# Applications of Dominant Set

Sebastiano Vascon, PhD

DAIS 09/05/2017



Ca' Foscari
University
of Venice

# Recap on the Dominant Set technique

- Graph-based clustering technique
- A DS is subset of highly coherent nodes in a graph (high internal similarity and high external dissimilarity).
- Maximal clique in edge weighted graph
- Pros:
  - No need for k
  - Provide a quality value for each cluster (cohesiveness)
  - Provide a membership value for each element in a cluster
  - Undirected and directed graph
- Cons:
  - Require O($n^2$) to store the similarity matrix (does not scale for big data)

# Recap on the Dominant Set technique

- Given an edge-weighted graph G=(V,E,w) with no self loop
- A DS is found optimizing the following problem (1):

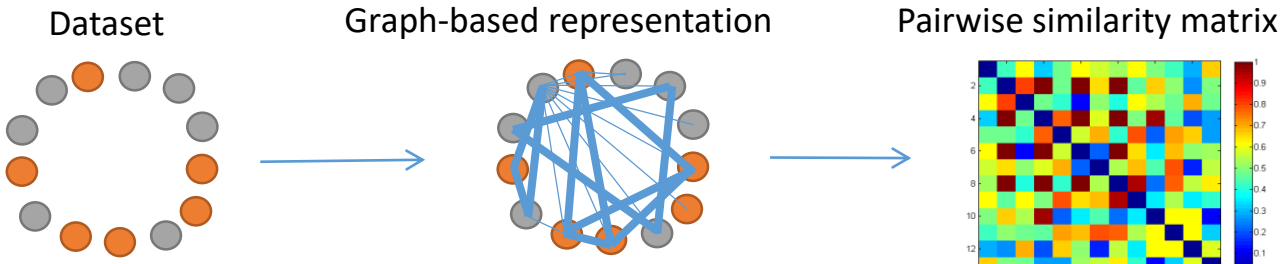
$$\max x'Ax$$
$$s.t.\ \ x \in \Delta^n$$

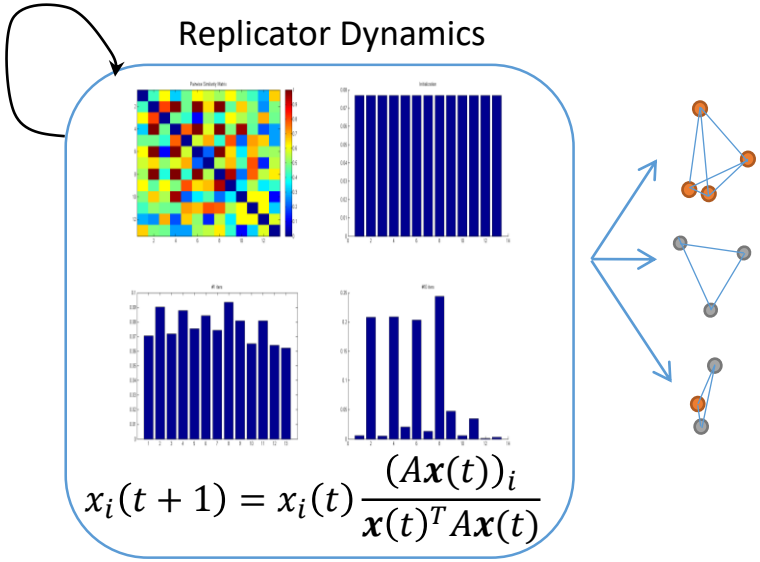
  where A is the affinity (similarity) matrix of G and $x$ is a probability distribution over V (usually set as a uniform distribution).

- Solution to (1) can be found with dynamical systems like:
  - Replicator Dynamics [1]
  - Exponential Rep Dynamics [1]
  - Infection Immunization [2]

# Recap on the Dominant Set technique

A dataset is modeled as a weighted graph $G = (V, E, \omega)$ with no self loop. The set of nodes *V* are the dataset's items and the edges are weighted by $\omega: V \times V \rightarrow \mathbb{R}_+$ that quantifies the pairwise similarity of the items. *G* is thus represented by an $n \times n$ adjacency matrix $A = (a_{ij})$



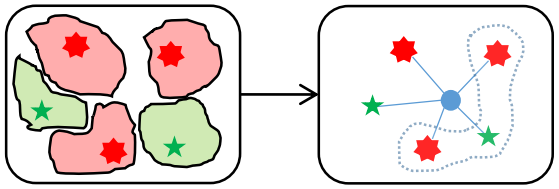

$\boldsymbol{x}$ is the *characteristic vector* and represents the degree of participation of the items in the cluster.

The support of $\boldsymbol{x}$, $\delta = \{i \mid x_i \geq \tau\}$ represents the set of nodes that are grouped into the same cluster.

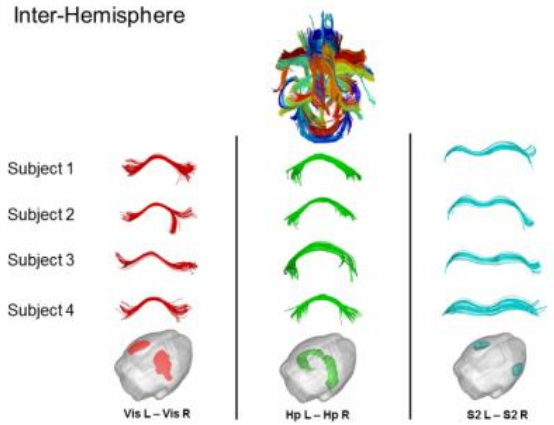
http://www.github.com/xwasco/DominantSetLibrary

# Applications

## Pattern Recognition

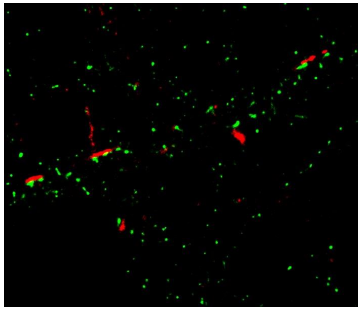


## Brain Connectomics



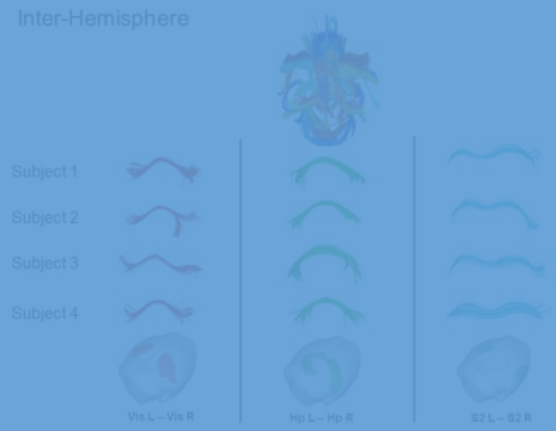

## Human Behavior

## Nano science

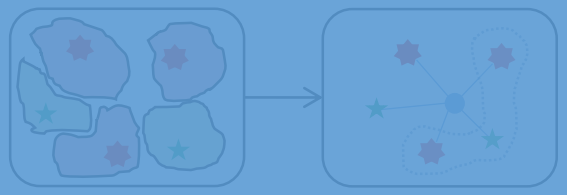


# Applications

## Brain Connectomics

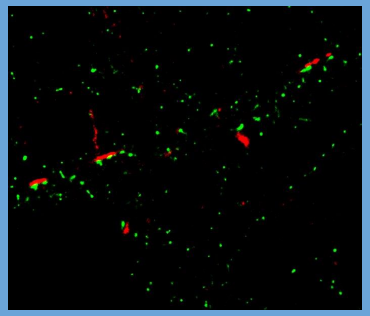



## Pattern Recognition



## Human Behavior

## Nano science

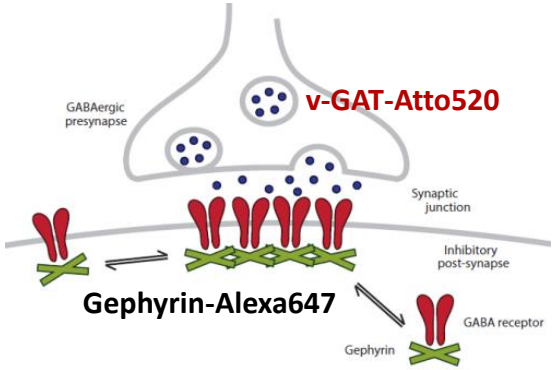


# Gephyrine & vGAT analysis tool

***Problem: Understanding the activity of Gephyrine and vGAT proteins.***

Gephyrine and vGAT are two proteins that takes parts into the synapse activation.

Gephyrine is a post-synaptic protein that sustain the grid of GABA receptors that receive the chemical stimuli in a synapse.



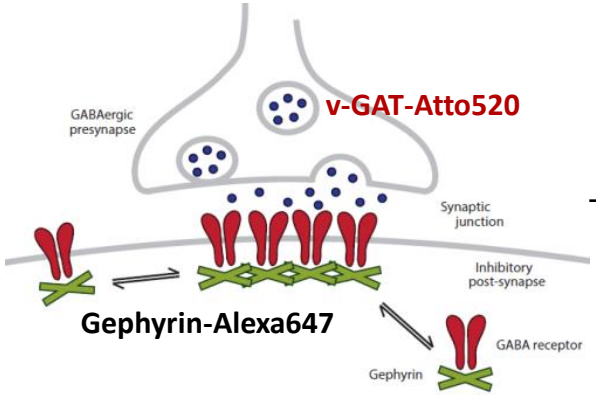

Analyze the morphological changes of this grid during the synapses activation is of crucial importance for the Nanophysicists (e.g. discovering disease).
These changes is reflected into the morphology and number of clusters of Gephyrine.

Finding an alignment with the v-GAT pre-synaptic protein clusters is important to understand when and where an accumulation of Gephyrine occurs.

F.Pennacchietti, S.Vascon, A. Del Bue, E. Petrini, A. Barberis, F.Cella, A. Diaspro - **Quantitative super-resolution by IML of anchoring proteins of the inhibitory synapse** – Workshop on Single Molecule Localization, PicoQuant , Berlin 2014

# Gephyrine & vGAT analysis tool

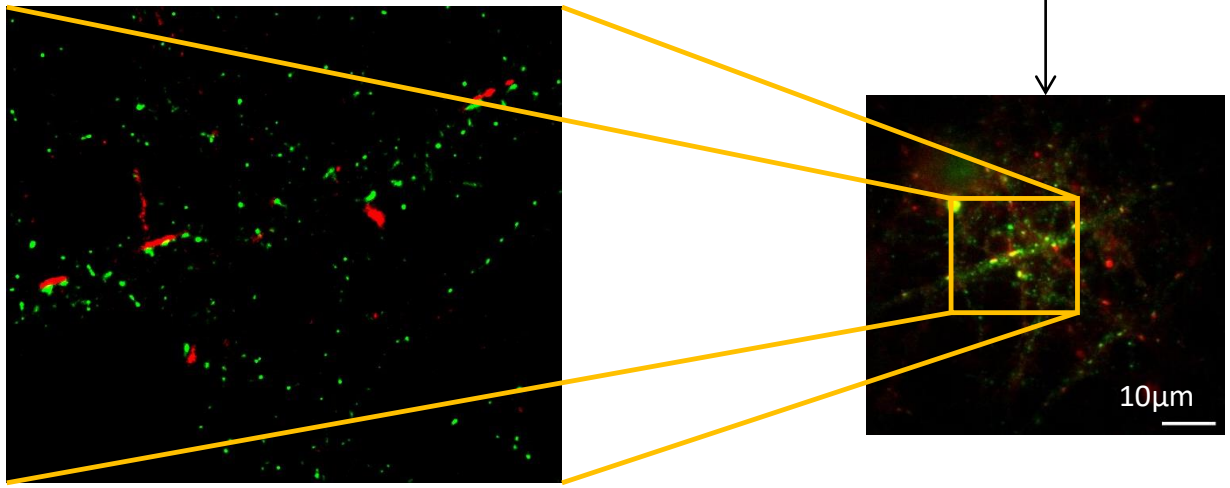
*Dataset: set of molecules position (x,y) for each channel (Gephyrine and vGAT)*




(x,y) locations of each molecule

Gephyrine

vGAT



# Gephyrine & vGAT analysis tool

***Aim:***

1. *Extract clusters of Gephyrine and vGAT based on the single molecules detection*

2. *Find associations between clusters of the two channel*

***Solution:***

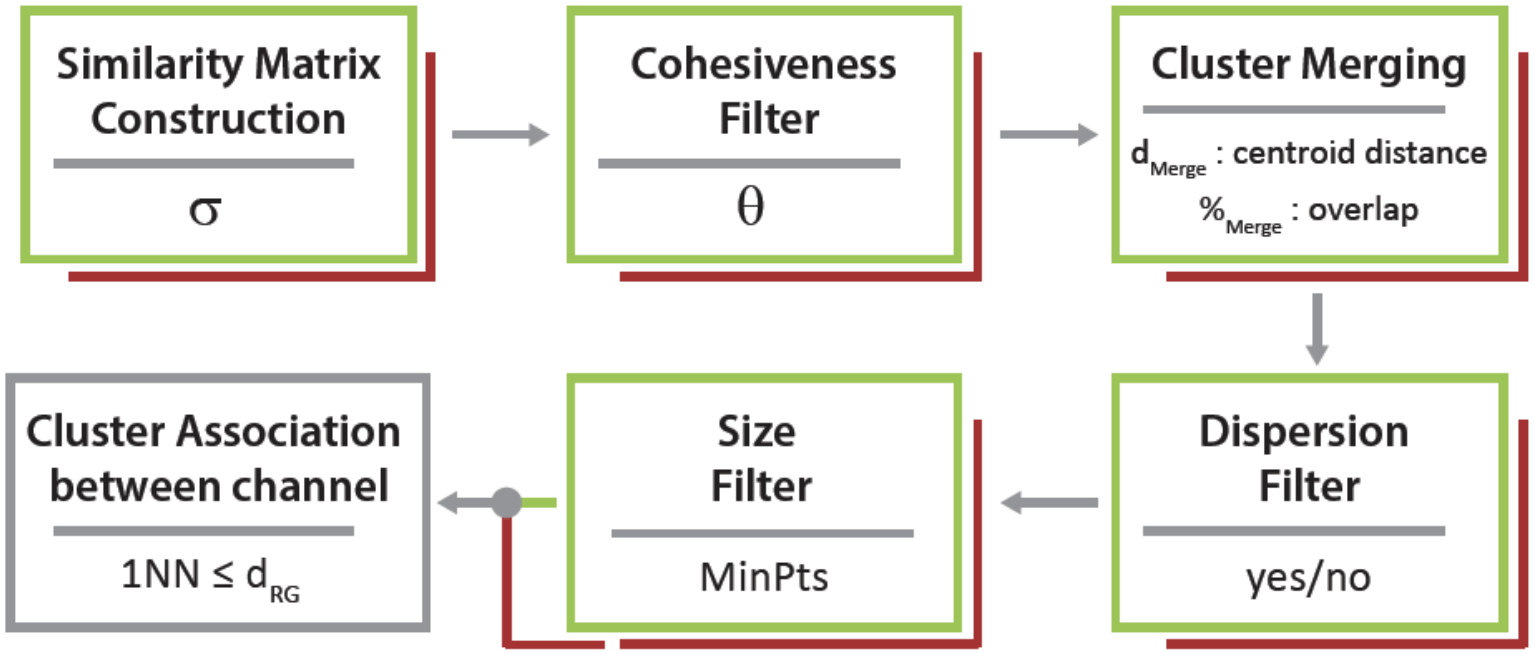
1. Create a graph-based representation of the points for each channel G(V,E,w) in which $w_{ij} = \begin{cases} e^{-\frac{||\, i-j \,||}{2\sigma^2}} & if\ i \neq j \\ 0 & otherwise \end{cases}$ and extract the clusters using the DS

2. Apply a chain of post processing filtering to merge the smaller clusters and remove the meaningless ones.

3. Find clusters associations between the two channels providing statistics

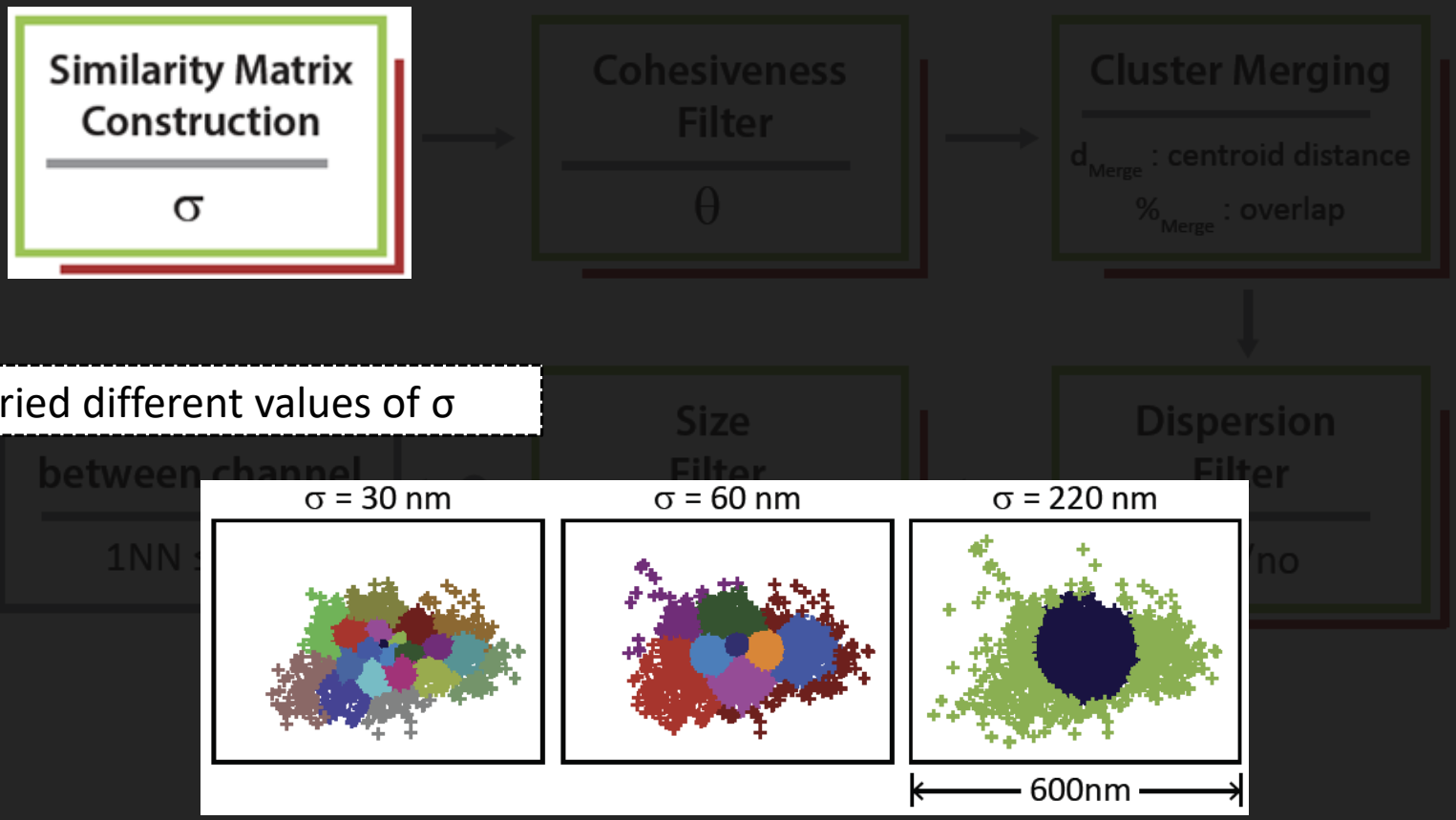
# Gephyrine & vGAT analysis tool

***Pipeline:***



# Gephyrine & vGAT analysis tool

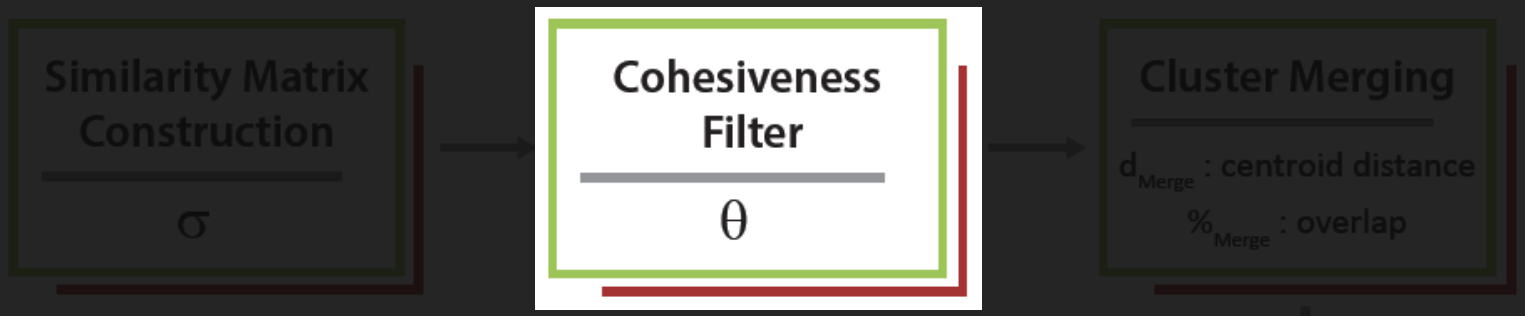
***Pipeline:***




We tried different values of σ

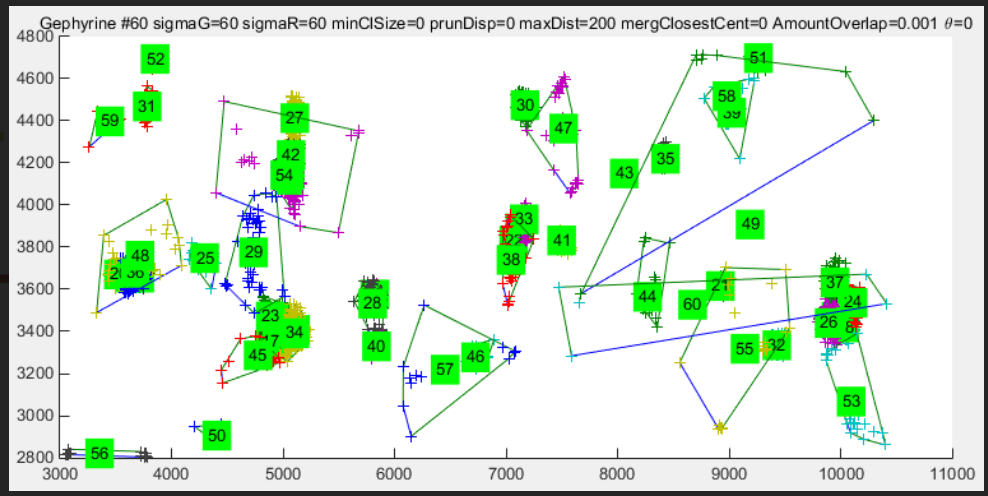
# Gephyrine & vGAT analysis tool

***Pipeline:***




Remove clusters having a cohesiveness ($x^T Ax$) values lower than a certain threshold $\theta$.

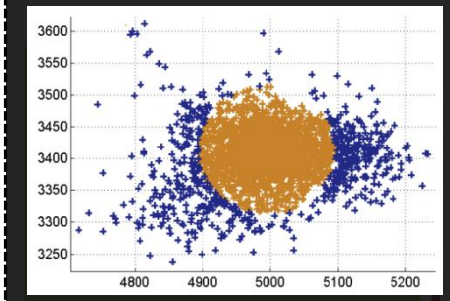
This remove clusters with few and spread points.



# Gephyrine & vGAT analysis tool

DS find circular and compact clusters … it is ok but ?

We merge clusters having the centroid (mean points) closer to a certain threshold or if their convex hull overlap for a certain %



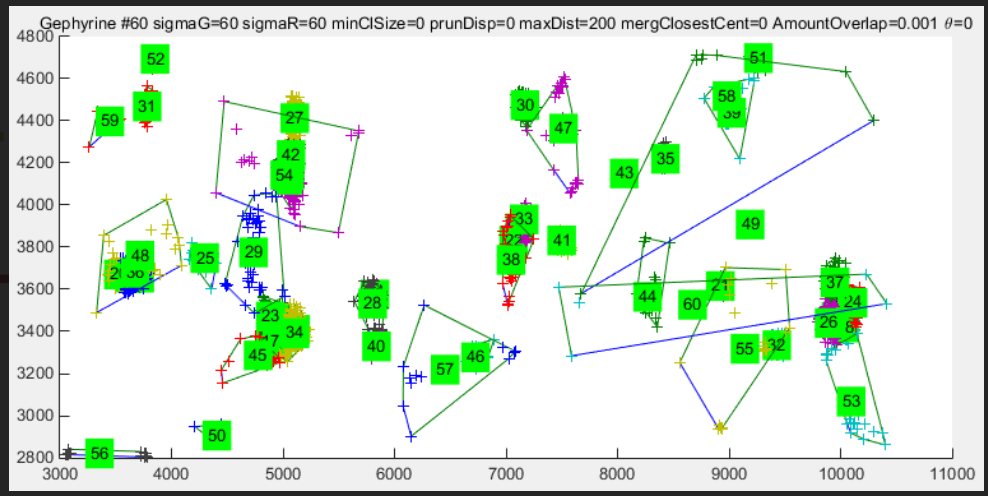

**Cluster Merging**

$d_{Merge}$ : centroid distance

$\%_{Merge}$ : overlap

**Cluster Association between channel**

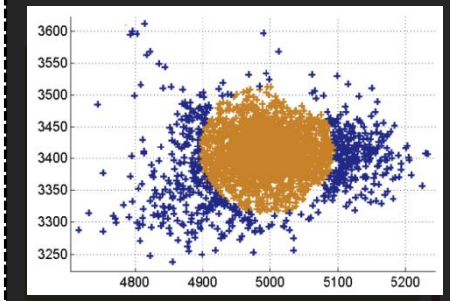
$1NN \leq d_{RG}$



# Gephyrine & vGAT analysis tool

DS find circular and compact clusters … it is ok but ?

We merge clusters having the centroid (mean points) closer to a certain threshold or if their convex hull overlap for a certain %



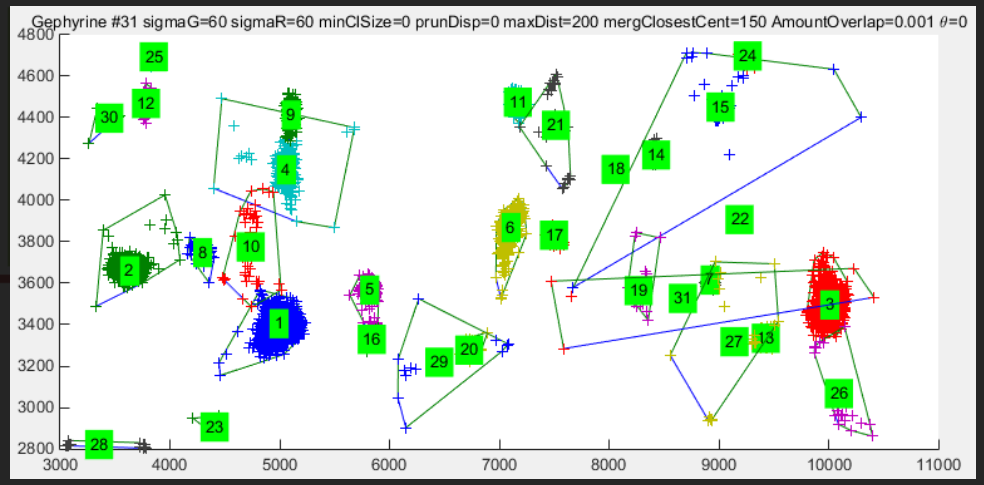

**Cluster Merging**

$d_{Merge}$ : centroid distance

$\%_{Merge}$ : overlap

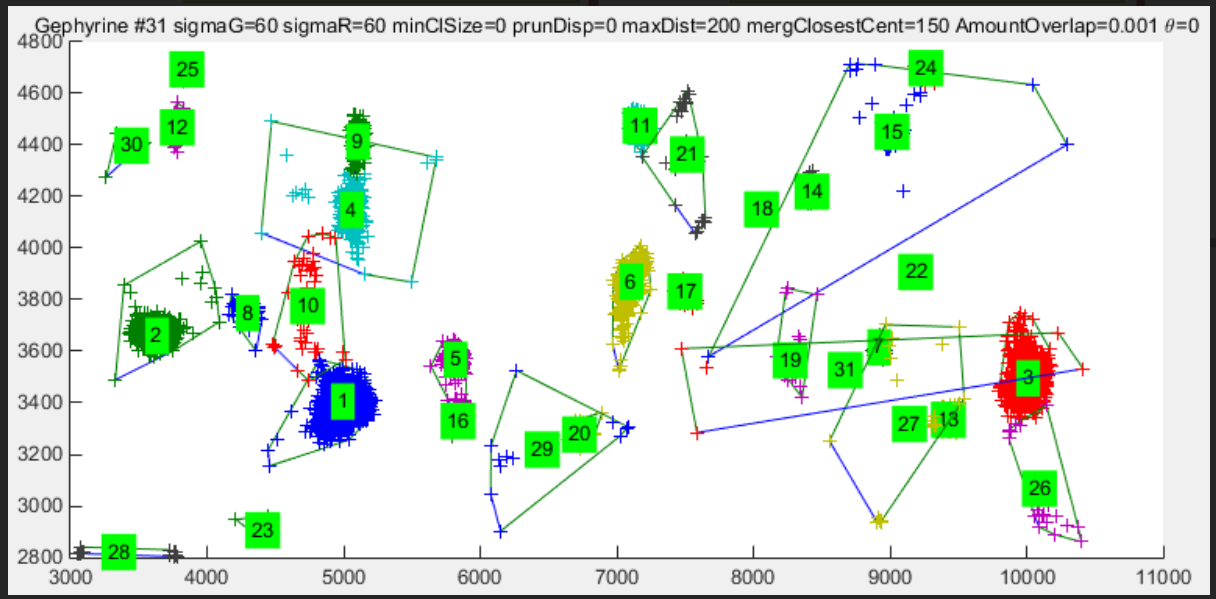
**Cluster Association between channel**

$1NN \leq d_{RG}$



# Gephyrine & vGAT analysis tool

Evaluate for each cluster the variance and remove the clusters having the variance above the mean variance of the clusters




Cohesiveness Filter

θ

Cluster Merging

$d_{Merge}$ : centroid distance

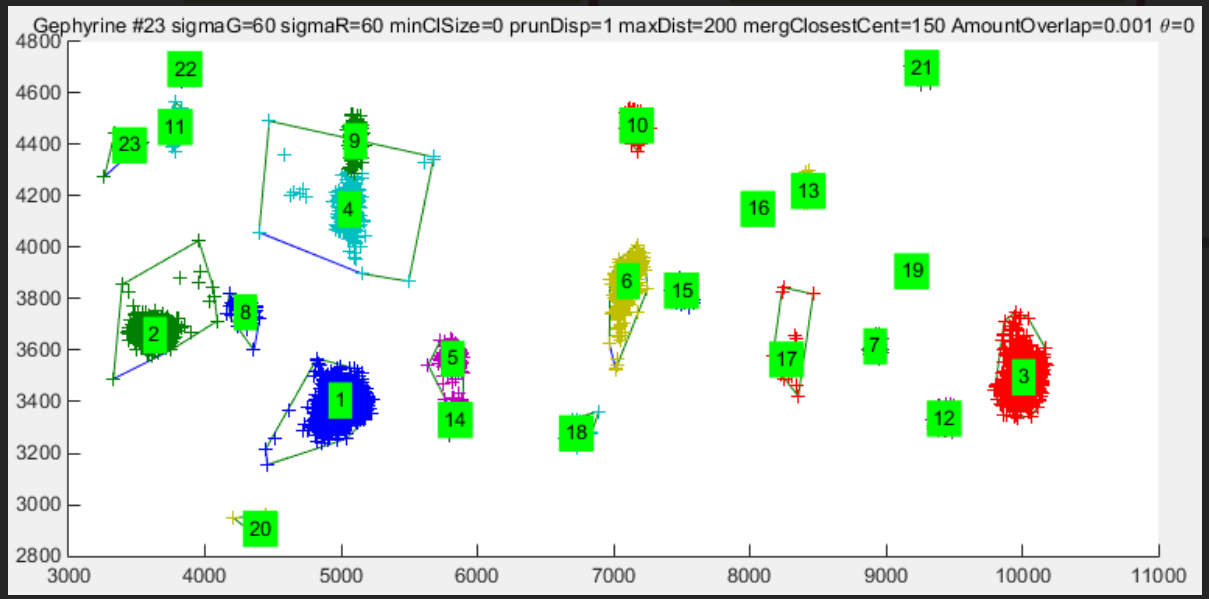
$\%_{Merge}$ : overlap

Dispersion Filter

yes/no

# Gephyrine & vGAT analysis tool

Evaluate for each cluster the variance and remove the clusters having the variance above the mean variance of the clusters




Cohesiveness Filter

θ

Cluster Merging

$d_{Merge}$ : centroid distance

$\%_{Merge}$ : overlap

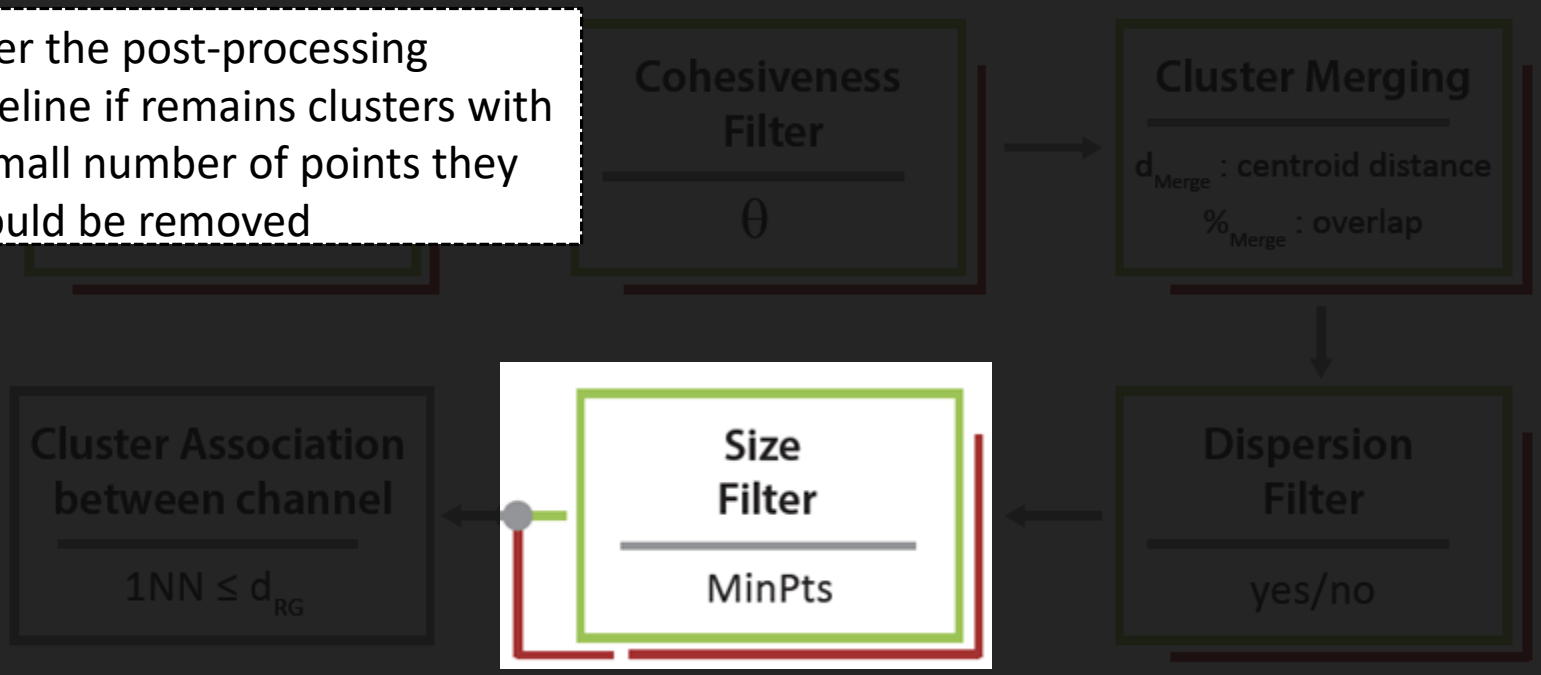
Dispersion Filter

yes/no

# Gephyrine & vGAT analysis tool

***Pipeline:***

After the post-processing pipeline if remains clusters with a small number of points they should be removed



# Gephyrine & vGAT analysis tool

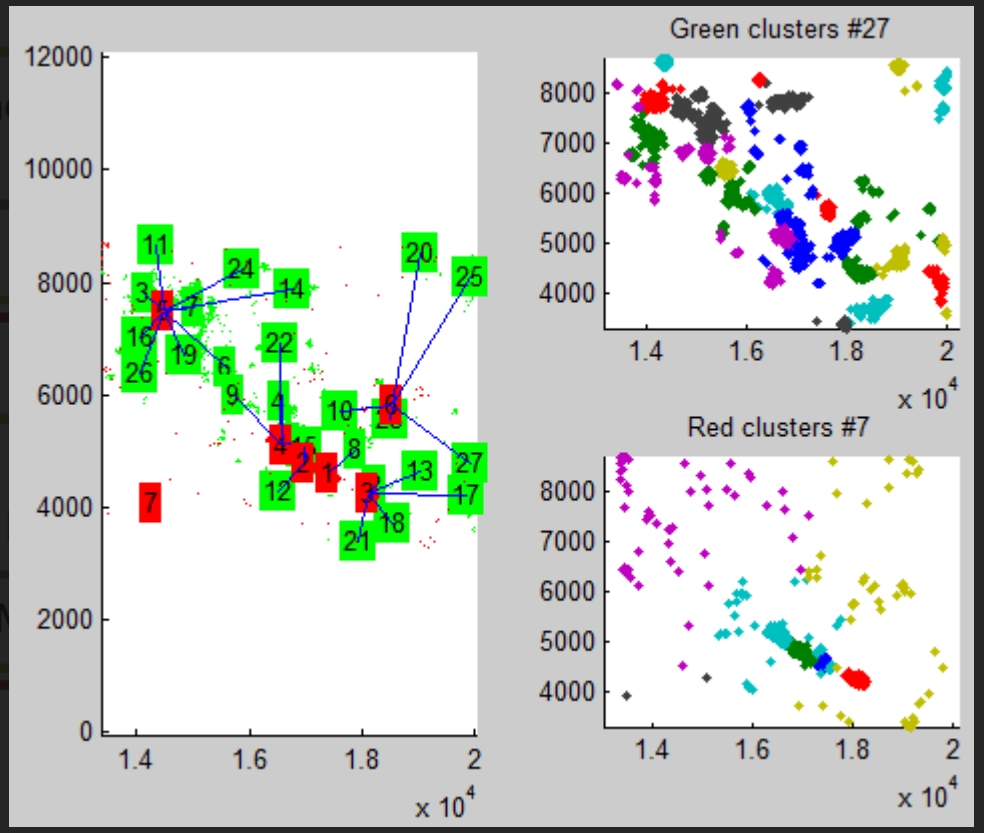
***Pipeline:***

1. Evaluate pairwise distances between green and red clusters centroid

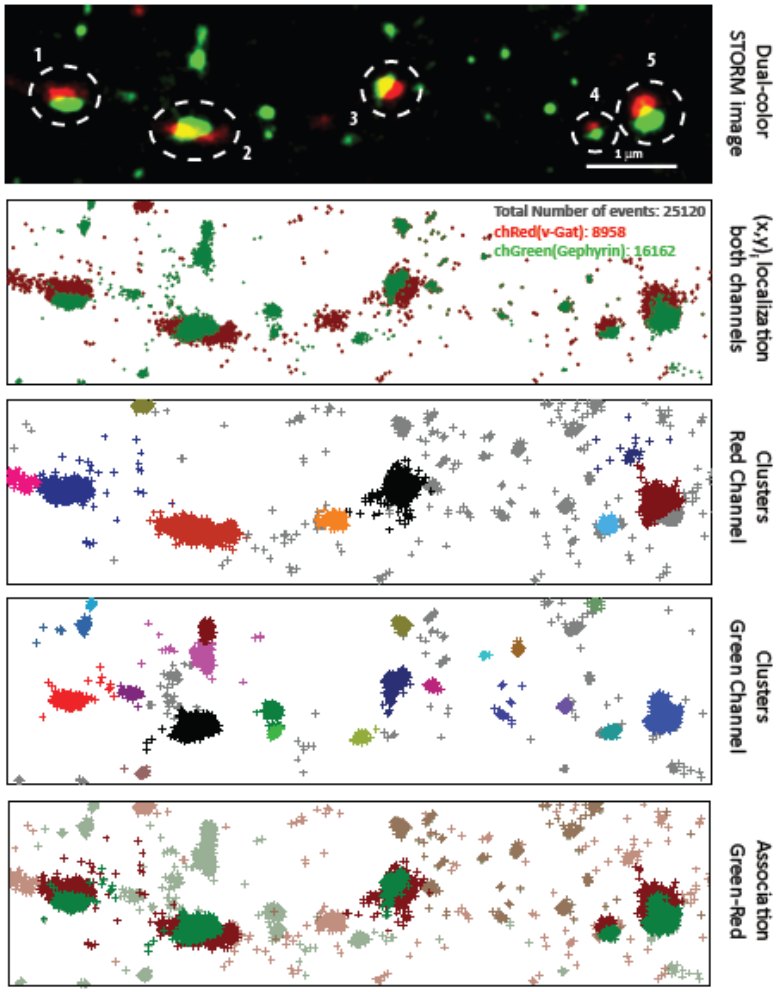
2. For each green cluster assign the 1-NN red cluster

**Cluster Association between channel**

$$1NN \leq d_{RG}$$



# Gephyrine & vGAT analysis tool




Cluster statistics for Gephyrine's clusters:

- Number of points
- Convex Hull area
- Variance
- Distance of the closest vGAT's cluster

Cluster statistics for vGAT's clusters:

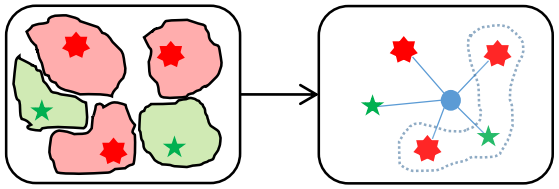
- Number of points
- Convex Hull area
- Variance
- Number of associated Gephyrine's cluster

Validation

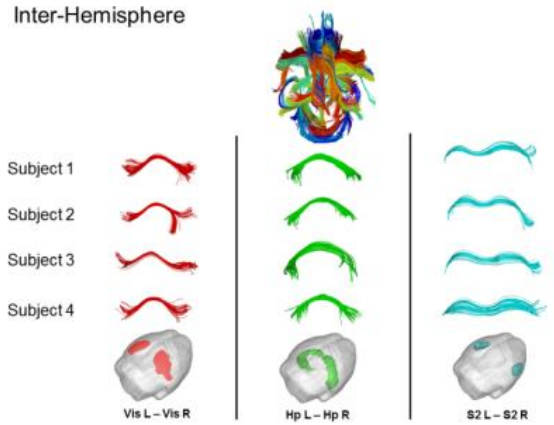
- Nanophysicists annotate a set of images
- Completeness/Correctness

# Applications

## Pattern Recognition

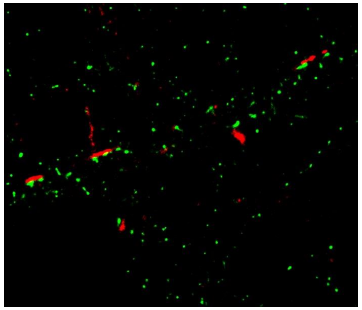


## Brain Connectomics



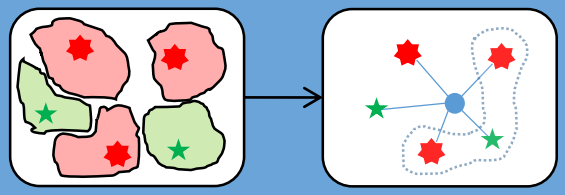

## Human Behavior

## Nano science

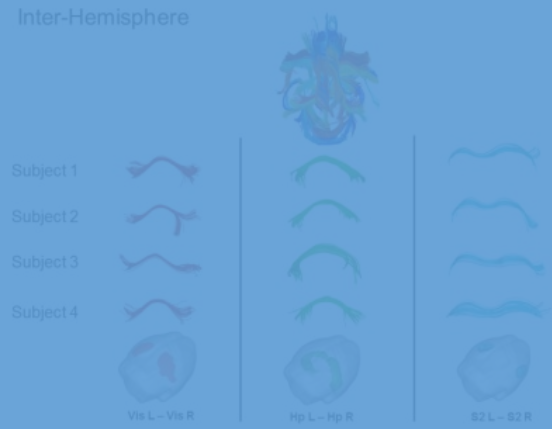


# Applications

## Pattern Recognition



## Brain Connectomics

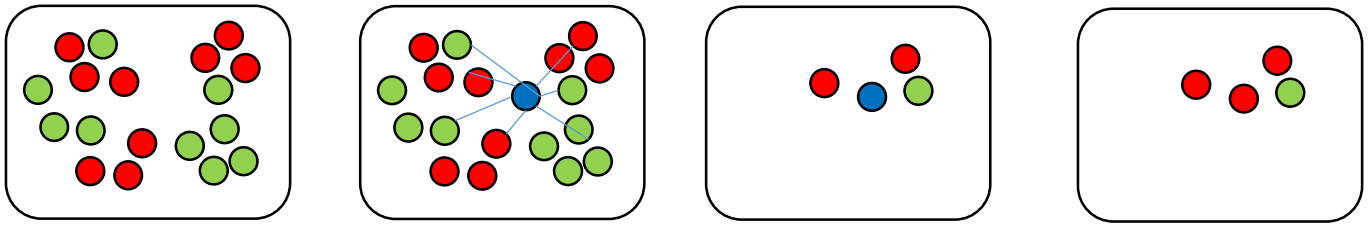



## Human Behavior

## Nano science

# Pattern Recognition: *k*-NN boosting

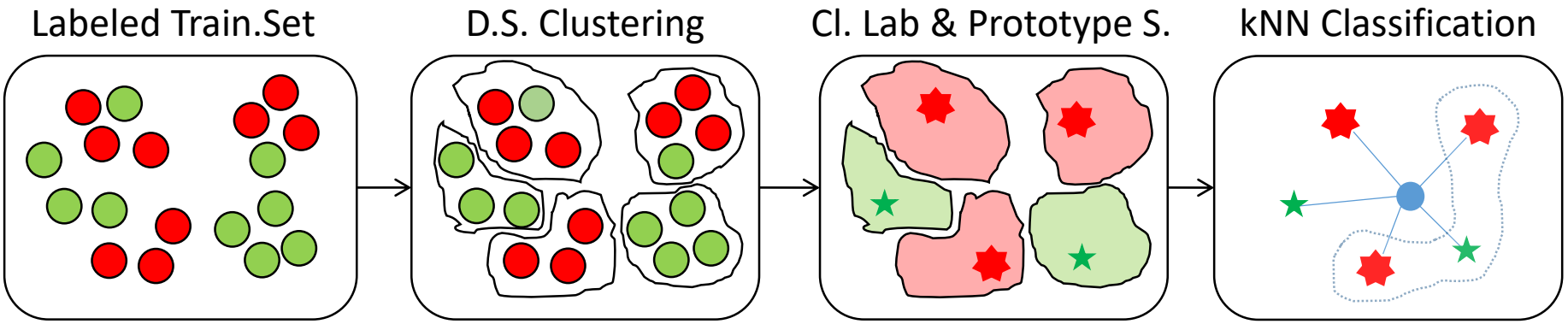
- *k*-NN classifier:
  Assign the class based on classes of the k nearest sample in the feature space.



- Problems of *k*-NN classifiers*:*
  - Sensitive to noise and outliers
  - Slow if the number of elements is high

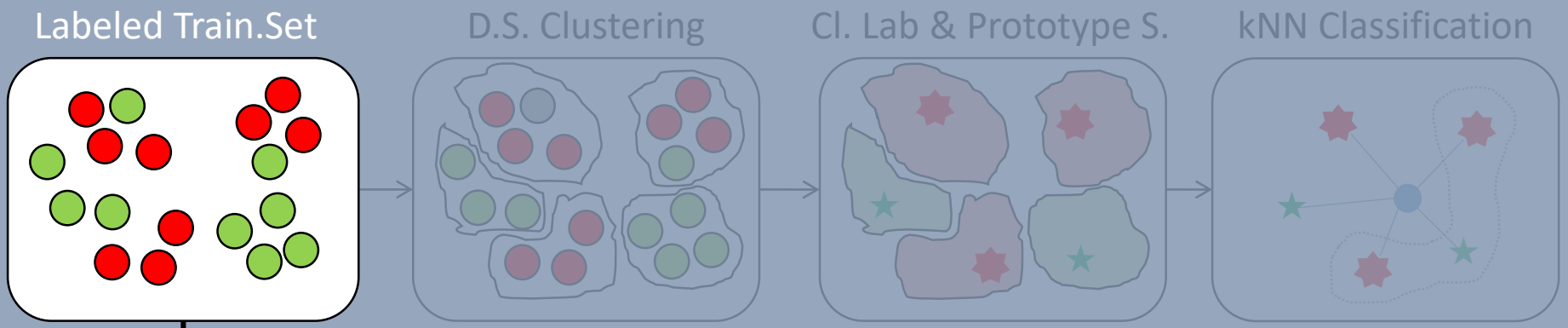
- Solution:
  - Reducing the space of search by using prototypes
  - Create/select prototypes such that the noise and outliers are minimized.

# Pattern Recognition: *k*-NN boosting

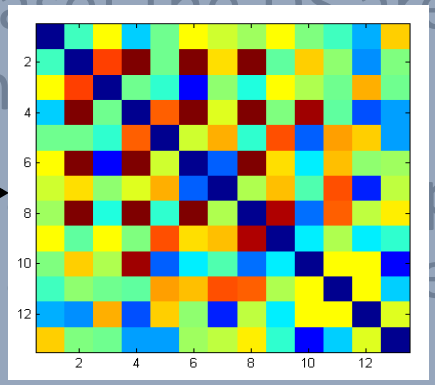



- Given a dataset the DS are used to extract the cluster and the centroid.
- The k-NN classification is performed on the prototypes and not on the entire set

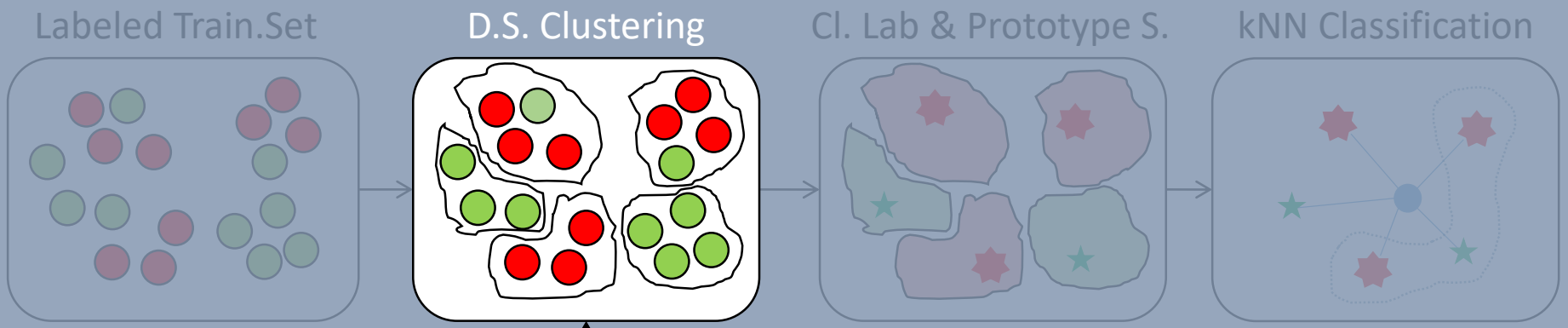
# Pattern Recognition: *k*-NN boosting



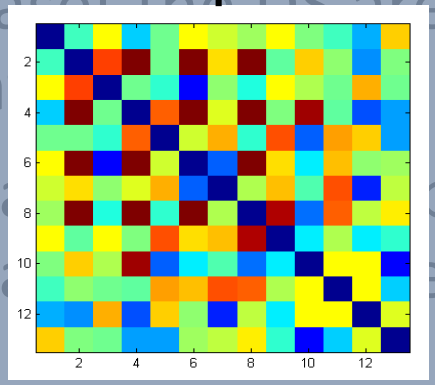

- Given a dataset the DS are used to extract the cluster and the cen
- The k-NN cl performed on the prototypes e entire set



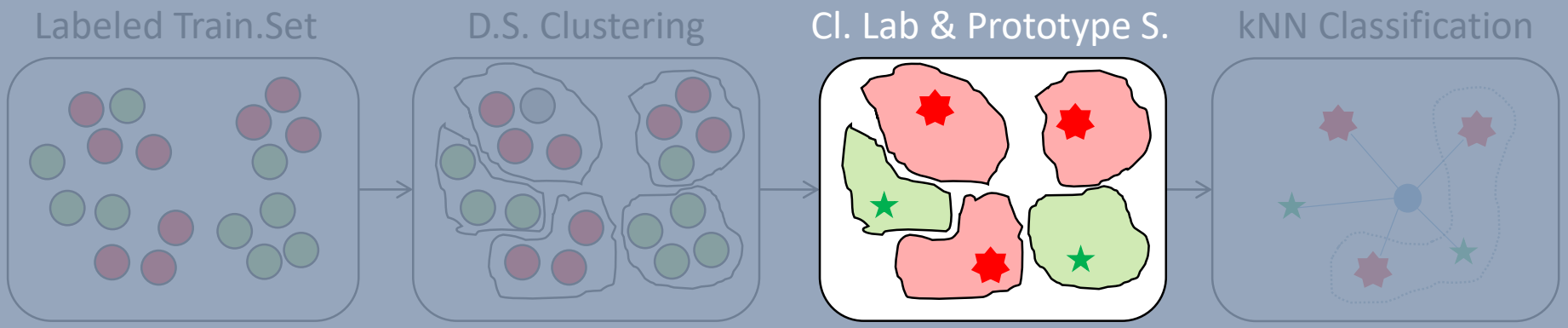
# Pattern Recognition: *k*-NN boosting




- Given a dataset the DS are used to extract the cluster and the cen
- The k-NN cl performed on the prototypes a e entire set

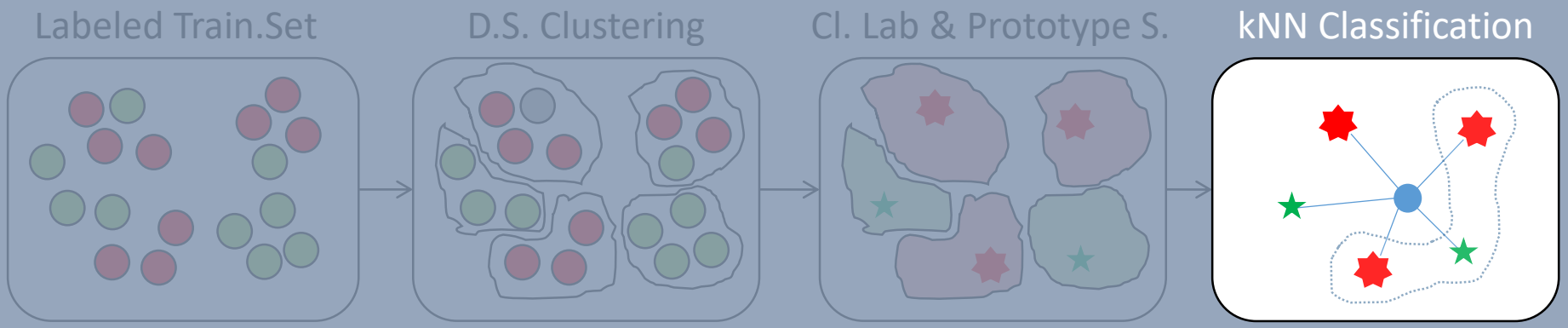


# Pattern Recognition: *k*-NN boosting




- Given a dataset the DS are used to extract the cluster and the centroid.
- The k-NN classification is performed on the prototypes and not on the entire set

# Pattern Recognition: *k*-NN boosting




- Given a dataset the DS are used to extract the cluster and the centroid.
- The k-NN classification is performed on the prototypes and not on the entire set

# Pattern Recognition: *k*-NN boosting

| Name | #ex | #att | Name | #ex | #att | Name | #ex | #att |
|---|---|---|---|---|---|---|---|---|
| appendicitis | 106 | 7 | haberman | 306 | 3 | sonar | 208 | 60 |
| australian | 690 | 14 | heart | 270 | 13 | spambase | 4597 | 57 |
| banana | 5300 | 2 | mammographic | 961 | 5 | spectfheart | 267 | 44 |
| bands | 539 | 19 | monk-2 | 432 | 6 | titanic | 2201 | 3 |
| bupa | 345 | 6 | pima | 768 | 8 | wisconsin | 699 | 9 |

- 15 binary classification datasets from UCI
- 25 different prototype methods
- 1 common benchmark [1]
- Accuracy, Compression rate and Exec. Time
- Evaluation of 1-NN and 3-NN performances

[1] Garcia, S. Et al : Prototype selection for nearest neighbor classification: taxonomy and empirical study. IEEE Transactions on Pattern Analysis and Machine Intelligence 34(3) (2012) 417-35

# Pattern Recognition: *k*-NN boosting

| Rank | 1-NN Classifier | |
|---|---|---|
| # | A×K×R | Name |
| 1 | 0,428 | 'CHC' |
| 2 | 0,393 | 'SSMA' |
| 3 | 0,393 | 'GGA' |
| 4 | 0,369 | 'RMHC' |
| 5 | 0,349 | 'RNN' |
| 6 | **0,340** | **AVG** |
| 7 | **0,332** | **WAVG** |
| 8 | **0,329** | **MAXCO** |
| 9 | **0,328** | **MAX** |
| 10 | 0,296 | 'CCIS' |
| 11 | 0,243 | 'MCNN' |
| 15 | 0,238 | 'CPruner' |

Table 2: 1-NN classifier ranking.

| Rank | 3-NN Classifier | |
|---|---|---|
| # | A×K×R | Name |
| 1 | 0,386 | 'GGA' |
| 2 | 0,382 | 'RMHC' |
| 3 | 0,344 | 'SSMA' |
| 4 | **0,334** | **AVG** |
| 5 | 0,328 | 'CHC' |
| 6 | **0,322** | **MAX** |
| **7** | **0,306** | **MAXCO** |
| 8 | 0,284 | 'RNN' |
| 9 | **0,268** | **WAVG** |
| 10 | 0,244 | 'CCIS' |
| 11 | 0,239 | 'DROP3' |
| 12 | 0,224 | 'HMNEI' |

Table 3: 3-NN classifier ranking.

| Rank | PS exec time (sec) | |
|---|---|---|
| # | Time | Name |
| 14 | 10,073 | 'DROP3' |
| 15 | **52,625** | **MAX** |
| 16 | **52,625** | **MAXCO** |
| 17 | **52,625** | **AVG** |
| 18 | **52,625** | **WAVG** |
| 19 | 80,508 | 'RNG' |
| 20 | 127,942 | 'Recons.' |
| 21 | 372,360 | 'CHC' |
| 22 | 391,666 | 'RMHC' |
| 23 | 513,965 | 'SSMA' |
| 24 | 874,246 | 'RNN' |
| 25 | 1525,734 | 'GGA' |

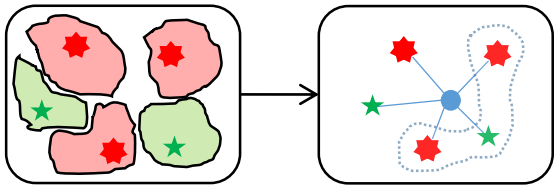
Table 4: Time needed for the prototypes extraction.

# Pattern Recognition: *k*-NN boosting

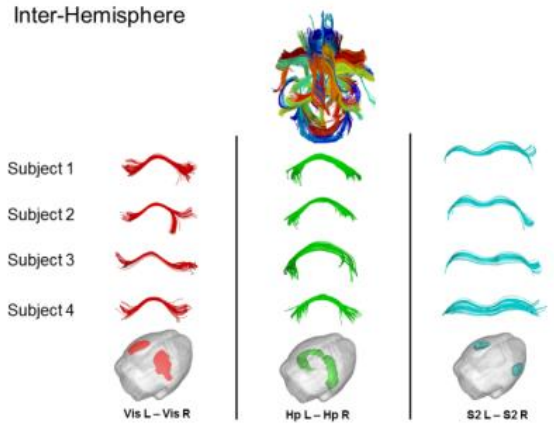
- Method strengthens:
  - Compression rate is around 90%
  - Good balance between accuracy, compression rate and exec time.
  - Time is an order of magnitude faster than the best competitors.
  - Method weakness:
    - Does not scale due to the quadratic requirement of the DS
  - Future work:
    - Extend the approach to handle multiple classes
- Publications:
  - **S Vascon**, M Cristani, M Pelillo, V Murino - Using Dominant Sets for k-NN Prototype Selection - International Conference on Image Analysis and Processing (ICIAP) 2013

# Applications

## Pattern Recognition

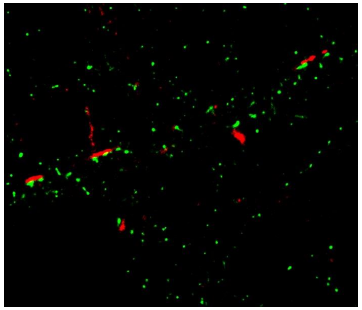


## Brain Connectomics



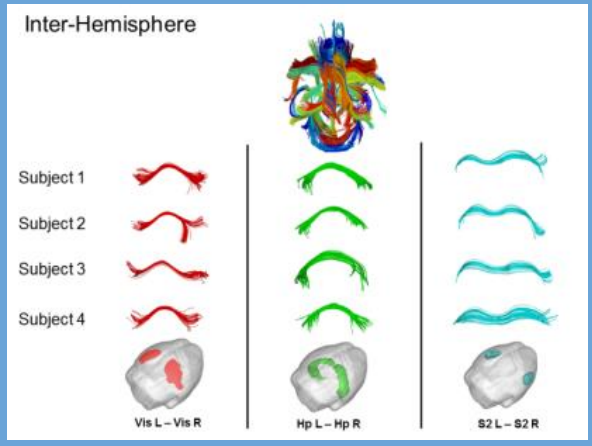

## Human Behavior

## Nano science



# Applications

## Brain Connectomics




## Pattern Recognition

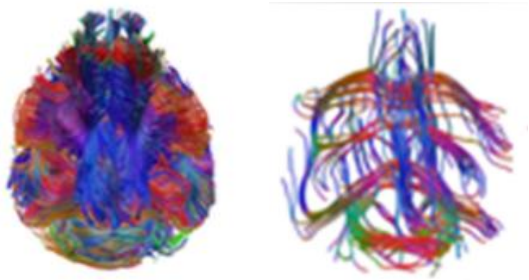
## Human Behavior

## Nano science

# Brain Connectomics: White matter multi-subject clustering

- White matter (WM) is a component of the central nervous system and consists mostly of cells that transmit signals from one region of the cerebrum to another.

- The studies of WM fibers organization is important in the diagnosis of diseases like Alzheimer or Multiple Sclerosis.



- The problem:
  - Simplify the complexity
  - Find common structure across subjects

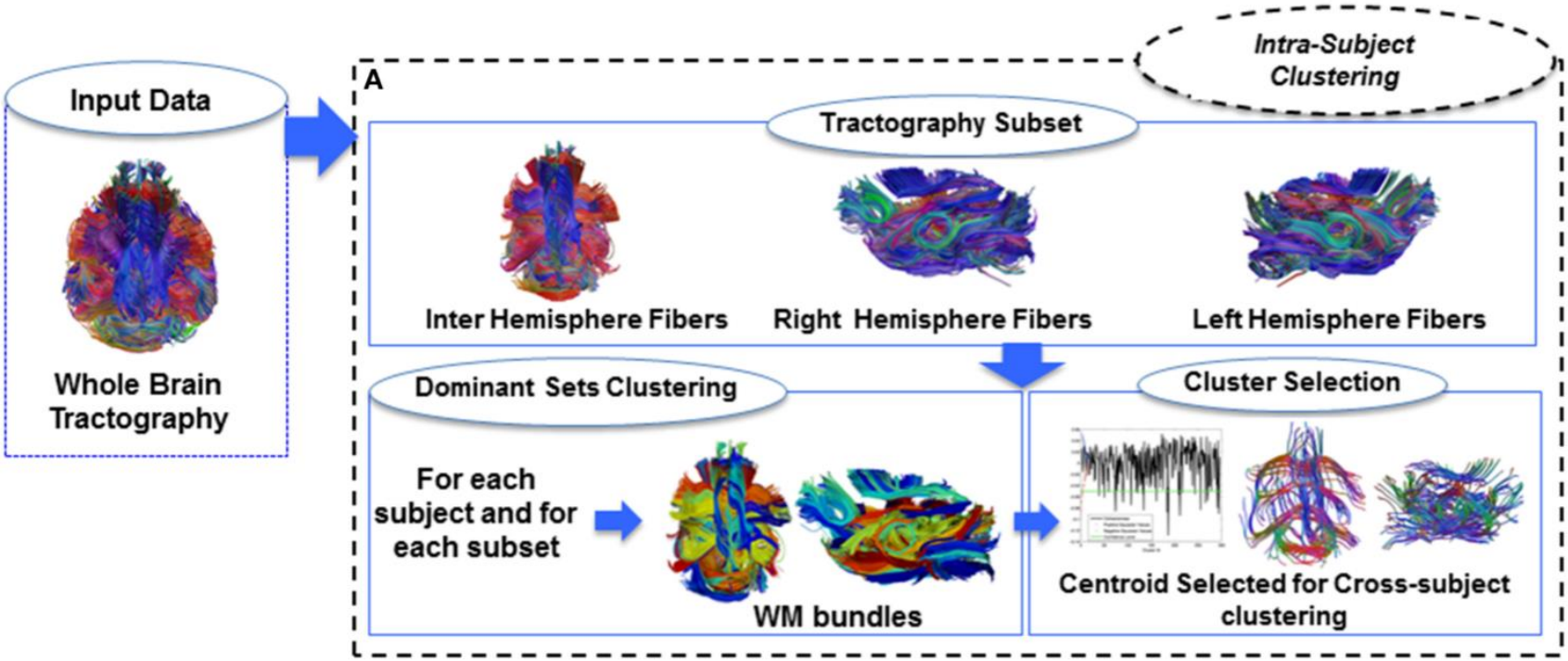
- Why ?
  - Neuroscientist needs an higher level of abstraction (manual investigation is prone to human error)
  - Automatic tool for white matter investigation and brain parcellation
  - Data-driven atlas of the brain avoiding neuroscientists bias

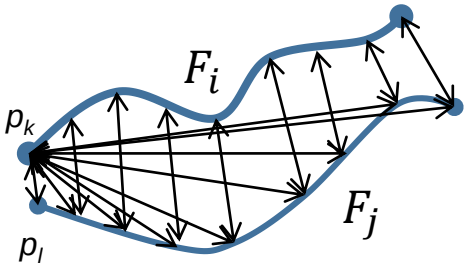
# Brain Connectomics: multi-subject clustering

- Other methods:
  - Hierarchical clustering [1]
  - Spectral clustering [2]
  - Stochastic processes [3]
- Problems:
  - Need an a-priori number of cluster
  - Need an a-priori level of the hierarchy
- Solution, a three steps algorithm:
  1. Reduce the complexity through brain abstraction
  2. Project the subject to a common space (landmark space)
  3. Performing a cross-subject clustering identifying the commonalities

[1] Guevara et al. Automatic fiber bundle segmentation in massive tractography datasets using a multisubject bundle atlas. NI2012
[2] O'Donnell et al. Automatic tractography segmentation using a high-dimensional white matter atlas. IEEET.Med.Img 2007
[3] Wang et al. Tractography segmentation using a hierarchical dirichlet processes mixture model.Neuroimage 2011

# Brain Connectomics: fiber bundle extraction

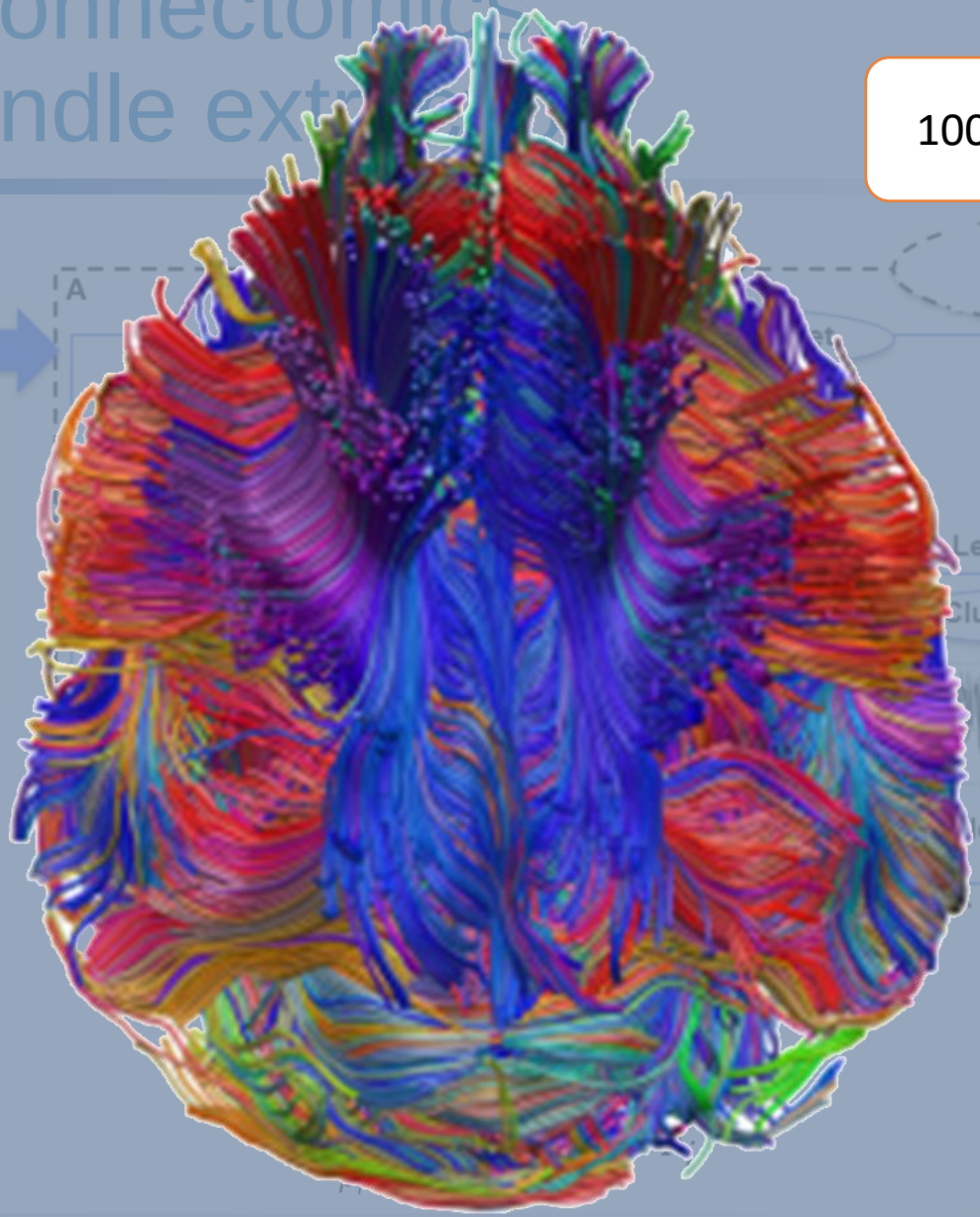



$$d(F_i, F_j) = \frac{1}{2}\left(d_m(F_i, F_j) + d_m(F_j, F_i)\right)$$

$$a_{ij} = \begin{cases} e^{-\frac{d(F_i,F_j)}{\sigma}} \\ 0 \end{cases}$$

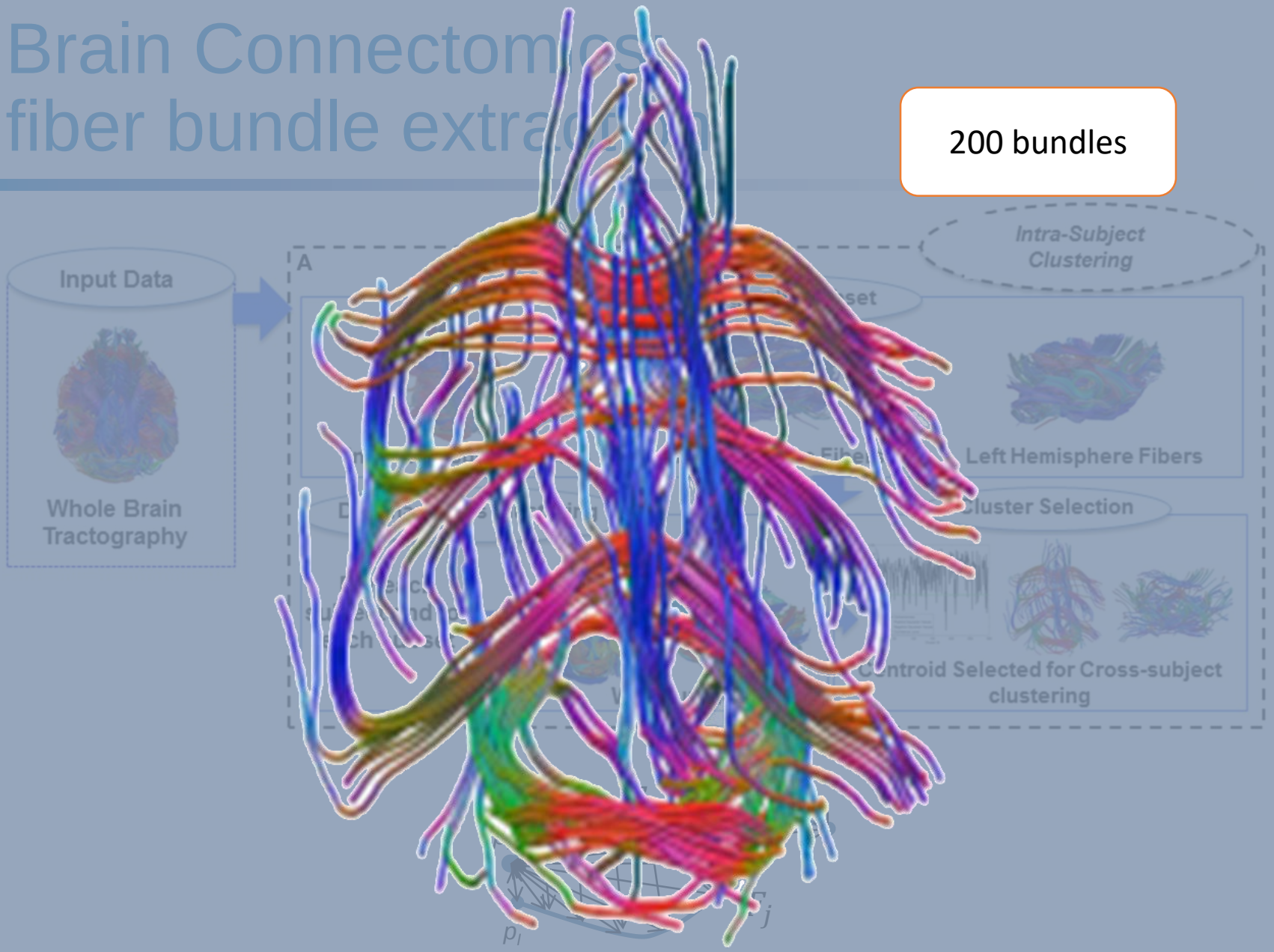
# Brain Connectomics: fiber bundle extr



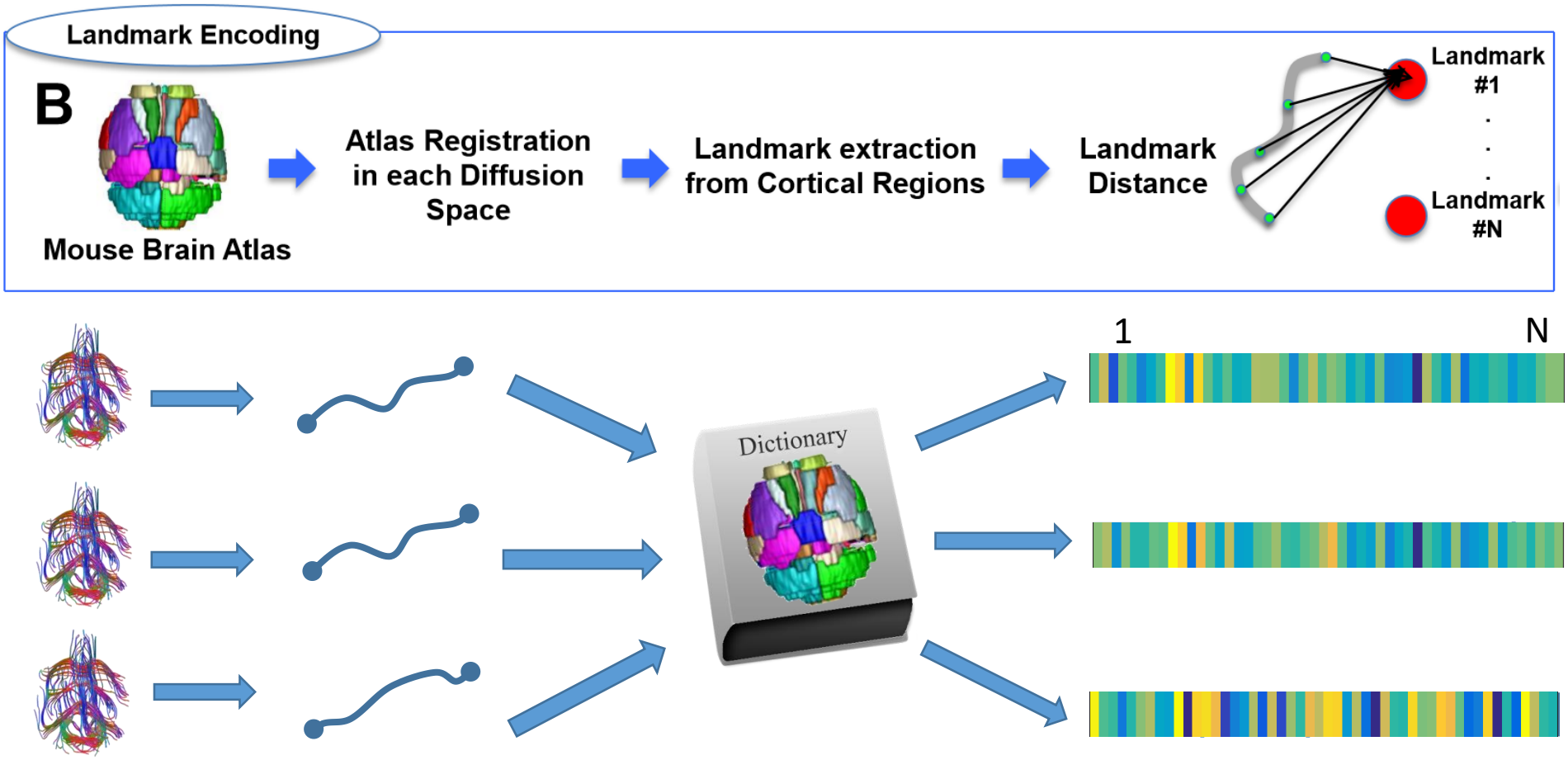
100000 fibers

# Brain Connectomics: fiber bundle extraction

200 bundles

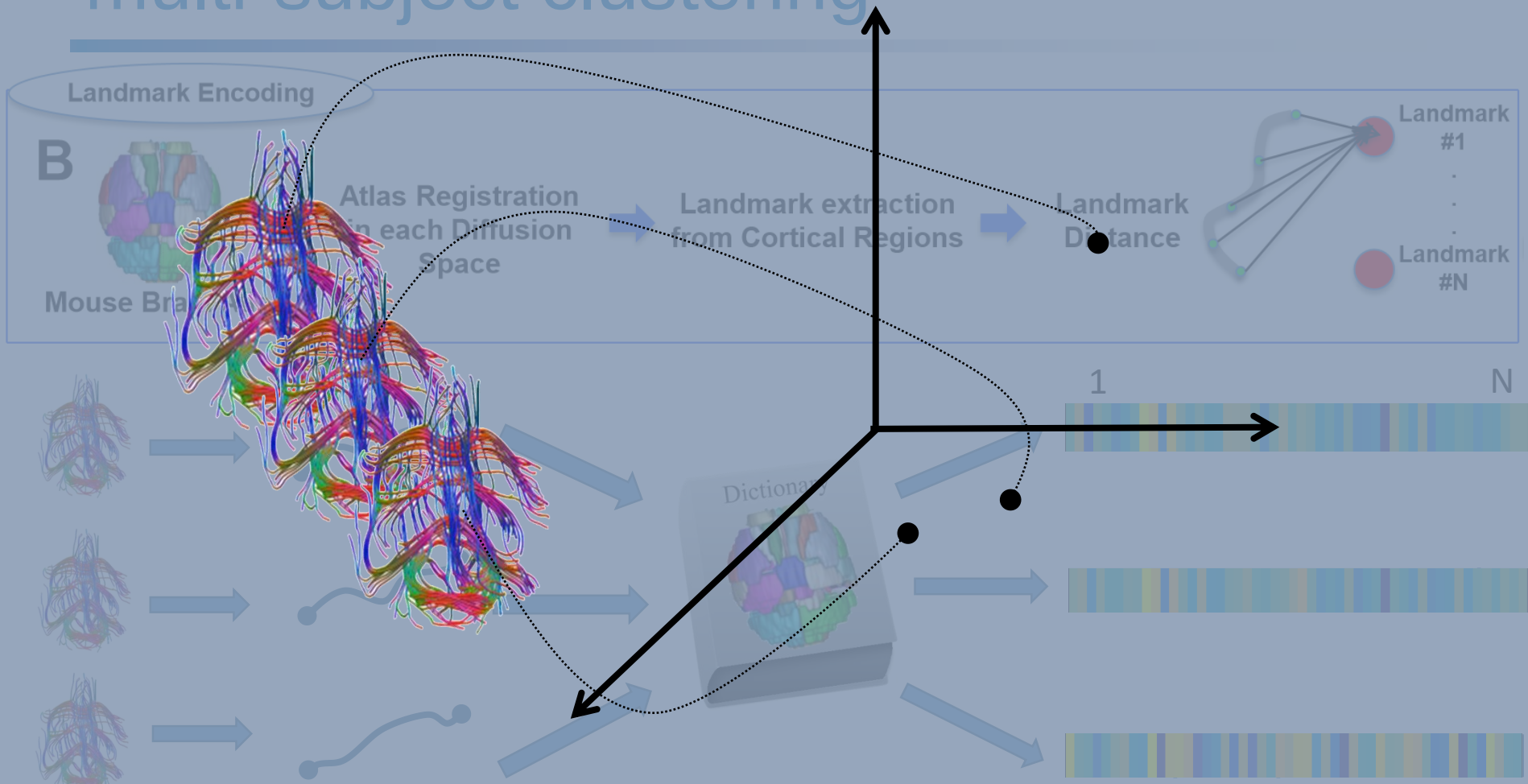


# Brain Connectomics: multi-subject clustering

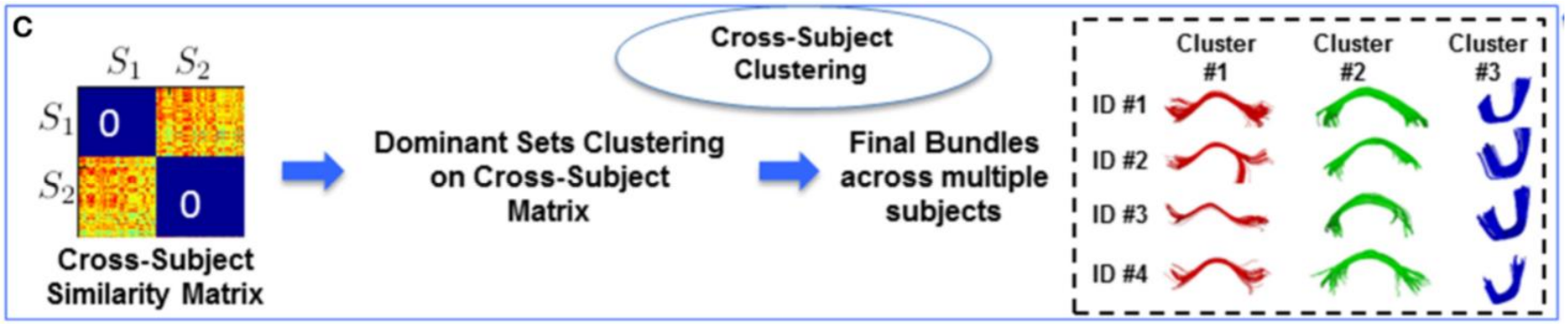


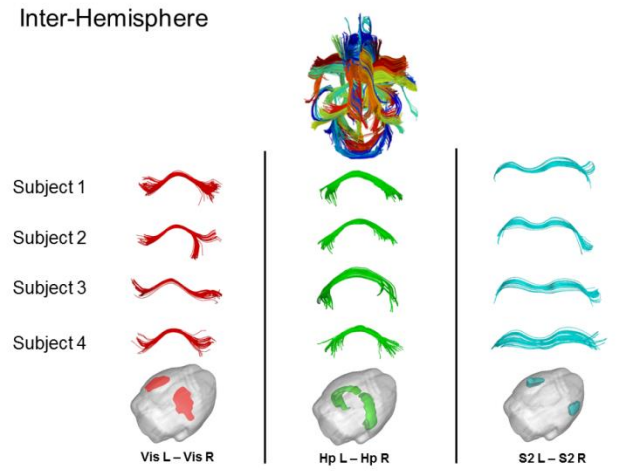
# Brain Connectomics: multi-subject clustering

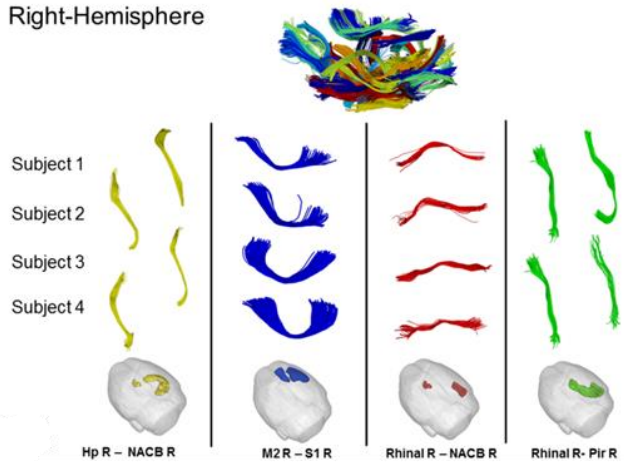
Landmark Space

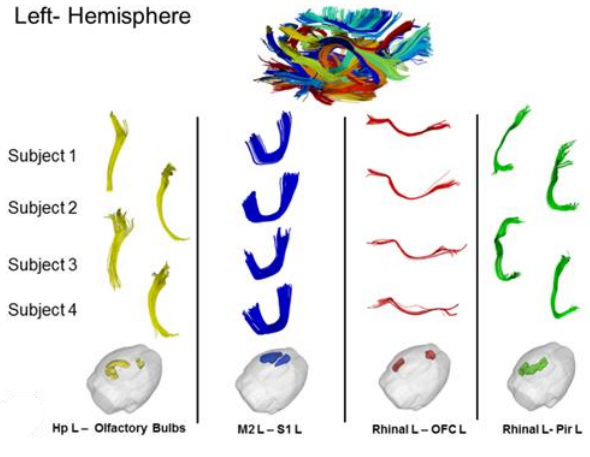


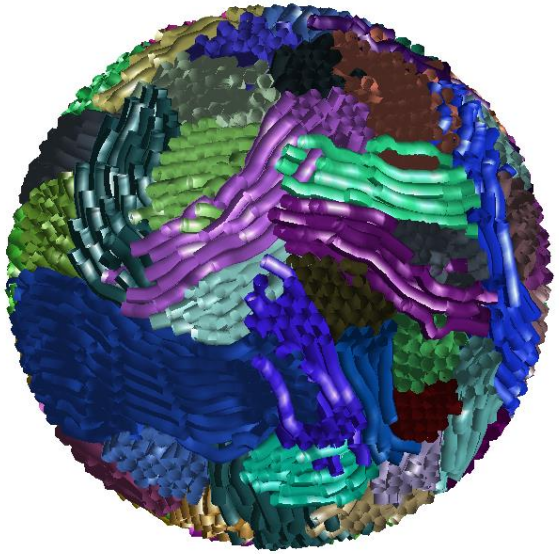
# Brain Connectomics: multi-subject clustering



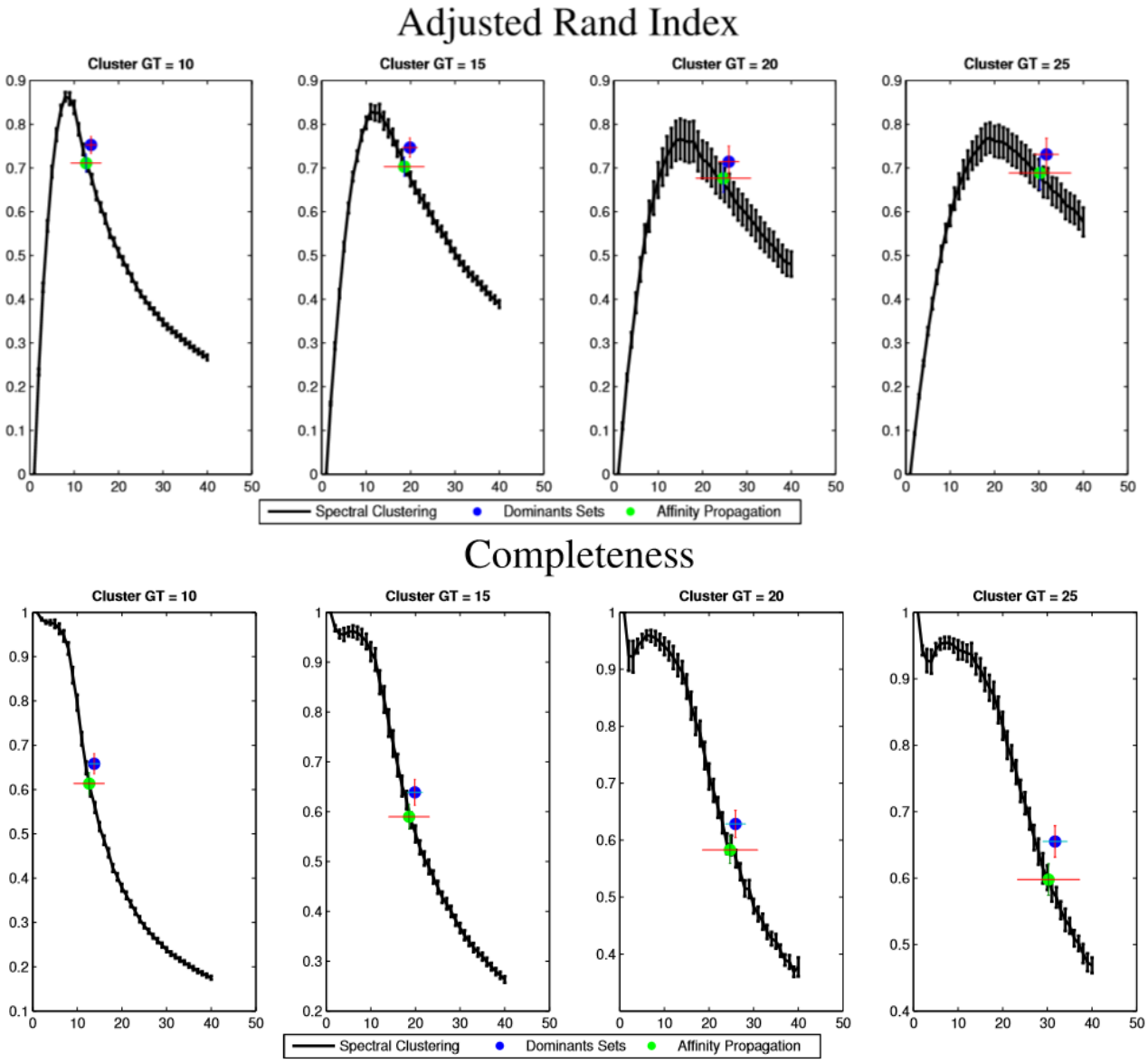





41±4 bundles
870 ± 37 fiber




Close, T. G et al. A software tool to generate simulated white matter structures for the assessment of fibre-tracking algorithms. Neuroimage 2009

# Brain connectomics: Conclusions

- Method strengthens:
  - Automatically extract the bundles (No prior on the number of clusters)
  - No need to register the tractography
  - Designed to cope with large set of subject (thanks to the first reduction)
  - Good performances if compared with both supervised and unsupervised clustering techniques.

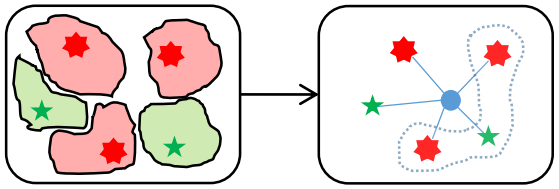
- Method weakness:
  - The method due to the quadratic complexity cannot scale to bigger dataset.

- Future Work:
  - Applied to human data-sets to build an atlas of WM bundles for clinical applications

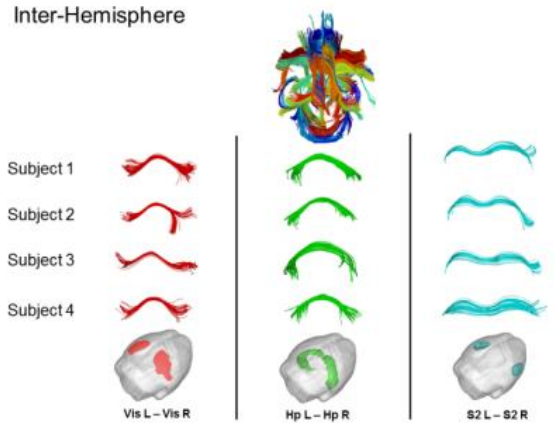
- Publications:
  - L Dodero, **S Vascon**, L Giancardo, A Gozzi, D Sona, V.Murino. Automatic white matter fiber clustering using dominant sets - Pattern Recognition in Neuroimaging (PRNI), 2013
  - **S Vascon**, L Dodero, V Murino, A Bifone, A Gozzi, D.Sona - Automated multi-subject fiber clustering of mouse brain using dominant sets. Fr.NeuroInf 2015

# Applications

## Pattern Recognition

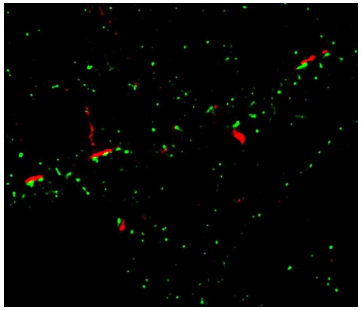


## Brain Connectomics



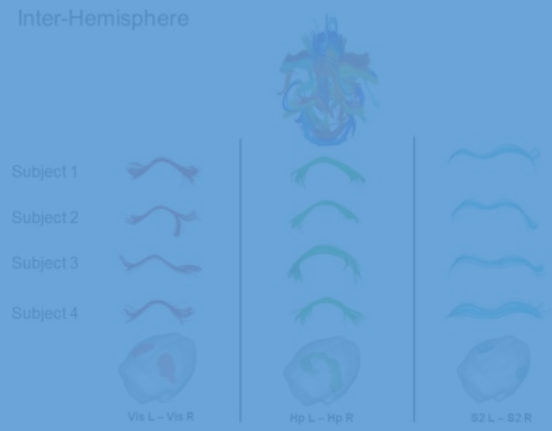

## Human Behavior

## Nano science

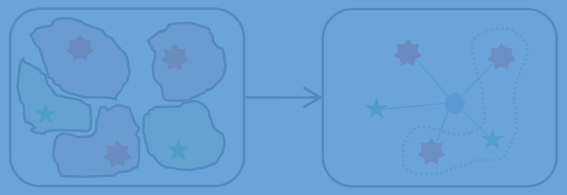


# Applications

## Brain Connectomics




## Pattern Recognition



## Human Behavior

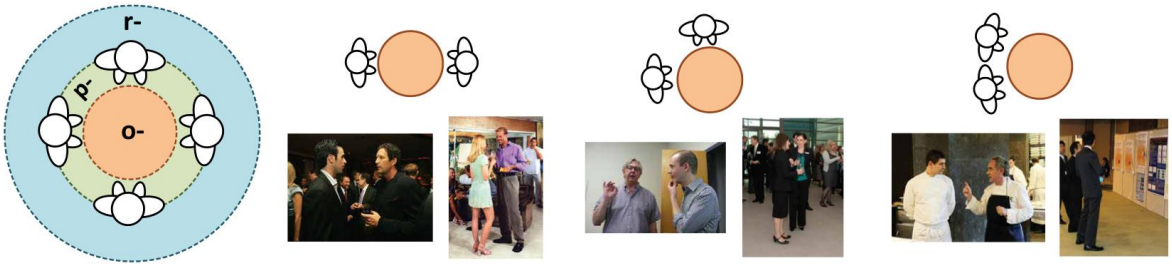
## Nano science

# The problem

- **Tasks:**
  - *Security & Surveillance*: who were with ?
  - *Scene understanding*: are there any groups of people ?
  - *Behavior analysis*: how we join and leave a group ?
  - *Social robotics*: how to interact with humans ?
  - …

- **Problems:**
  - Unreliability of the detectors
  - Grouping in a low density space (few persons per scene)
  - Respecting sociological constraints
  - Respecting biological constraints

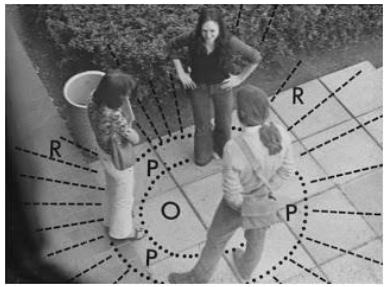
# Constraints




a) *Circular* arrangement b) *Vis-a-vis* arrangement c) *L*-arrangement d) *Side-by-side* arrangement

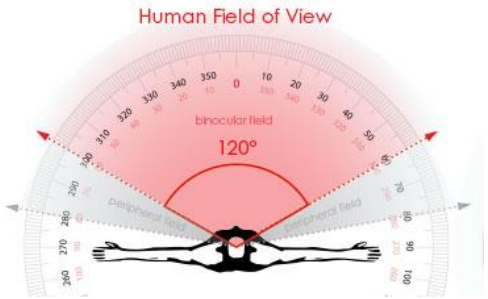
- Sociological constraints:

  F-Formation: "*whenever two or more individuals in close proximity orient their bodies in such a way that each of them has an easy, direct and equal access to every other participant's transactional segment*" [1]




- Biological Constraints:

  *Human field of view is the range [120°- 190°]* [2]

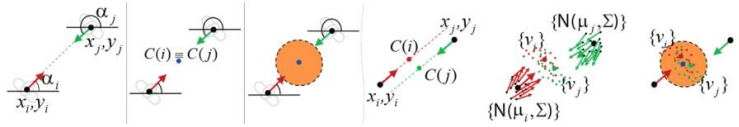



[1] Ciolek, T.M., Kendon, A.: Environment and the Spatial Arrangement of Conversational Encounters. Sociological Inquiry 50 (1980)
[2] I.P. Howard and B.J. Rogers. Binocular Vision and Stereopsis. Oxford psychology series. Oxford University Press, (1995).

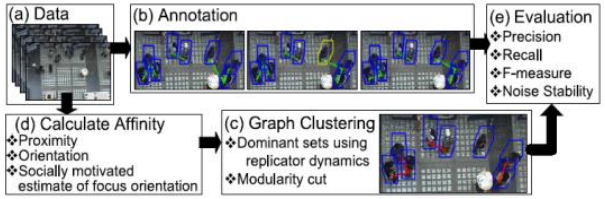
# State of the art

## F-Formation detection algorithms:

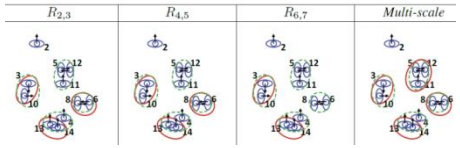
- Hough voting [1]
  - Samples vote for an o-space
  - O-space with the majority of votes is taken.



- Graph Based[2,3]
  - A scene is represented as a weighted graph G.
  - An F-F is found partitioning the graph (graph-cut, max clique)



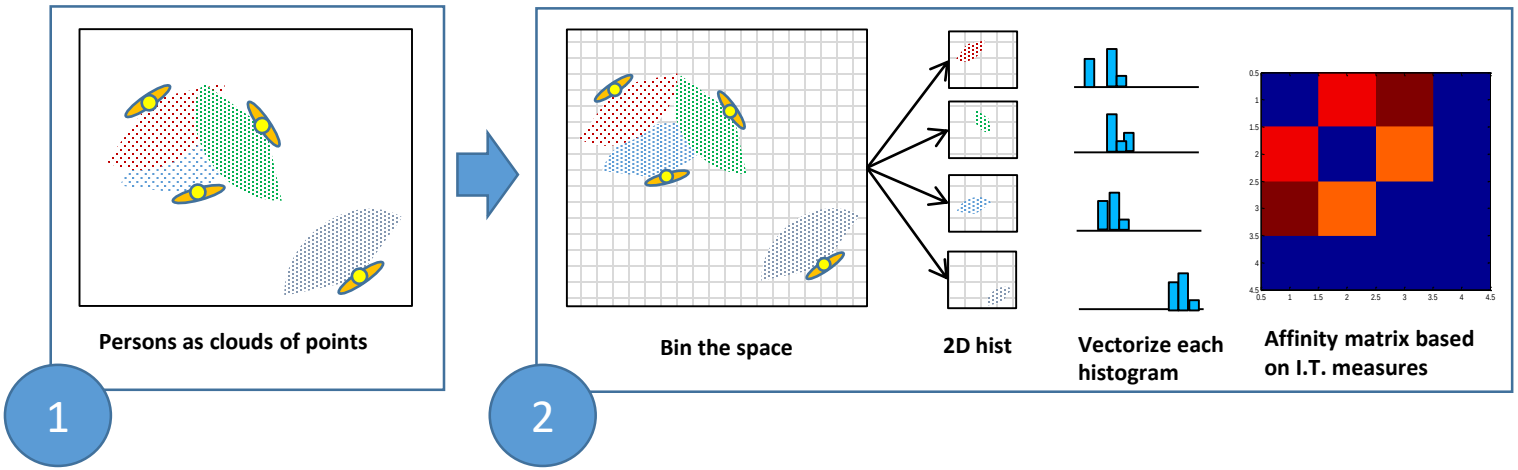

- Multi-Scale [4]
  - Based on [2] Hough Voting schema but for different F-F sizes.



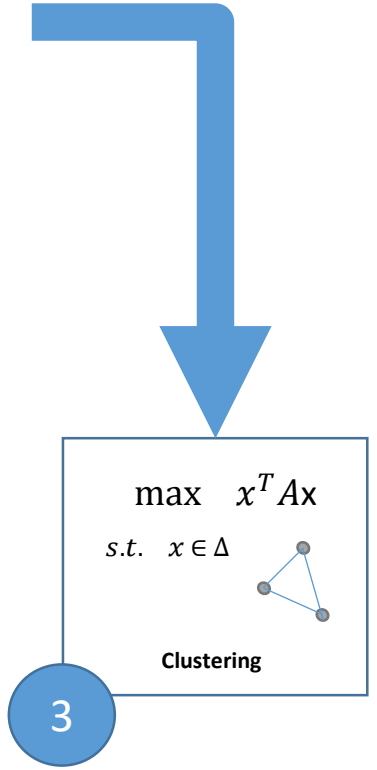


[1] Cristani et al: Social interaction discovery by statistical analysis of F-formations. In: Proc. Of BMVC, BMVA Press (2011)
[2] Hung, H., Krose, B.: Detecting F-formations as dominant sets. In: ICMI. (2011)
[3] Setti, F., Lanz, O., Ferrario, R., Murino, V., Cristani, M.: Multi-Scale F-Formation Discovery for Group Detection. In: ICIP. (2013

# Group Detection: Our method



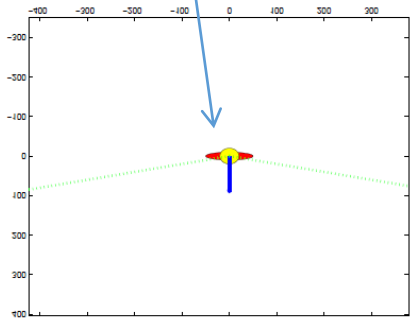

1. **Probabilistic model of Frustum of Visual Attention**
2. **Quantify interactions in a pairwise matrix using Information-Theoretic measures**
3. **Game-theoretic clustering for finding groups**



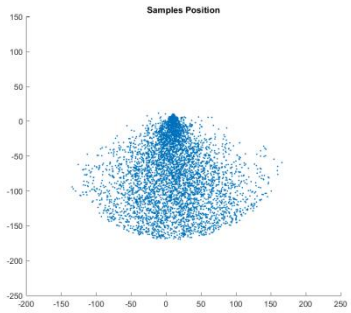
# Our method - 1 Frustum

- A person in a scene is described by his/her position *(x,y)* and the head orientation $\vartheta$
- The frustum of visual attention is defined by an aperture (160°) and by a length $l$ [1].

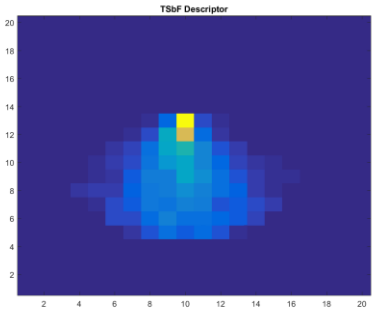
$(x, y, \theta)$



Samples drawn from a Gaussian and a Beta distribution

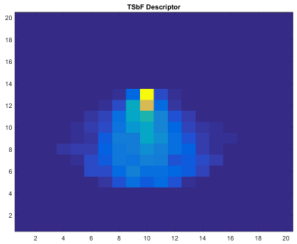



Normalized 2D histogram of the samples. 20x20 grid




[1] Vinciarelli et al. Social Signal Processing: Survey of an emerging domain.IJCV 2009.

# Our method - 2
# Quantify Pairwise Interaction




- Given two histogram $P$ and $Q$ their distance is:

| Kullback-Leibler divergence (A-Sym) | Jensen-Shannon divergence (Sym) |
|---|---|
| $KL(P \mid\mid Q) = \sum_{i=1}^{n} \left( \log(p_i) \frac{p_i}{q_i} \right)$ | $JS(P,Q) = \frac{KL(P \mid\mid M) + KL(Q \mid\mid M)}{2}$ <br> $M = \frac{1}{2}(P+Q)$ |

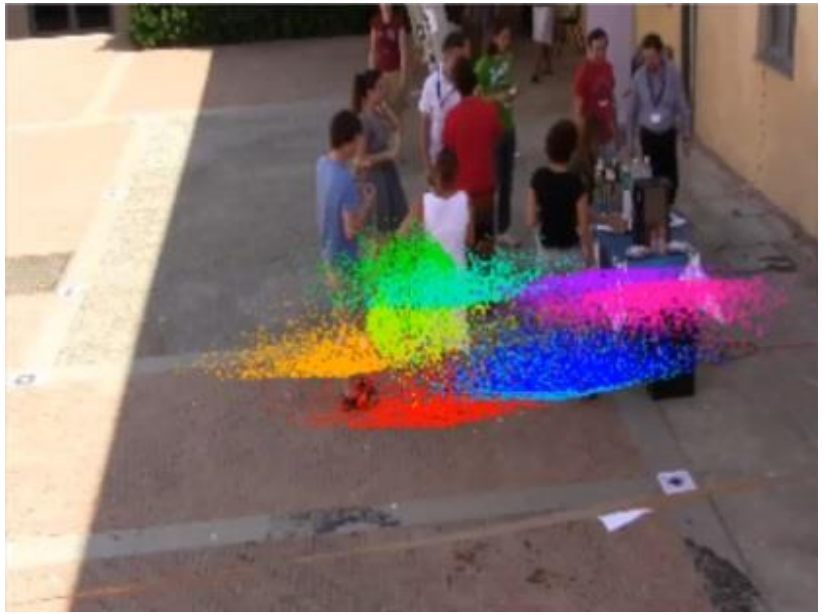
- A measure of affinity is obtained through a Gaussian Kernel

$$a_{P,Q} = exp\left\{ -\frac{d(P,Q)}{\sigma} \right\}$$

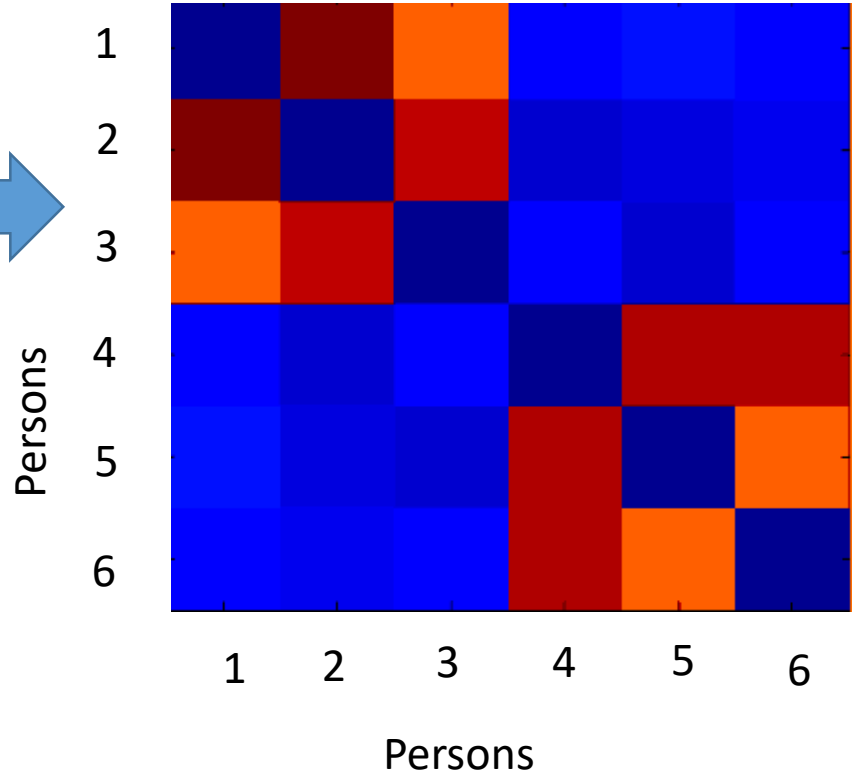
where P,Q are the frustum of two persons, d(…) could be either KL or JS and σ act as normalization term.

# Our method - 2
# Quantify Pairwise Interaction

Frame + Frustum



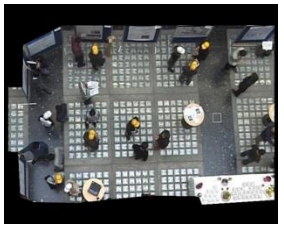
Payoff matrix



# Experiments

| Dataset | #Sequences | #Frames × seq. | Consecutive Frames | Automated Tracking |
|---|---|---|---|---|
| CoffeeBreak | 2 | 45,74 | Y | Y |
| CocktailParty | 1 | 320 | Y | Y |
| GDet | 5 | 132,115,79,17,60 | N | Y |
| PosterData | 82 | 1 | N | N |
| Synth | 10 | 10 | N | N |



- Evaluation criteria:

  As in [1] a group is correctly detected if at least $\left\lceil \frac{2}{3}|G| \right\rceil$ of its members matches the ground truth.

- Metrics: *Precision, Recall, F1-Score* (averaged over the frames)

[1] Setti, F., Hung, H., Cristani, M.: Group Detection in Still Images by F-formation Modeling: a Comparative Study. In: WIAMIS. (2013)

# Results

| | CoffeeBreak (S1+S2) | | | PosterData | | | Gdet | | |
|---|---|---|---|---|---|---|---|---|---|
| *Method* ⋆ | Prec | Rec | F1 | Prec | Rec | F1 | Prec | Rec | F1 |
| IRPM | 0.60 | 0,41 | 0,49 | - | - | - | **-** | **-** | **-** |
| HFF | 0,82 | 0,83 | 0,82 | **0,93** | 0,96 | 0,94 | 0,67 | 0,57 | 0,62 |
| DS | 0,68 | 0,65 | 0,66 | **0,93** | 0,92 | 0,92 | **-** | **-** | **-** |
| MULTISCALE | 0,82 | 0,77 | 0,80 | - | - | - | **-** | **-** | **-** |
| R-GTCG | **0,86** | **0,88** | **0,87** | 0,92 | **0,96** | **0,94** | **0,76** | **0,76** | **0,76** |
| | $\sigma$=0.2 , $l$=145 | | | $\sigma$=0.25 , $l$=115 | | | $\sigma$=0.7 $l$=180 | | |

| | Cocktail Party | | | Synth | | |
|---|---|---|---|---|---|---|
| *Method* ⋆ | Prec | Rec | F1 | Prec | Rec | F1 |
| IRPM | - | - | - | 0,71 | 0,54 | 0,61 |
| HFF | 0,59 | 0,74 | 0,66 | 0,73 | 0,83 | 0,78 |
| MULTISCALE | 0,69 | 0,74 | 0,71 | 0,86 | 0,94 | 0,90 |
| R-GTCG | **0,87** | **0,82** | **0,84** | **1,00** | **1,00** | **1,00** |
| | $\sigma$=0.6 , $l$=170 | | | $\sigma$=0.1 , $l$=75 | | |

# Conclusions

- Method strengthens:
  - Based on sociological and biological constraints
  - No assumption on the size or shape of the F-F
  - Designed to cope with very different realistic scenario
  - Work on top of a tracker or person detection algorithms (15-20 fps)
  - State of the art in all publicly available datasets.
  - Comparable performances on non dedicated datasets.

- Method weakness:
  - Pairwise Affinity matrix does not scale on thousands of detections per frame (unlikely situation)

- Future work:
  - Group tracking

- Publications:
  - A Game-Theoretic Probabilistic Approach for Detecting Conversational Groups.
    **S Vascon**, Z Eyasu, M Cristani, H Hung, M Pelillo, V Murino. Asian Conference in Computer Vision 2014
  - Detecting conversational groups in images and sequences: A robust game-theoretic approach.
    **S Vascon**, EZ Mequanint, M Cristani, H Hung, M Pelillo, V Murino Computer Vision and Image Understanding 2015
  - Group detection and tracking with sociological features. **S.Vascon**, L.Bazzani. Book chapter *submitted*