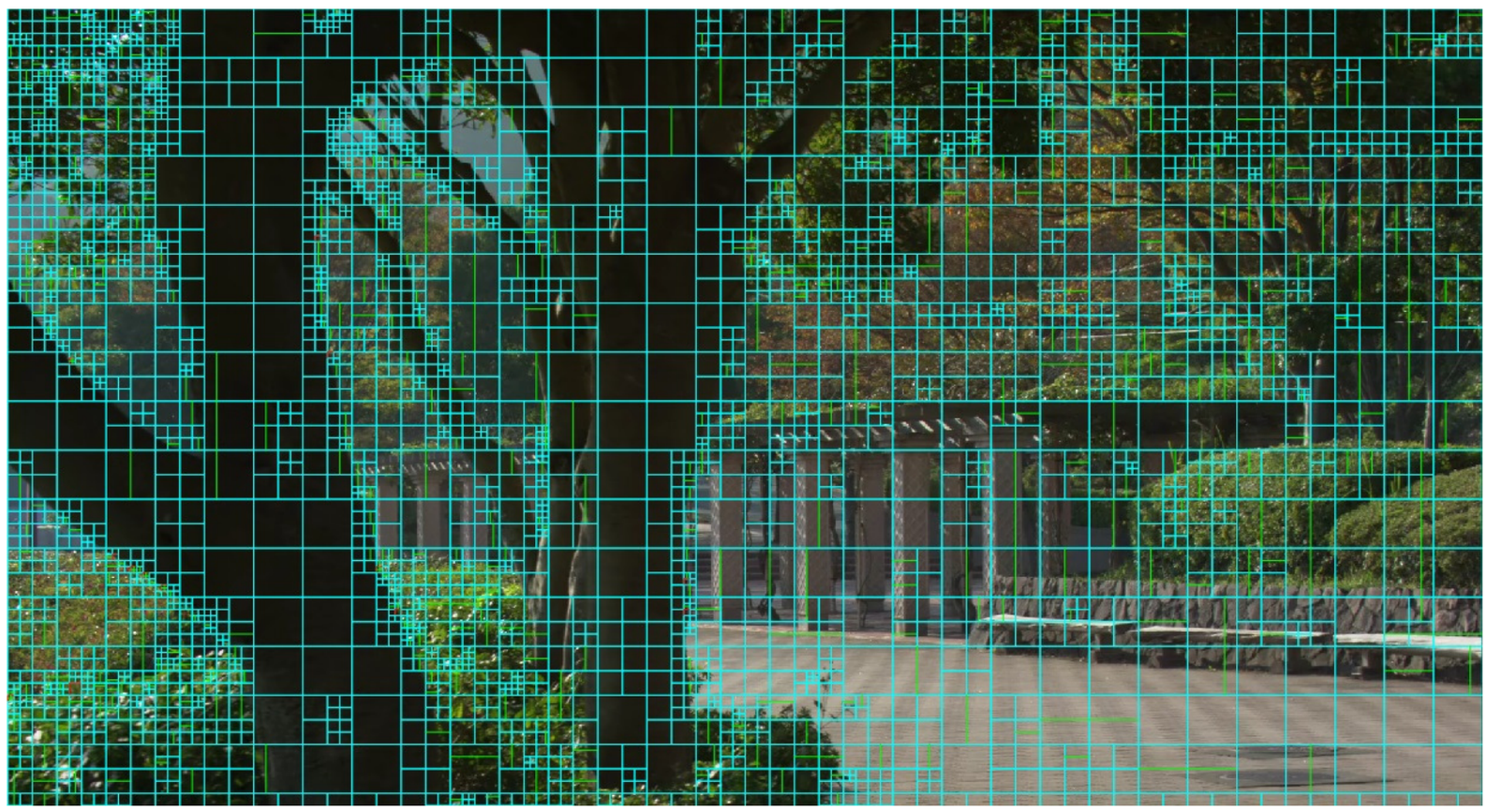
Adaptive Fast Quadtree Level Decision



Proceso de Aprendizaje de Modelos

- Modelo de Clasificación Supervisada: Split or NotSplit
- Se ha aprendido varios modelos uno para cada nivel (0,1) así como para cada modelo de energía.
- Además del tipo de “frame” Ramdom Access, Low Delay B and Low Delay P.
- Las características para los modelos son:
    - Características extraídas de la codificación fuente en el proceso de descodificación.
    - Características de complejidad espacial y temporal del frame.
    - Características numéricas extraídas del proceso de transcodificación.
    - Características del HEVC que se puede extraer de forma dinámica en la etapa actual.
- Se han utilizado Naive Bayes, discretizando variables, con selección de variables y con umbral adaptativo dinámico.





Resultados

	AFQLD		ECU		AFQLD+ESD+CFM		ECU+ESD+CFM	
	BDR (%)	TR (%)	BDR (%)	TR (%)	BDR (%)	TR (%)	BDR (%)	TR (%)
Class A	2.5	54.75	2.8	32.55	4.2	64.25	6.3	51.10
Class B	3.5	59.45	2.2	44.81	5.3	68.47	5.6	56.33
Class C	2.2	48.32	1.9	33.33	3.9	59.92	5.1	46.02
Class D	2.3	48.39	2.2	31.97	4.1	58.63	5.9	46.52
Average	2.7	53.70	2.3	37.89	4.4	63.64	5.7	50.74

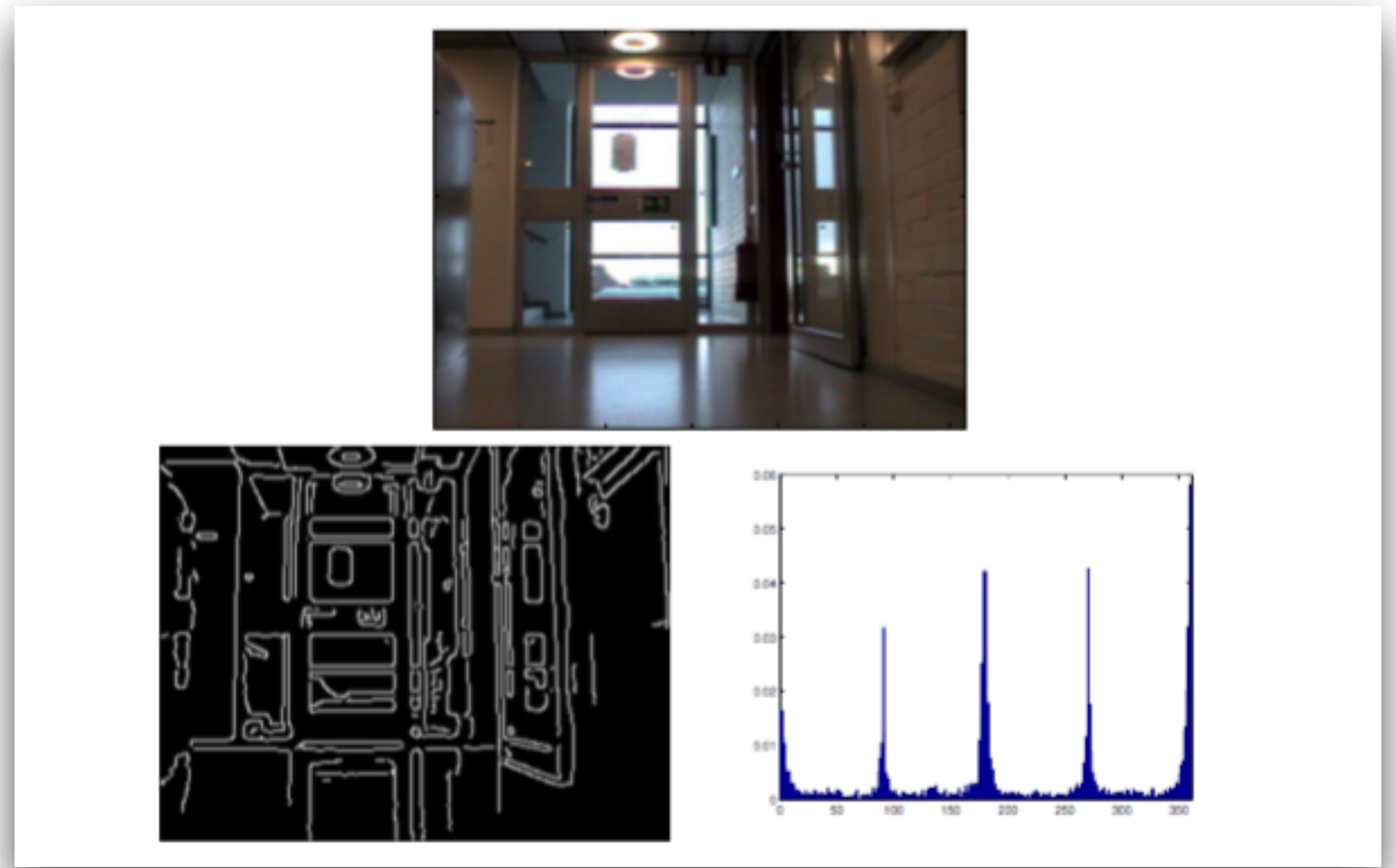
Index

- Predicción reingreso COPD
- H.264/HEVC Video Transcoder
- Scene Classification from images by means of Bayesian Networks and using contextual information

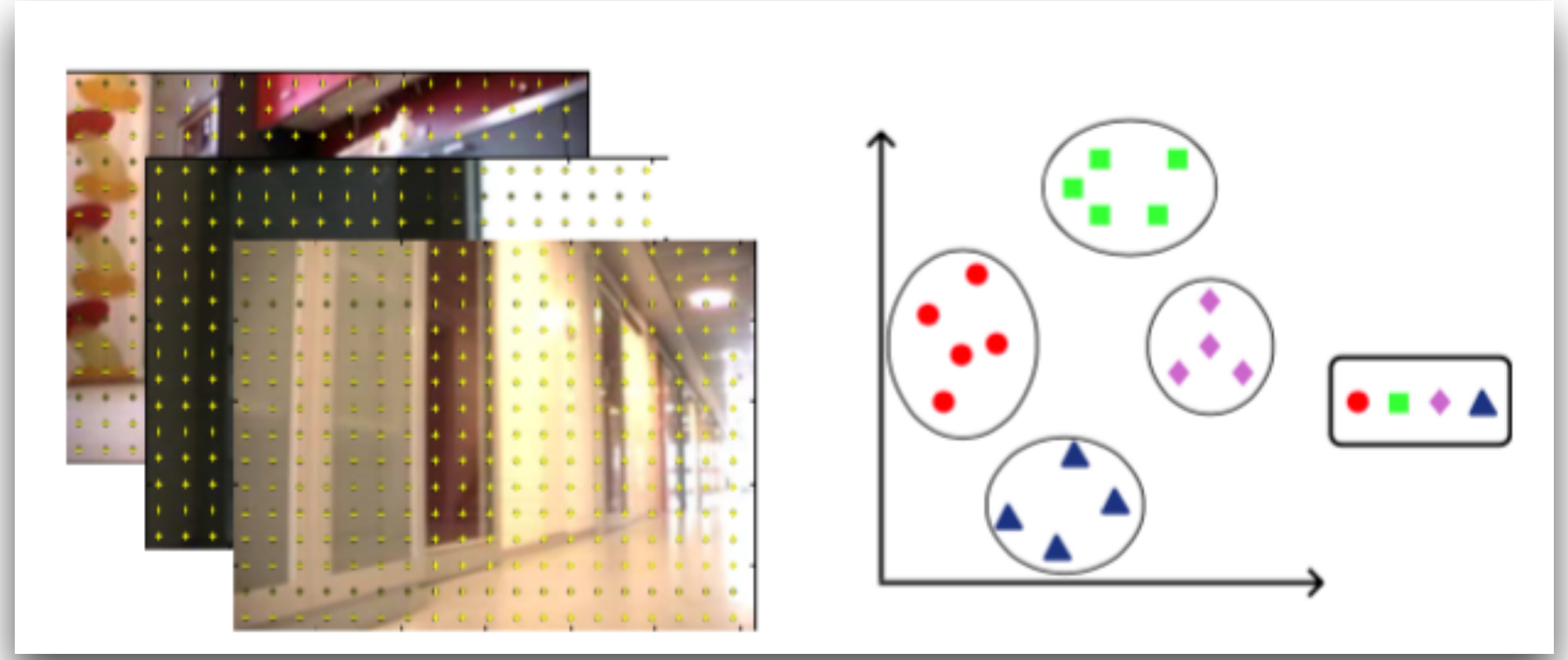
Scene Classification from images by means of Bayesian Networks and using contextual information

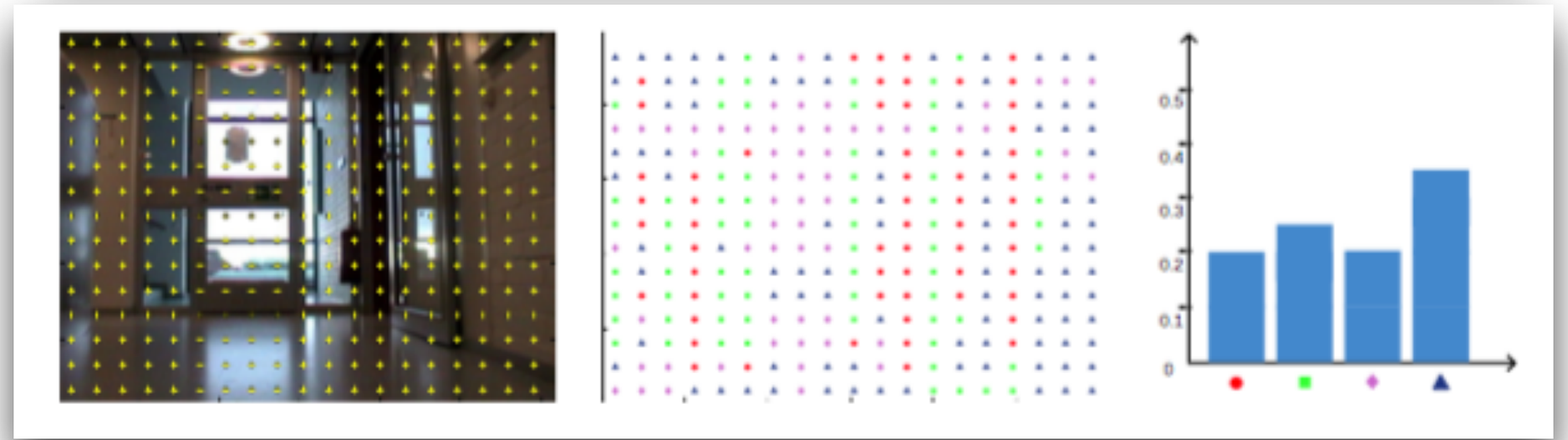
- Aplicado a Localización semántica de Robots.
- Las localizaciones son etiquetas y se plantea como un problema de clasificación.
- La localización se realiza a través de “frames” / imágenes y la extracción de características de ellas.
- Sin embargo existe la posibilidad de utilizar información adicional de la imagen: anotaciones, condiciones, etiquetas de objetos, etc.
- En este trabajo se aborda el estudio de integrar dicha información contextual en el problema de localización semántica de robots
- Se evalúan clasificadores Bayesianos y SVM.

Descriptores de Imagenes: HoG



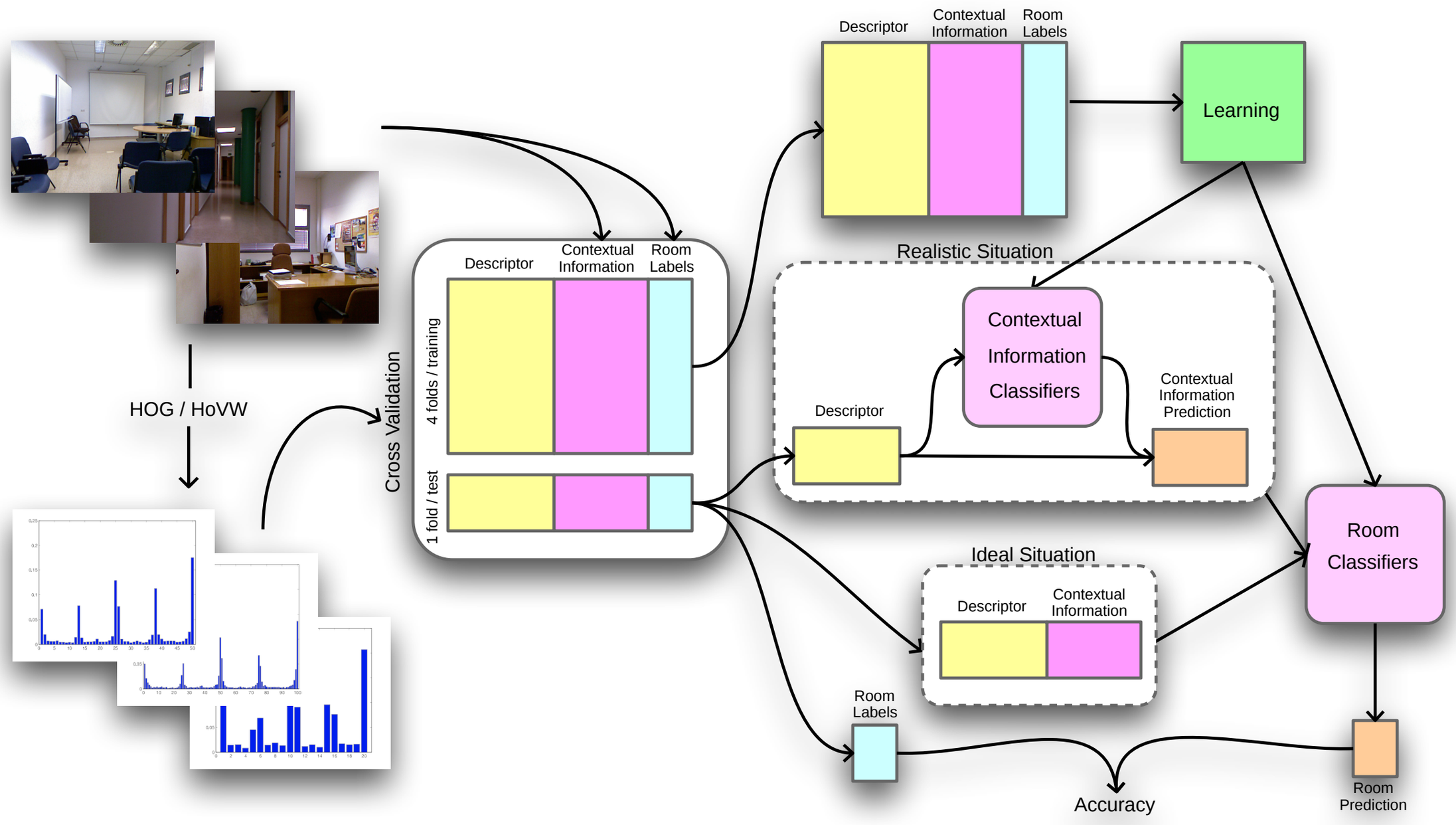
Descriptores Imagenes: HoVW (Sift)



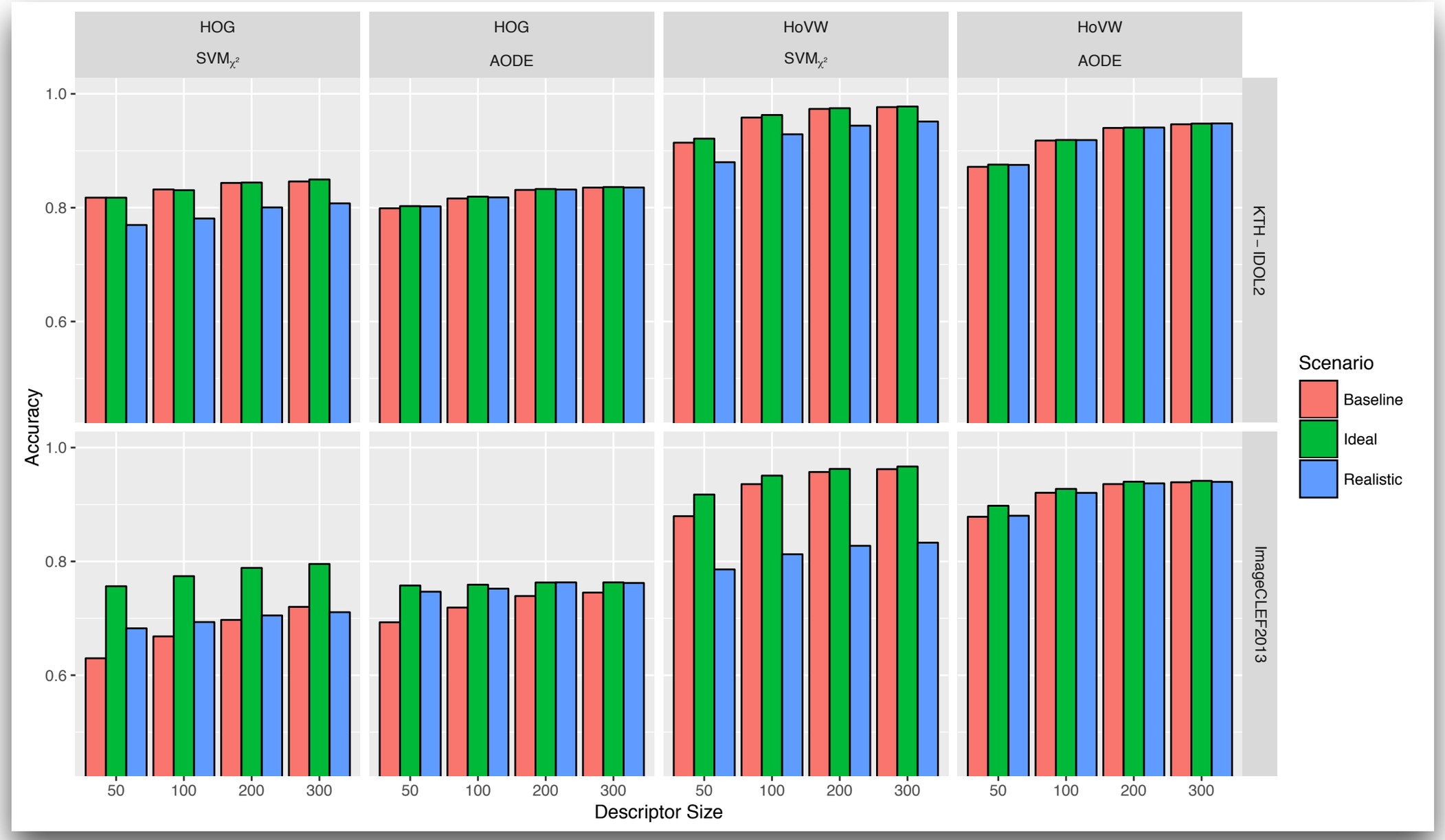


Información Contextual

Evaluación


HOG / HoVW
Cross Validation
4 folds / training
1 fold / test
Descriptor
Contextual Information
Room Labels
Learning
Realistic Situation
Contextual Information Classifiers
Descriptor
Contextual Information Prediction
Ideal Situation
Descriptor
Contextual Information
Room Classifiers
Room Labels
Accuracy
Room Prediction

Resultados


HOG
SVM$_{\chi^2}$
HOG
AODE
HoVW
SVM$_{\chi^2}$
HoVW
AODE
KTH – IDOL2
ImageCLEF2013
Accuracy
1.0
0.8
0.6
50
100
200
300
Descriptor Size
Scenario
Baseline
Ideal
Realistic