

# Visual Analytics in Bio-Medical Applications

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- “Visual Analytics is the science of analytical reasoning supported by a highly interactive visual interface.” [Wong and Thomas 2004]
- “Visual Analytics combines **automated analysis techniques** with **interactive visualisations** for an effective **understanding, reasoning and decision making** on the basis of **very large and complex datasets**” [Keim 2010]



- First step: preprocess and transform data
  - Data cleaning, normalization, grouping, data fusion

- **Automated methods**

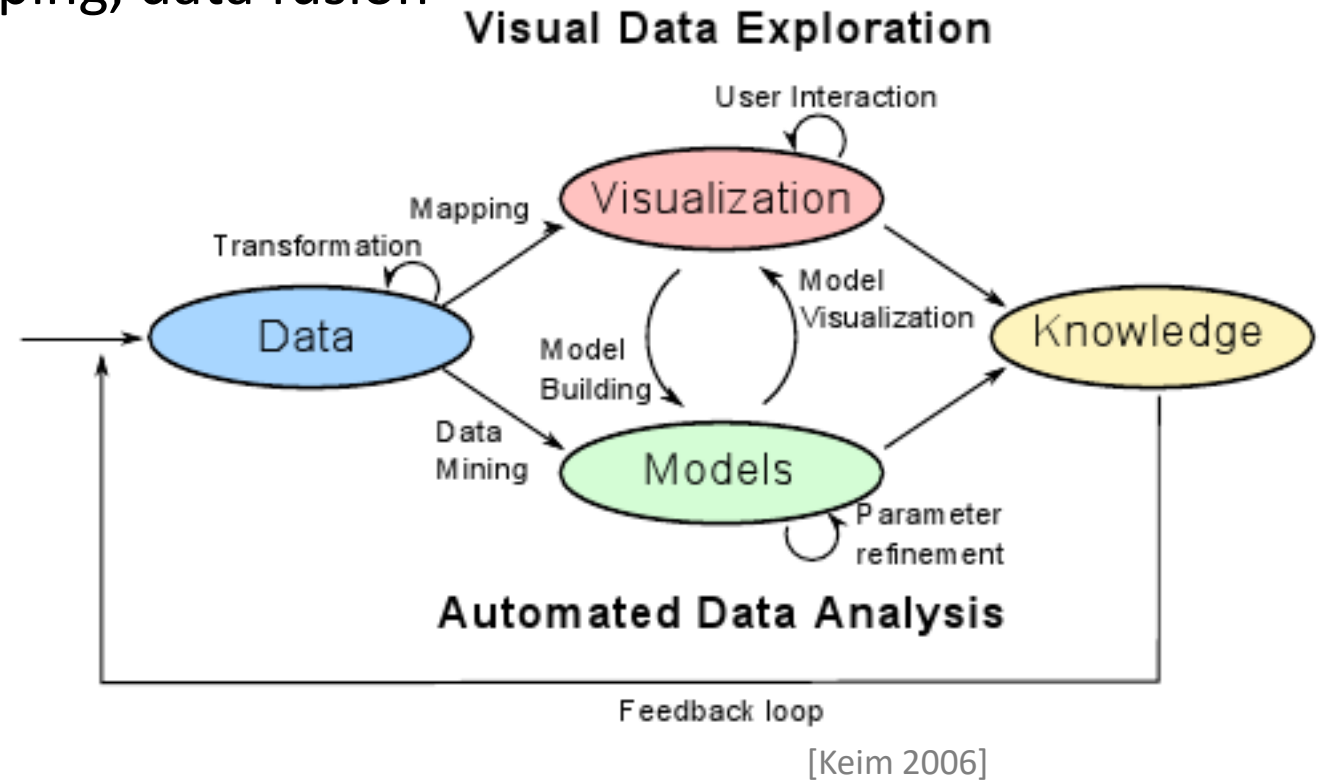
- + Scale well
- Get stuck in local optima
- Run in a black box fashion

- **Visualization**

- + Interactive data analysis
- Scalability

- Visual Analytics integrates both

- Tied together by the user
- Alternating between visual and automatic methods

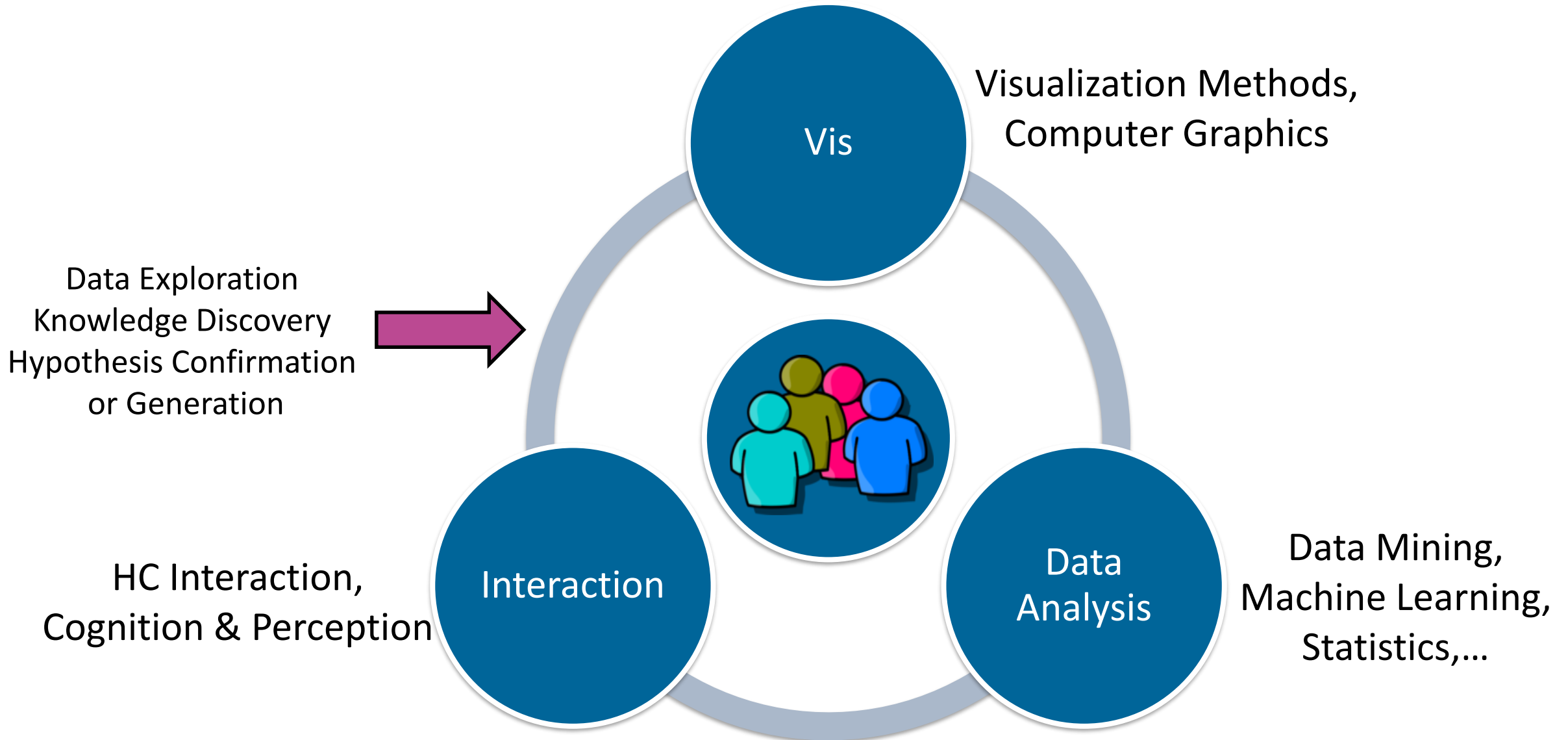


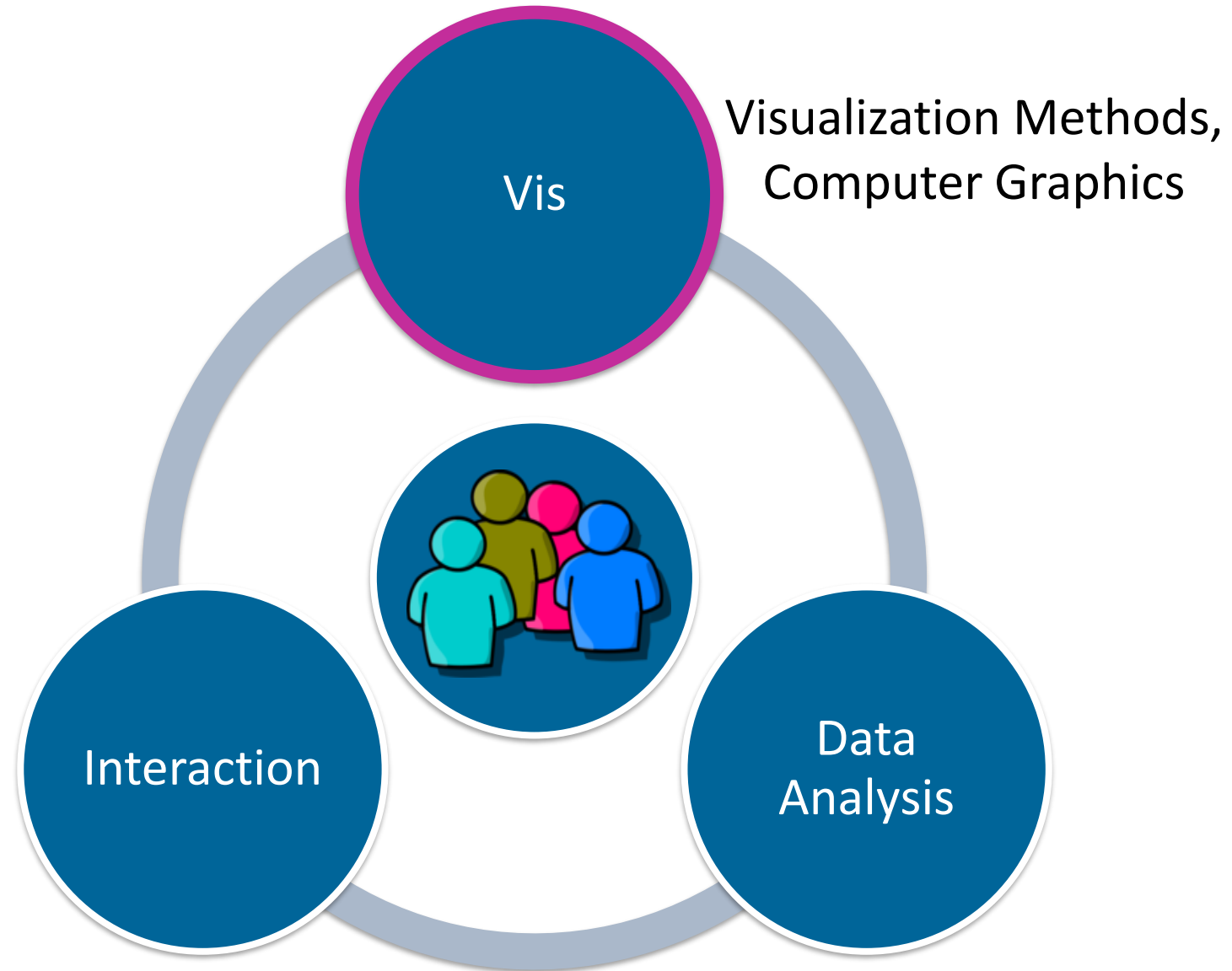
Creation of tools and techniques to enable users to:

- Synthesize information and derive insight from massive, dynamic, ambiguous, and often conflicting data
- Detect the expected and discover the unexpected
- Provide timely, defensible, and understandable assessments
- Communicate these assessment effectively for action



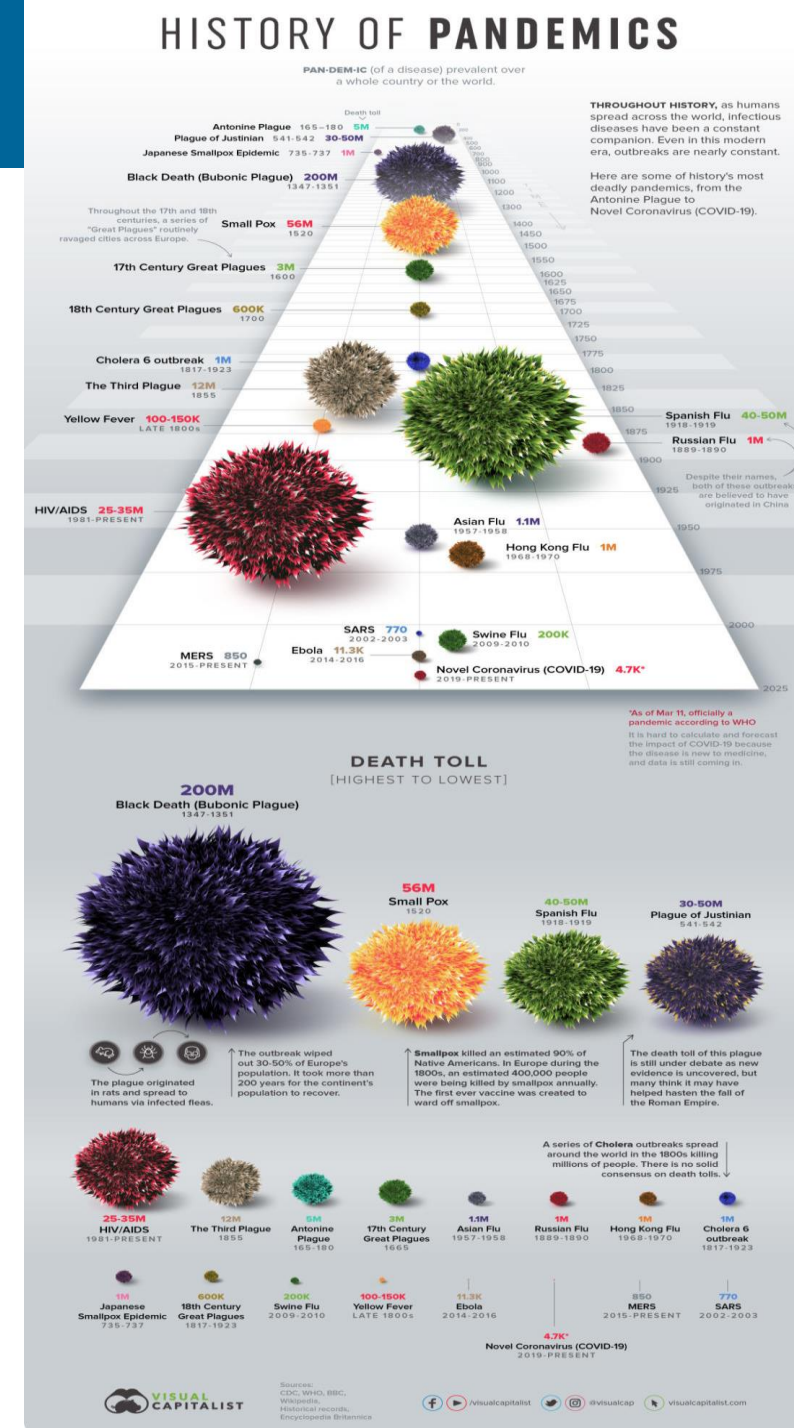






# Why Graphics?

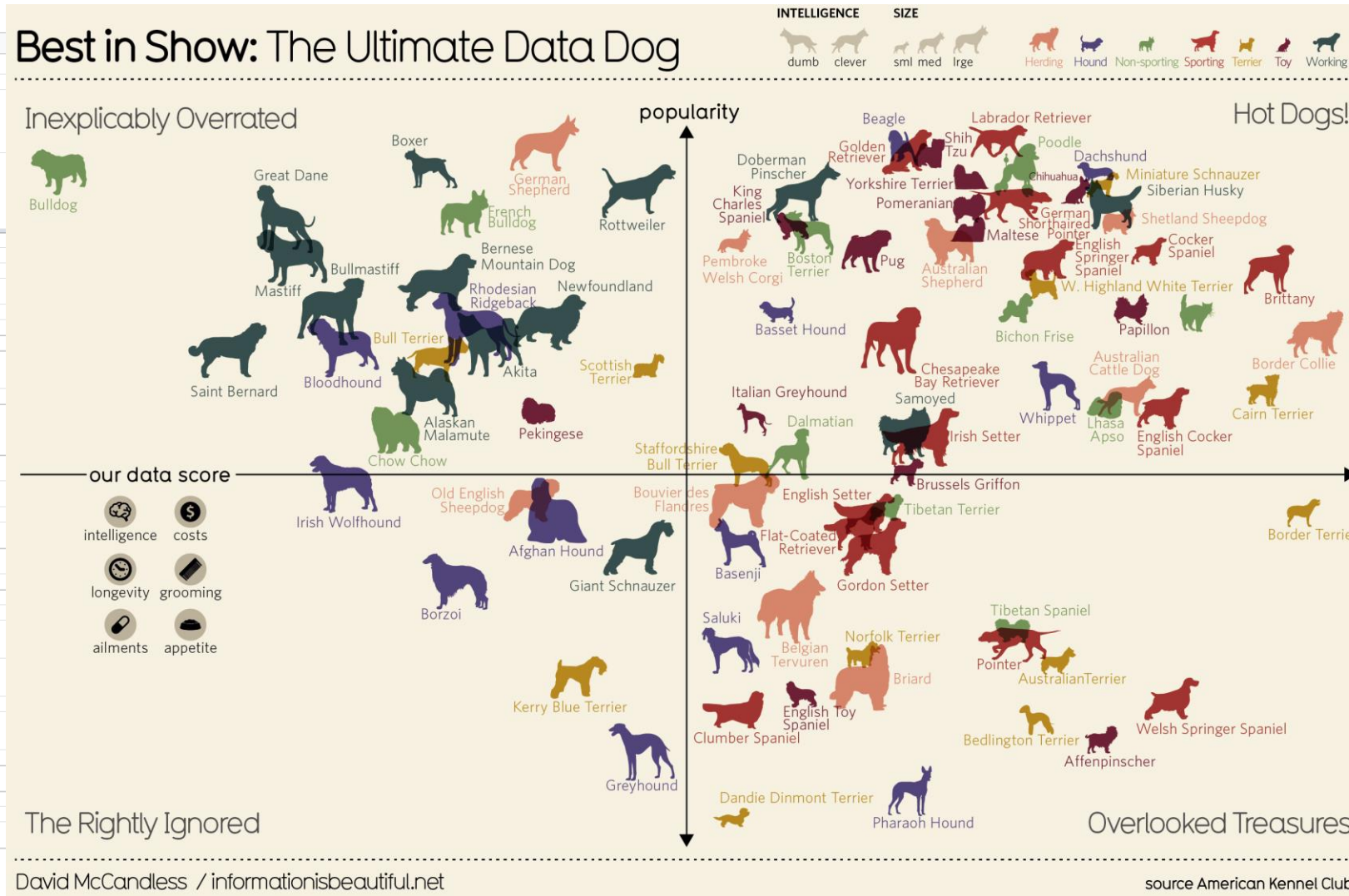
- Figures are **richer**; provide more information with less clutter and in less space.
- Figures provide the ‘Gestalt’ effect: they give an overview; **make structure more visible**.
- Figures are **more accessible**, easier to understand, **faster to grasp**, more comprehensible, **more memorable**, more fun, and less formal.



# Why Graphics?

“The art of making the unseen visible” [Clifford Pickover]

	A	B	C	D	E
1	Best in show?	largest value			
2	we rated 87 dog breeds	smallest value			
3	Sources - see bottom right Dog breed	category		datadog score	
4		American Kennel Club group			
5	Border Collie	herding		3.64	
6	Border Terrier	terrier		3.61	
7	Brittany	sporting		3.54	
8	Cairn Terrier	terrier		3.53	
9	Welsh Springer Spaniel	sporting		3.34	
10	English Cocker Spaniel	sporting		3.33	
11	Cocker Spaniel	sporting		3.3	
12	Papillon	toy		3.26	
13	Australian Cattle Dog	herding		3.25	
14	Shetland Sheepdog	herding		3.22	
15	Siberian Husky	working		3.22	
16	Lhasa Apso	non-sporting		3.21	
17	Affenpinscher	toy		3.2	
18	Dachshund	hound		3.19	
19	Miniature Schnauzer	terrier		3.19	
20	Chihuahua	toy		3.15	
21	Australian Terrier	terrier		3.11	
22	Whippet	hound		3.11	
23	English Springer Spaniel	sporting		3.09	
24	West Highland White Terrier	terrier		3.08	
25	Bedlington Terrier	terrier		3.07	
26	Poodle	non-sporting		3.04	
27	Bichon Frise	non-sporting		3.03	
28	German Shorthaired Pointer	sporting		3.03	
29	Pointer	sporting		3.03	
30	Tibetan Spaniel	non-sporting		3.02	
31	Labrador Retriever	sporting		2.97	
32	Maltese	toy		2.93	



	AA	AB	AC
1			
2			
3	ULTIMATE TOP DATA DOG MEGA RANKING - without kids	ULTIMATE TOP DATA DOG MEGA RANKING - with kids	ULTIMATE TOP DATA DOG MEGA SCORE
4			intelligenece + longevity + ailments + 50% (purchase price + food costs + grooming score). highest possible score: 4.5
5	1	29	3.64
6	2	1	3.61
7	3	11	3.54
8	4	2	3.53
9	5	4	3.34
10	6	5	3.33
11	7	6	3.30
12	8	22	3.26
13	9	52	3.25
14	11	8	3.22
15	10	3	3.22
16	12	7	3.21
17	13	26	3.20
18	14	54	3.19
19	14	27	3.19
20	16	55	3.15
21	17	30	3.11
22	17	30	3.11
23	19	9	3.09
24	20	10	3.08
25	21	35	3.07
26	22	39	3.04
27	25	16	3.03
28	23	12	3.03
29	24	13	3.03
30	26	14	3.02
31	27	15	2.97
32	29	65	2.93



**Anscombe's quartet**

I		II		III		IV	
x	y	x	y	x	y	x	y
10.0	8.04	10.0	9.14	10.0	7.46	8.0	6.58
8.0	6.95	8.0	8.14	8.0	6.77	8.0	5.76
13.0	7.58	13.0	8.74	13.0	12.74	8.0	7.71
9.0	8.81	9.0	8.77	9.0	7.11	8.0	8.84
11.0	8.33	11.0	9.26	11.0	7.81	8.0	8.47
14.0	9.96	14.0	8.10	14.0	8.84	8.0	7.04
6.0	7.24	6.0	6.13	6.0	6.08	8.0	5.25
4.0	4.26	4.0	3.10	4.0	5.39	19.0	12.50
12.0	10.84	12.0	9.13	12.0	8.15	8.0	5.56
7.0	4.82	7.0	7.26	7.0	6.42	8.0	7.91
5.0	5.68	5.0	4.74	5.0	5.73	8.0	6.89



Statistics profile is the same for all!

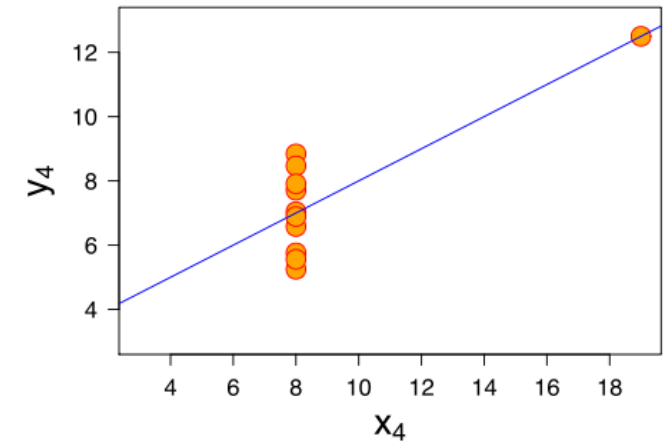
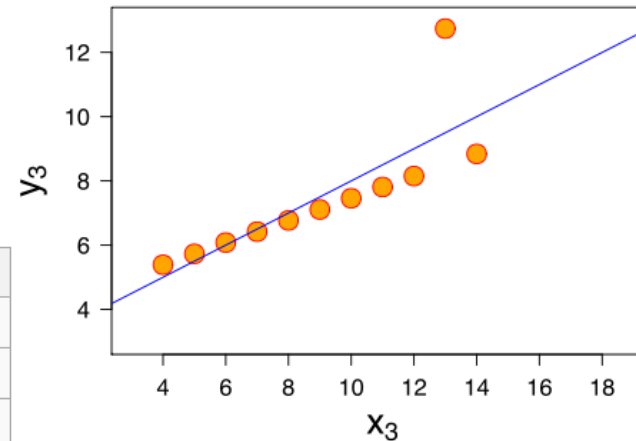
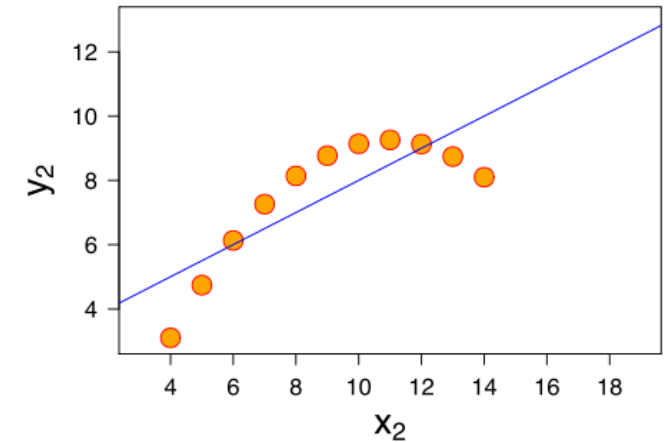
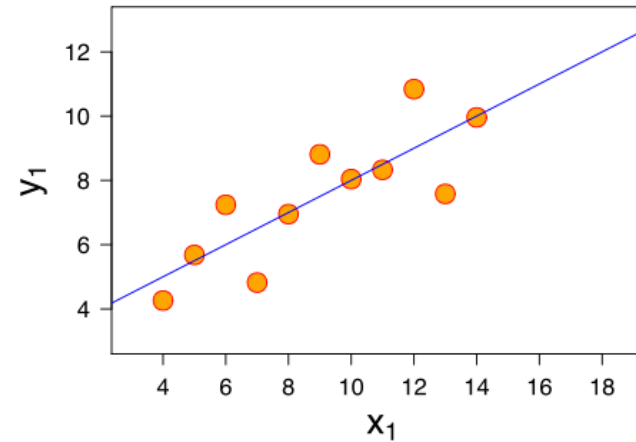
Property	Value
Mean of $x$ in each case	9 (exact)
Variance of $x$ in each case	11 (exact)
Mean of $y$ in each case	7.50 (to 2 decimal places)
Variance of $y$ in each case	4.122 or 4.127 (to 3 decimal places)
Correlation between $x$ and $y$ in each case	0.816 (to 3 decimal places)
Linear regression line in each case	$y = 3.00 + 0.500x$ (to 2 and 3 decimal places, respectively)





# Anscombe's Quartet

Four datasets that have identical simple statistical properties, yet appear very different when graphed.



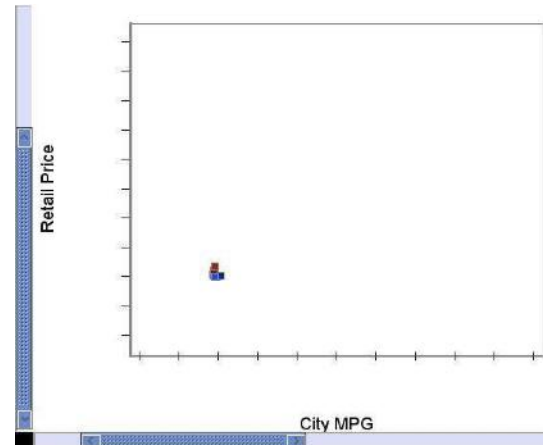
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Wikimedia Commons

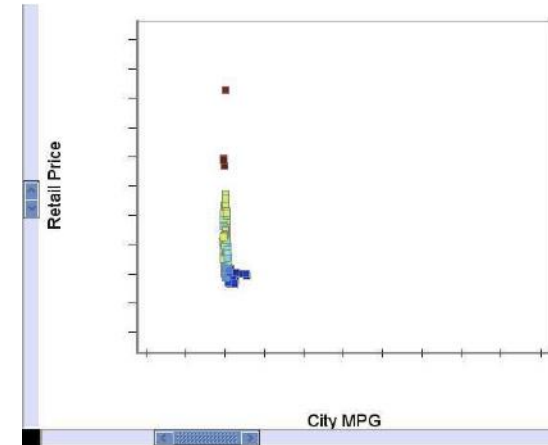


[Ward, Grinstein, Keim 2011]

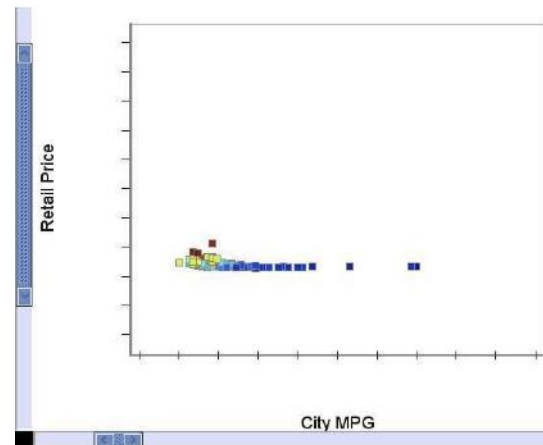
The same data plotted with different scales is perceived dramatically differently.



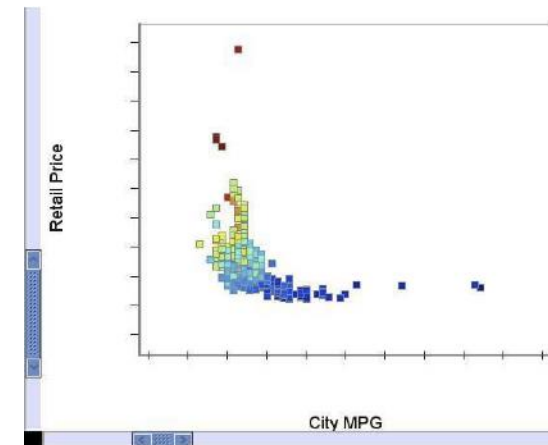
(a) Equally (uniformly) large scale in both x and y



(b) Large scale in x



(c) Large scale in y



(d) Scale determined by range of x- and y-values.



Overview first, zoom/filter, details on demand

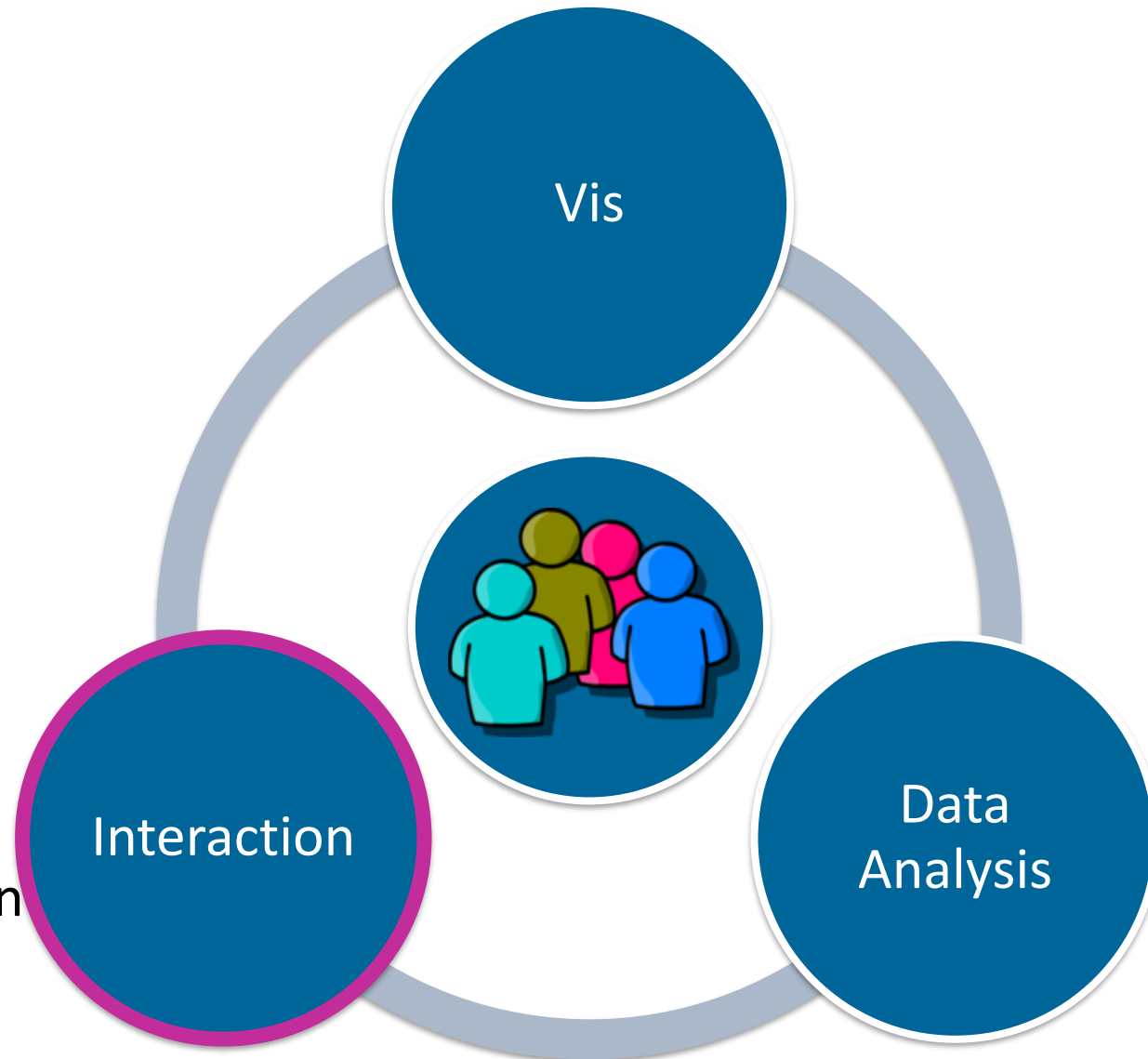
[Shneiderman, 1996]

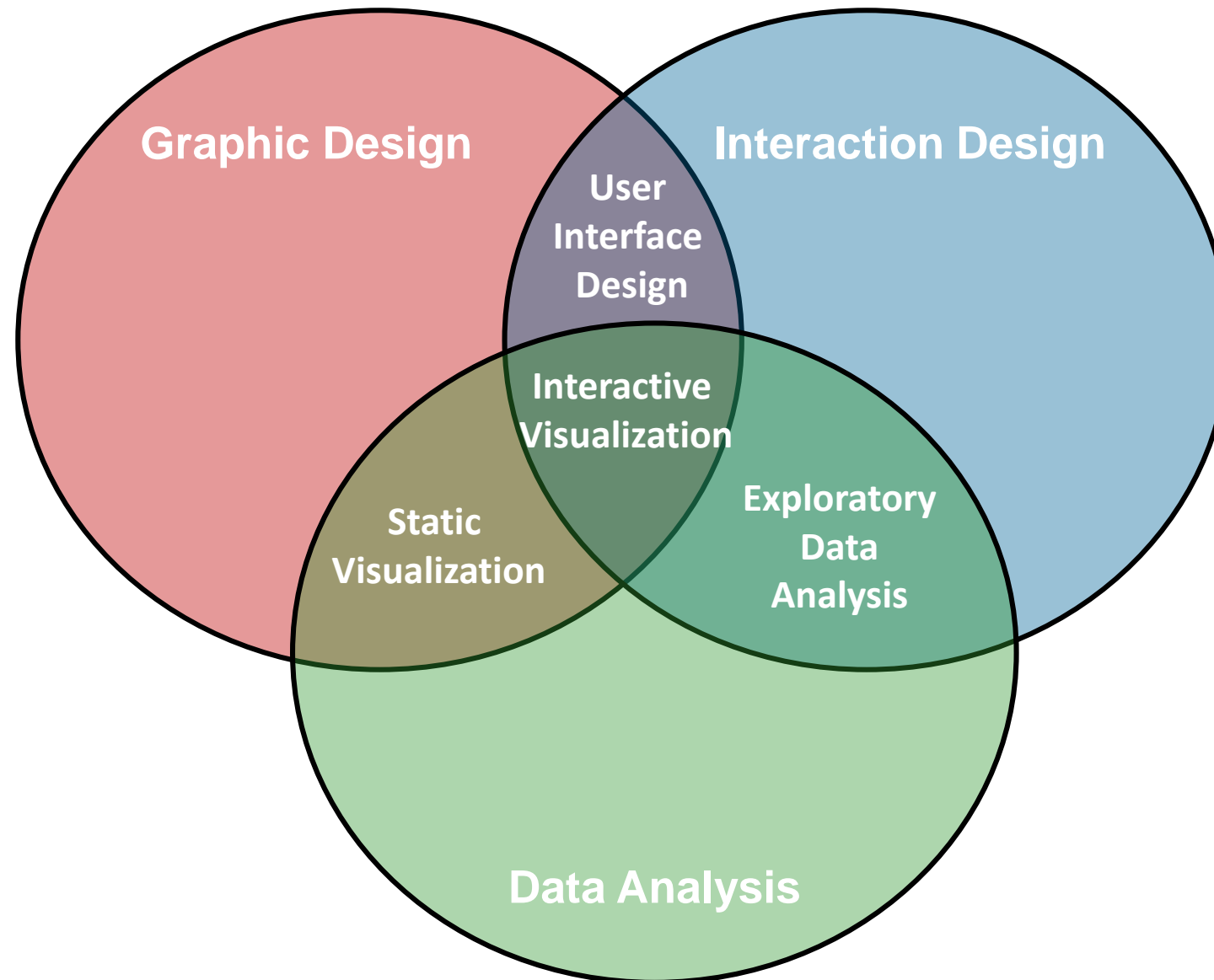


Analyze first, show the important, zoom/filter, analyze further,  
details on demand [Keim, 2006]

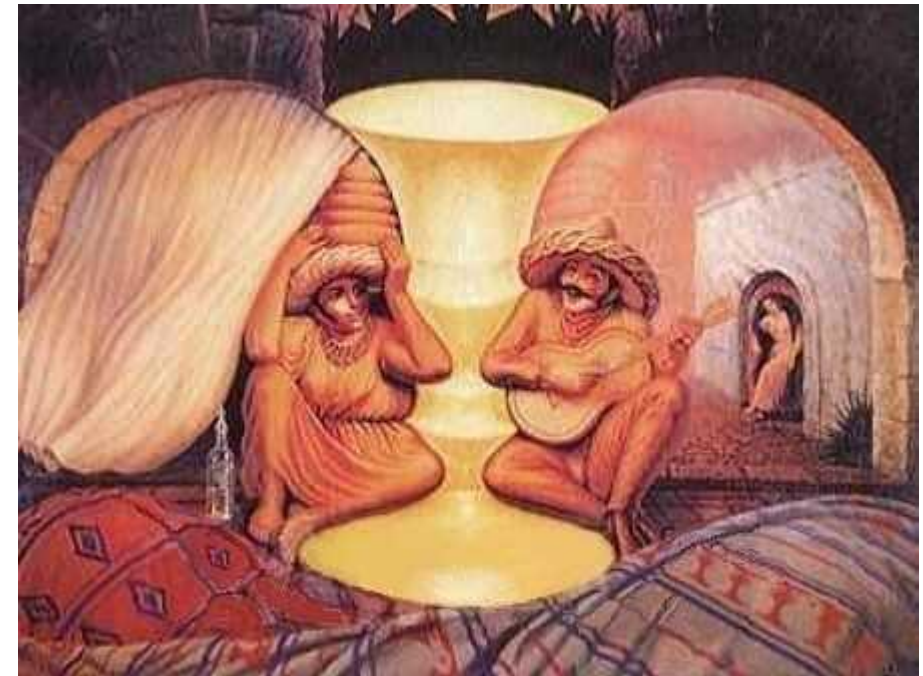
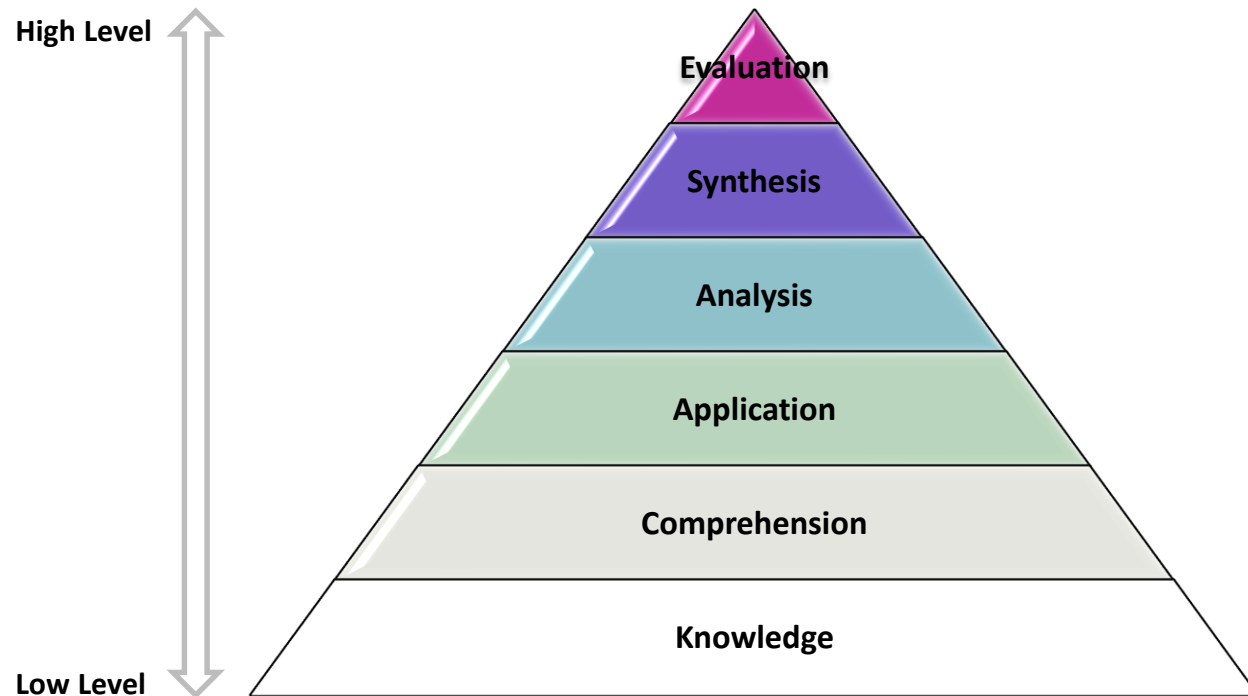


HC Interaction,  
Cognition & Perception

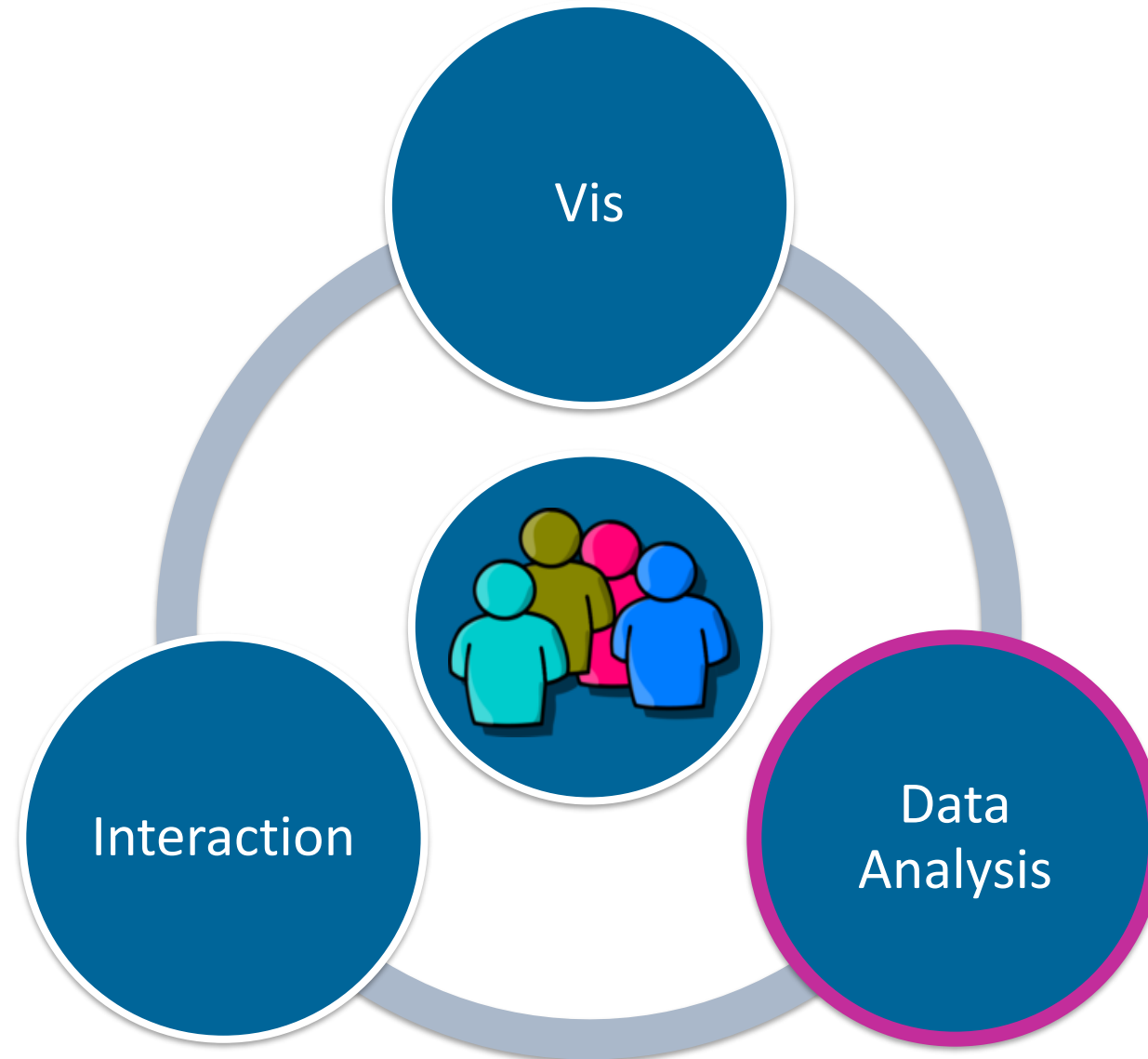




- Cognition: the **mental processes** which assist us to remember, think, know, judge, solve problems, etc.
- Perception: the process by which we interpret the things around us **through sensory stimuli**.

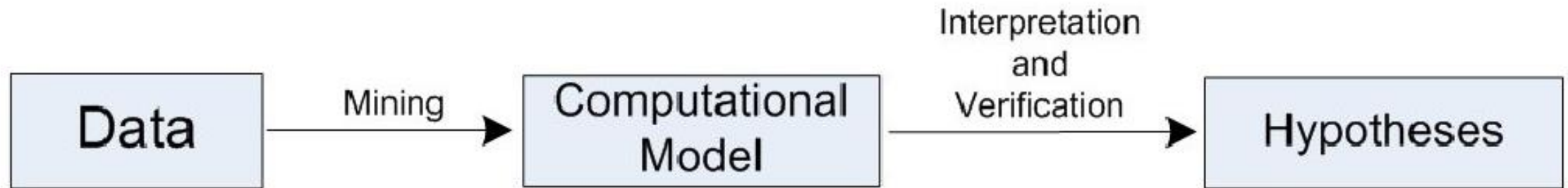






Data Mining,  
Machine Learning,  
Statistics,...

Automatic algorithmic extraction of valuable information  
from raw data



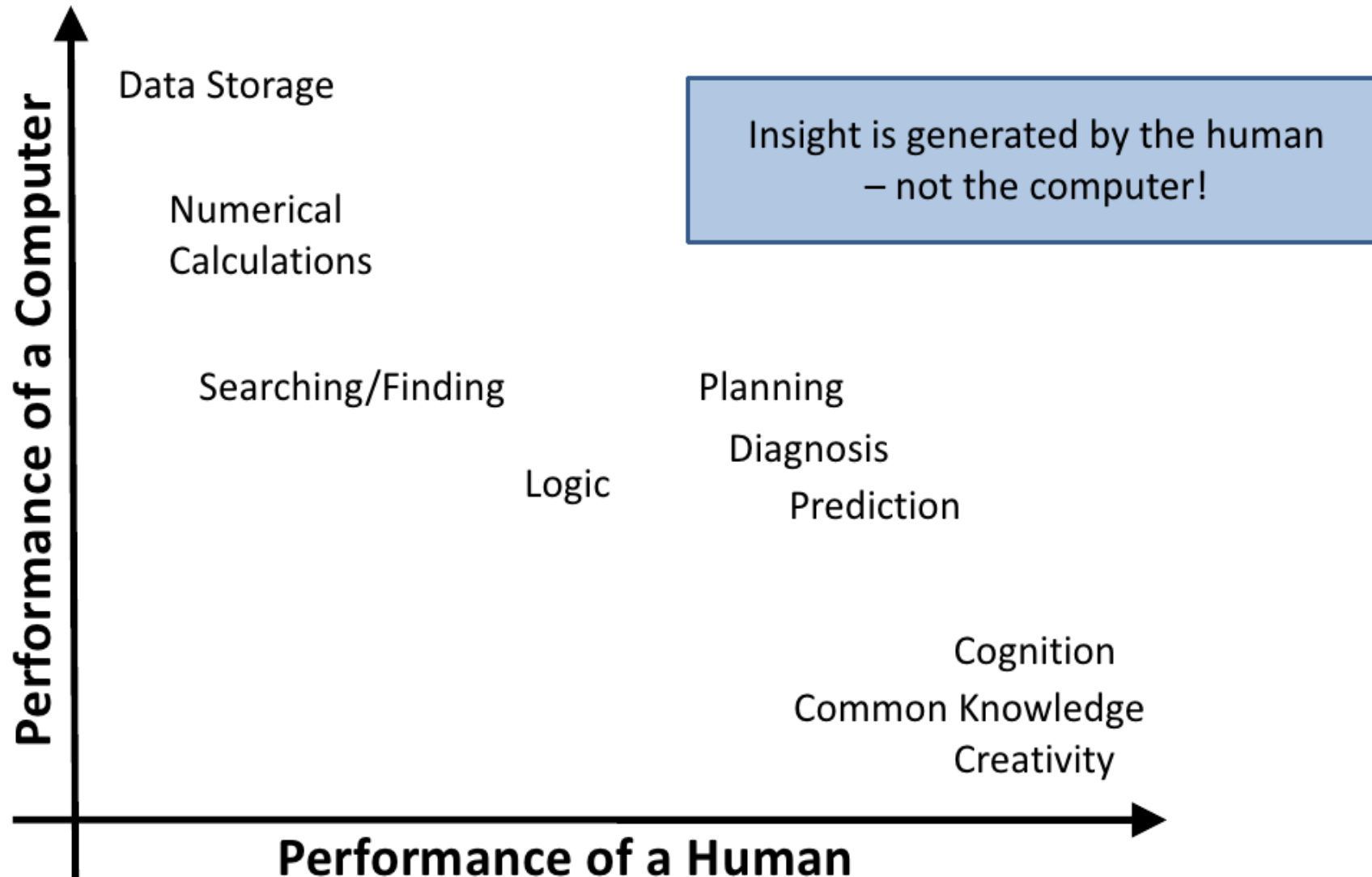
Descriptive vs. Predictive tasks



- Semi or fully automated analysis of massive data sets
- Contributions are more about general methodologies
- Black-box methods in the hands of end users
  - Users need to understand the algorithms for using them
  - What attributes to use? What similarity measure? etc.
  - Often trial and error



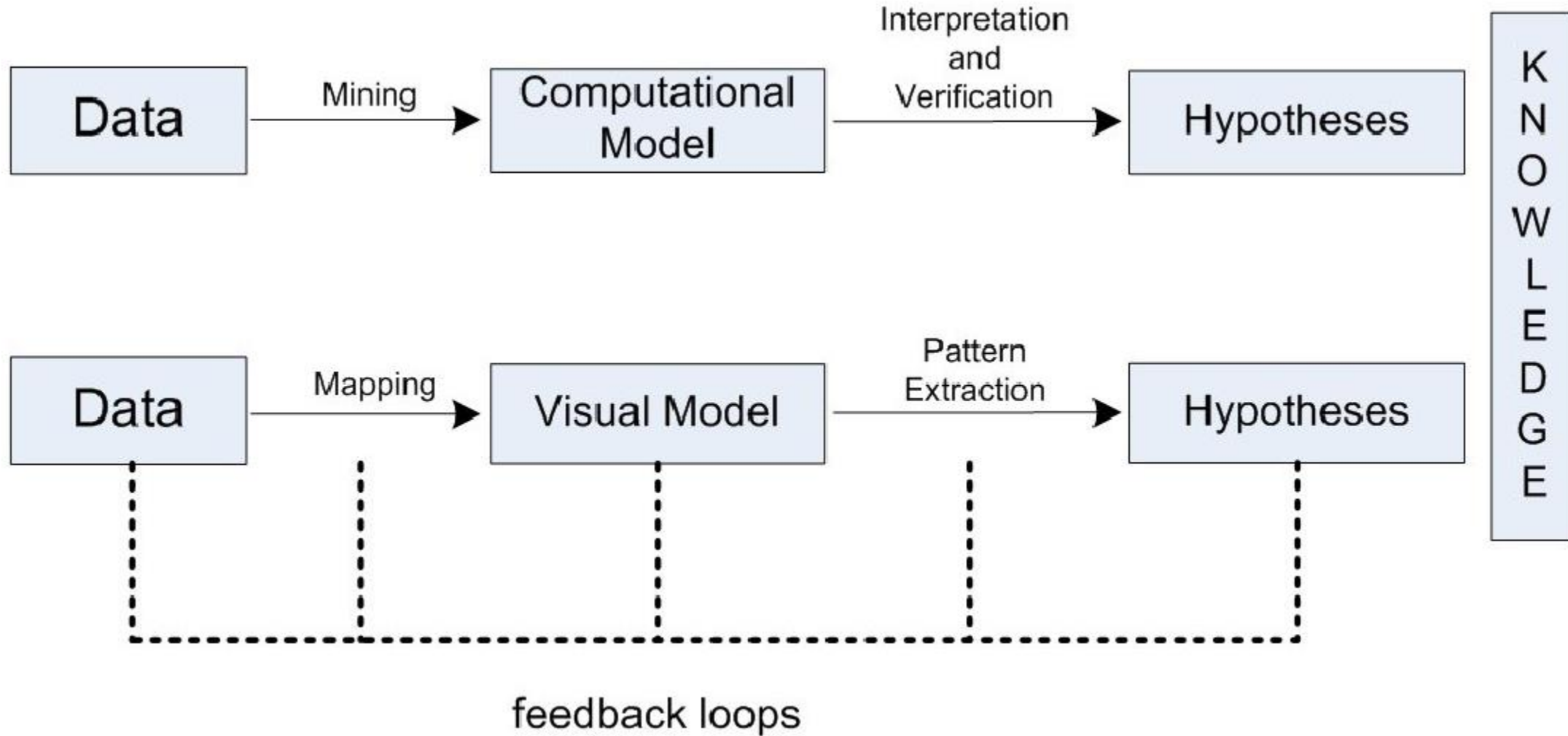
# The Ability Matrix

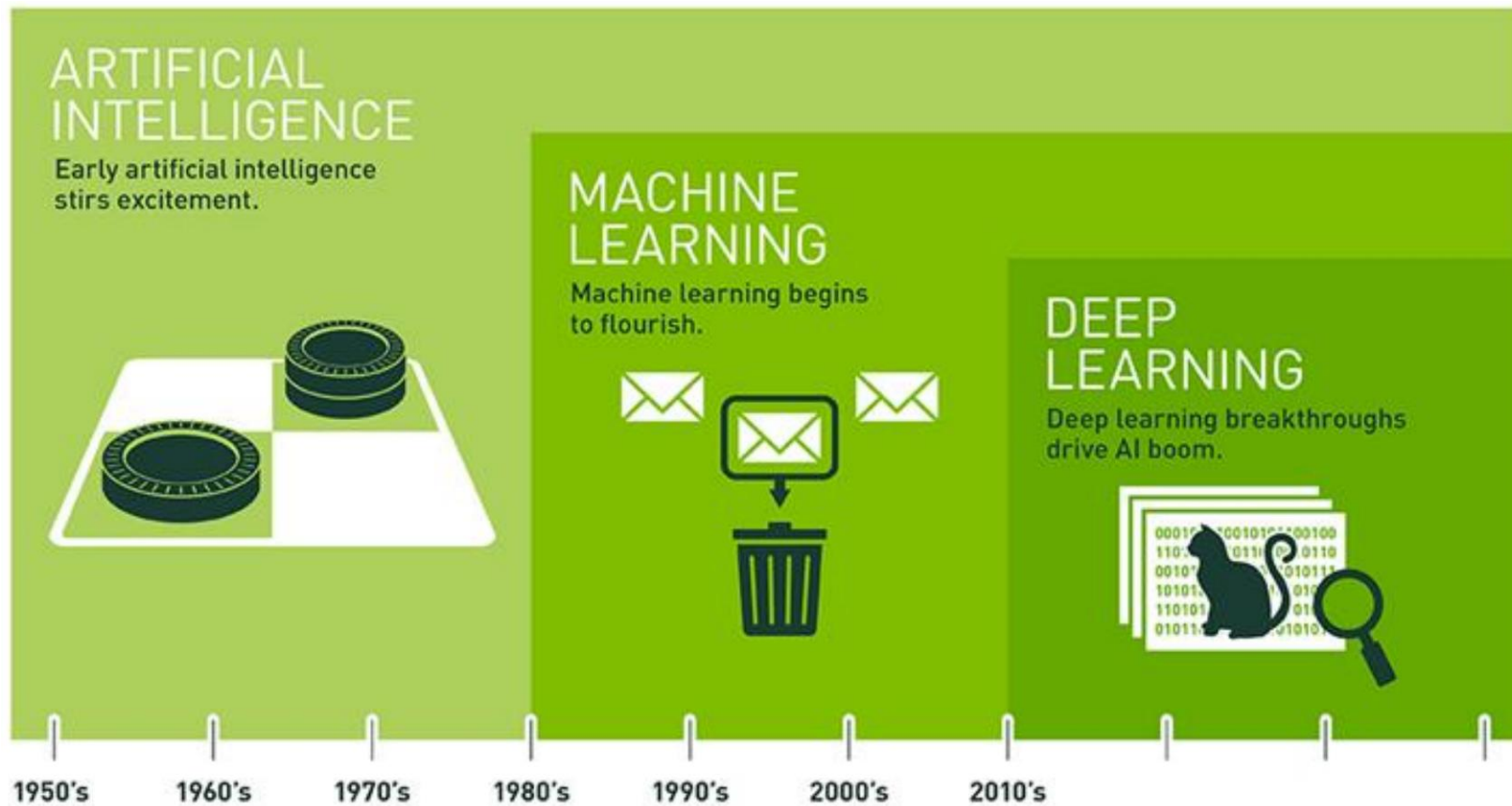


adapted from Daniel Keim, Uni. Konstanz



# Traditional Data Mining vs. Visual Analysis Processes





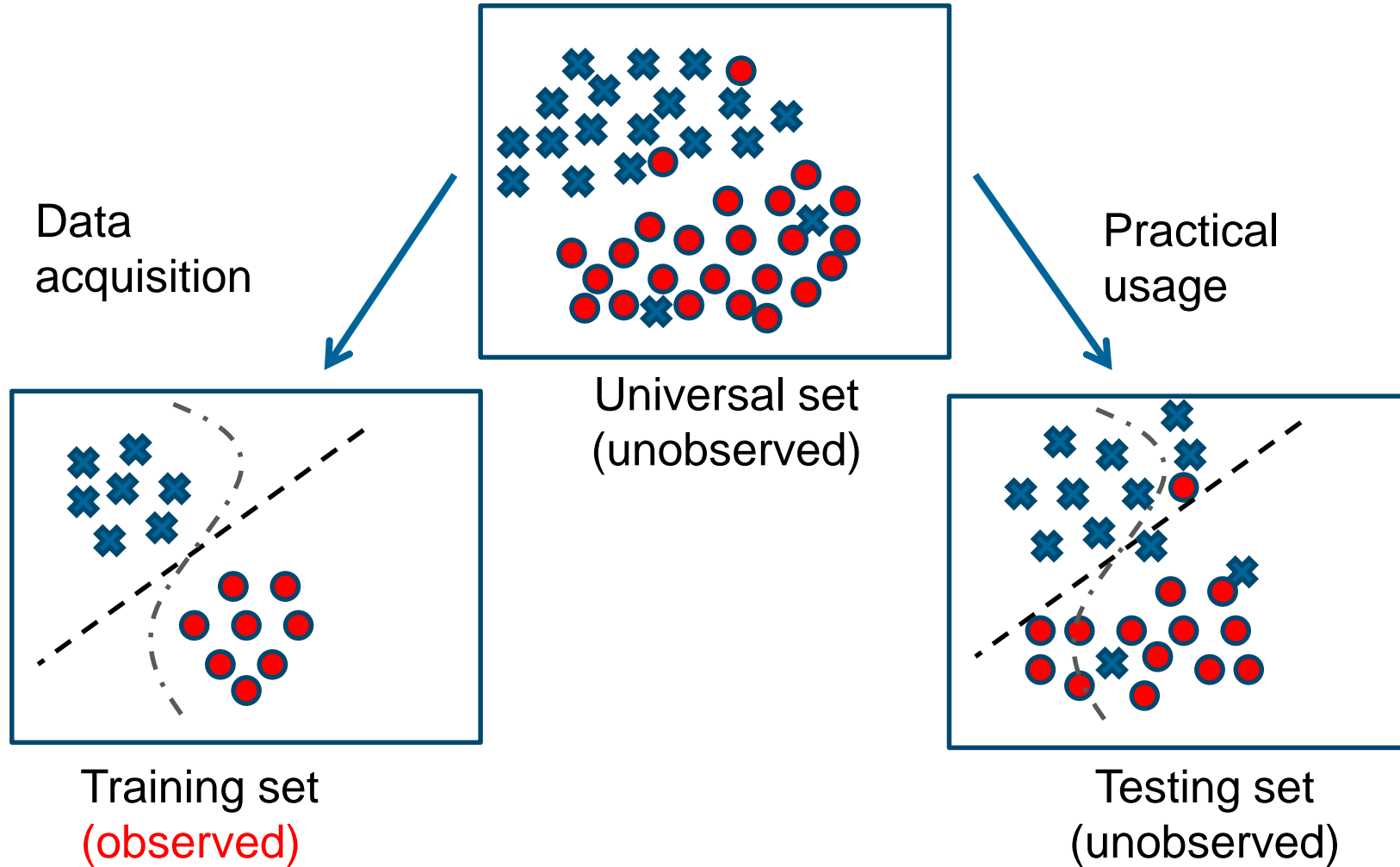


# What is machine learning?

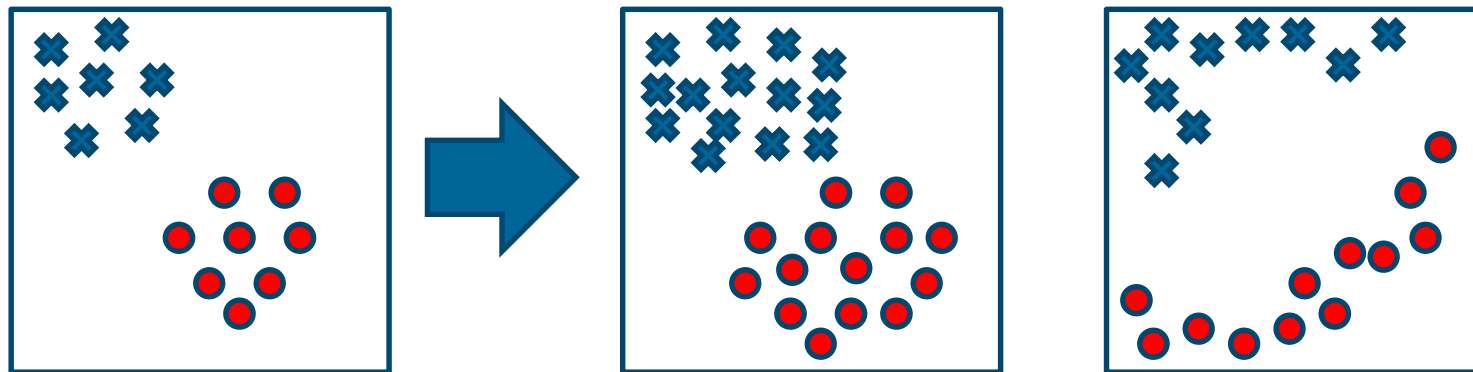
- A branch of artificial intelligence, concerned with the design and development of algorithms that allow computers to evolve behaviors based on empirical data.
- As intelligence requires knowledge, it is necessary for the computers to acquire knowledge.

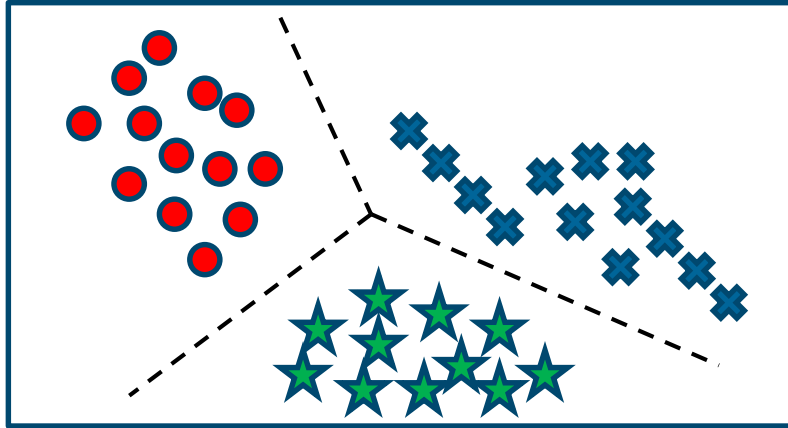


# Training and testing

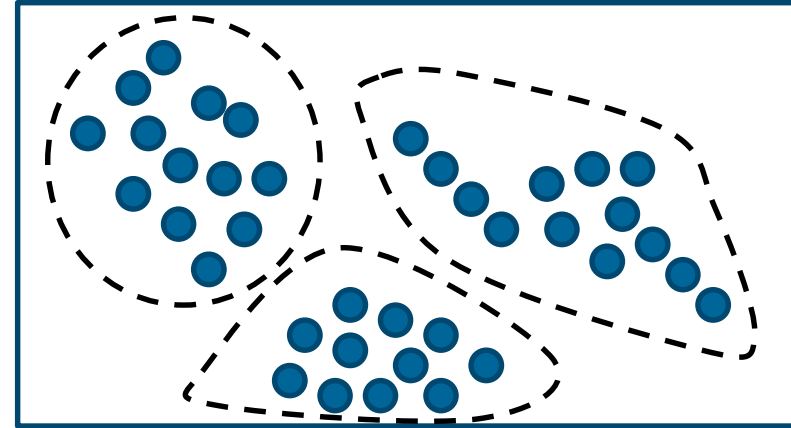


- Training is the process of making the system able to learn.
- No “free-lunch” rule:
  - Training set and testing set come from the same distribution
  - Need to make some assumptions or bias

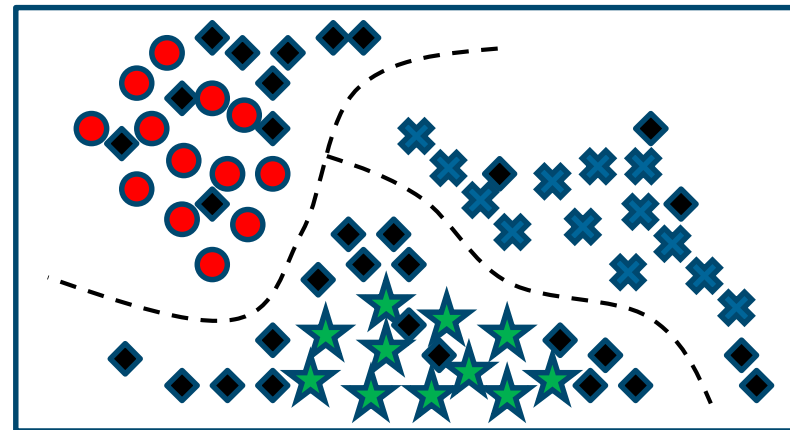




Supervised learning



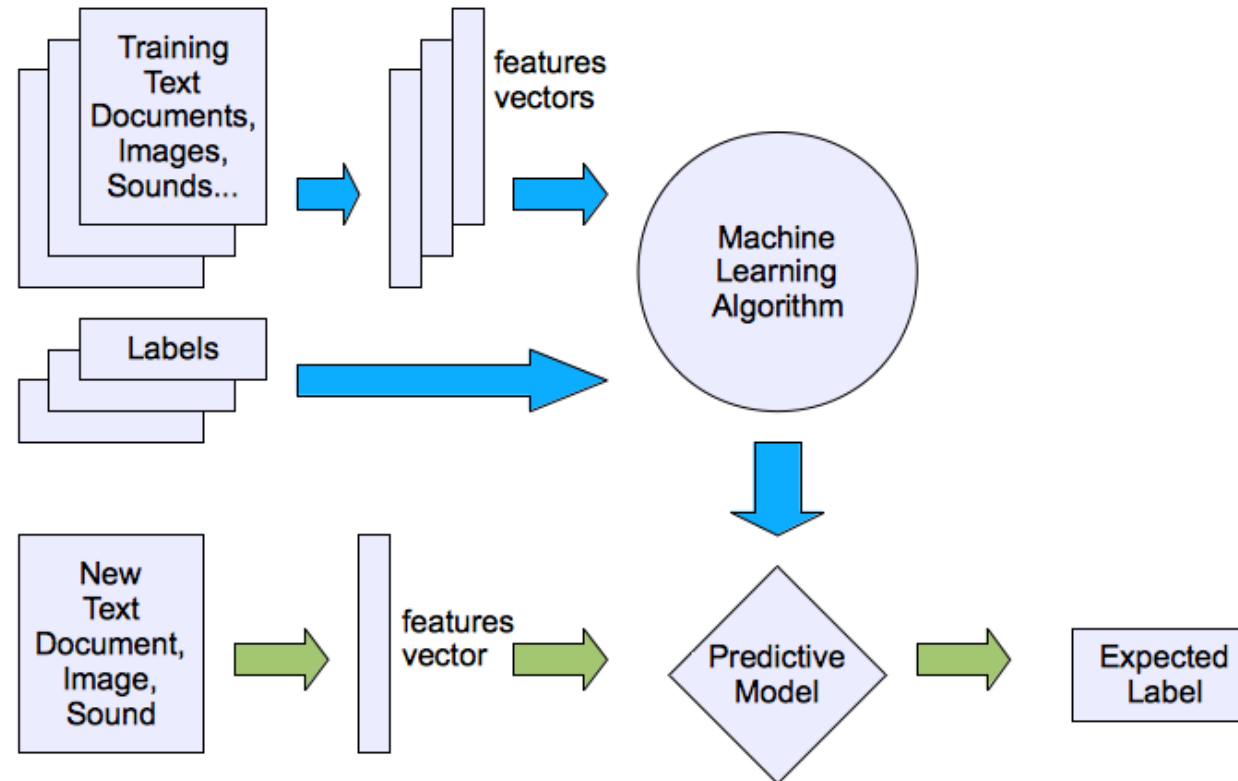
Unsupervised learning



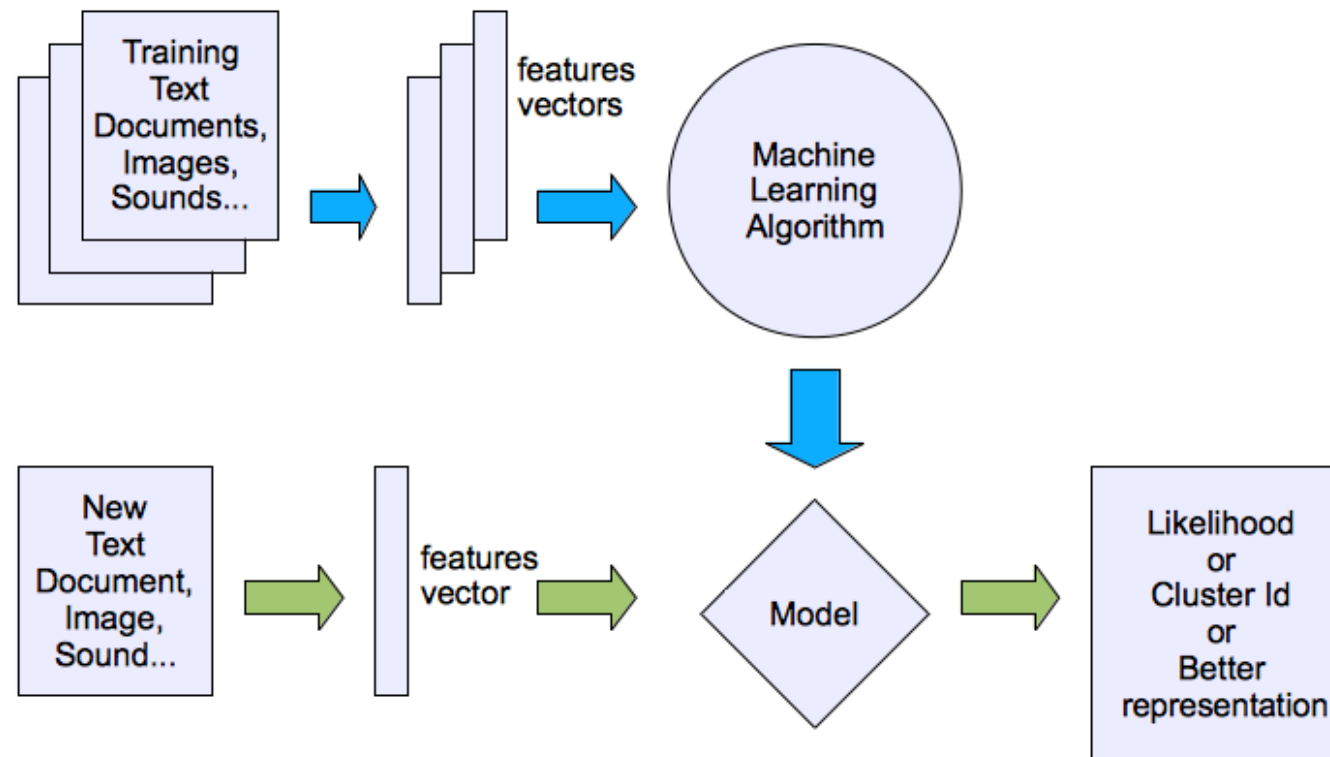
Semi-supervised learning



## Supervised learning



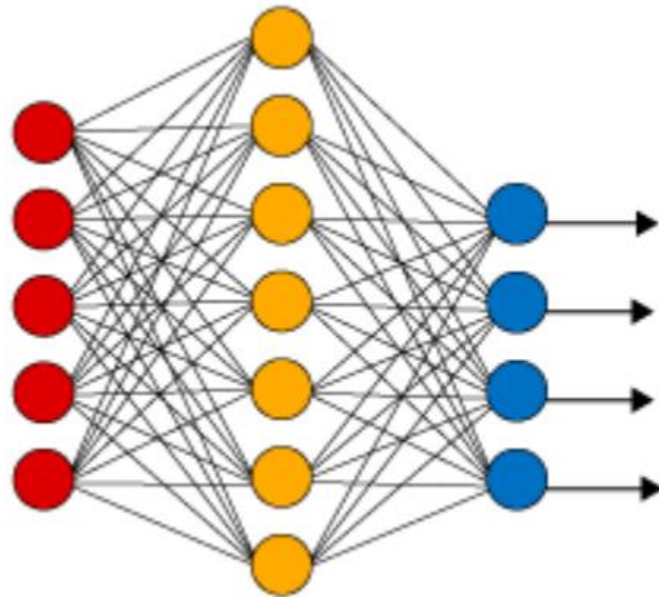
## Unsupervised learning



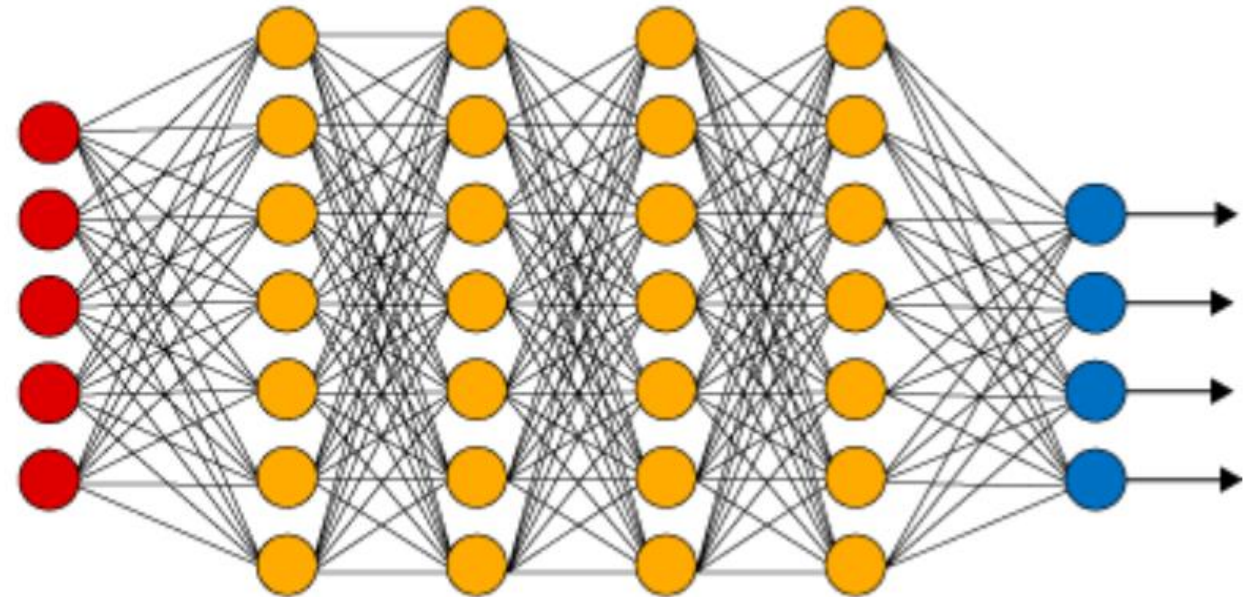



Construct layers of increasingly meaningful representations of the data

## Simple Neural Network



## Deep Learning Neural Network

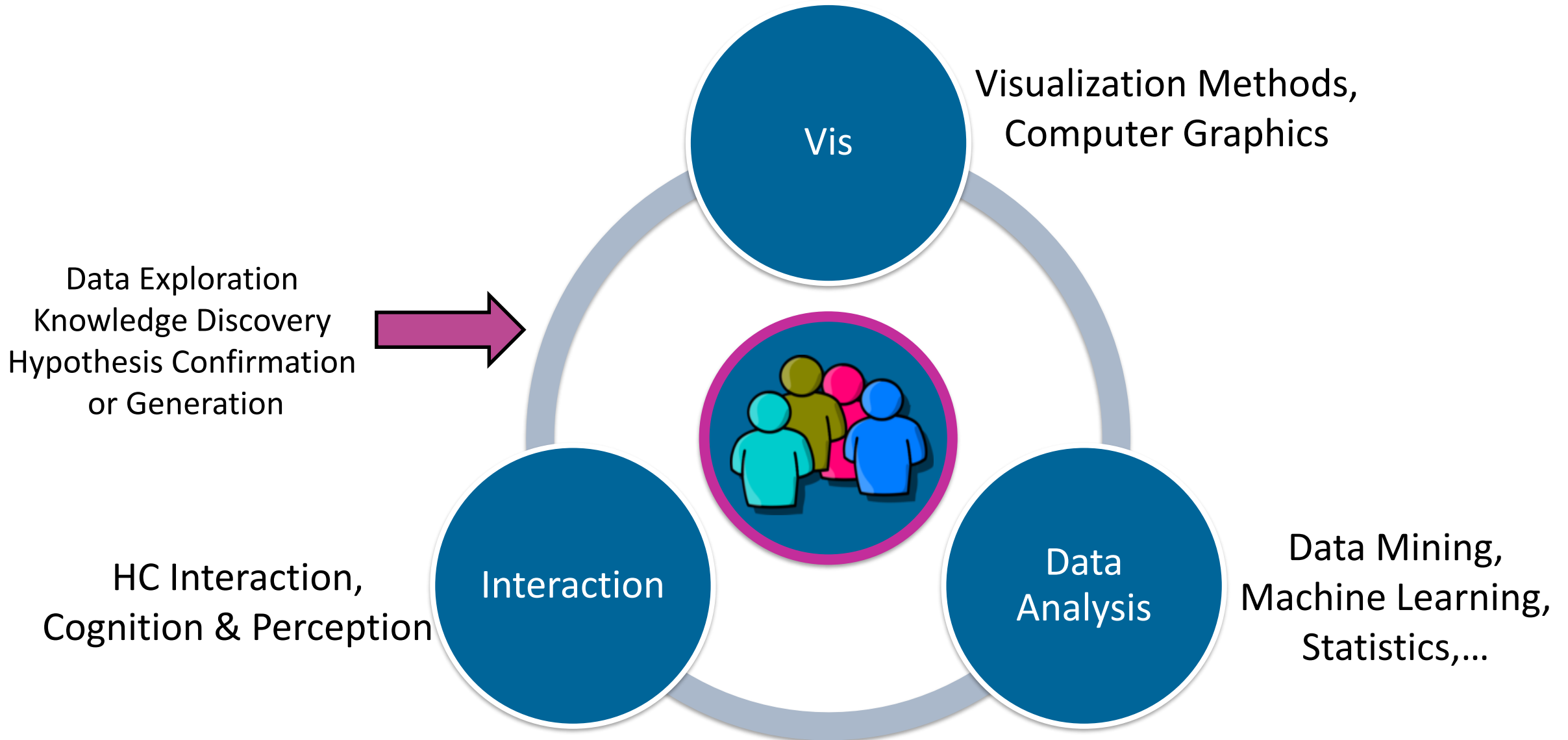


 Input Layer

 Hidden Layer

 Output Layer





- Data → Dealing with very large, diverse, variable quality datasets
- Users → Meeting the needs of the users
- Design → Assisting designers of visual analytic systems
- Technology → Providing the necessary infrastructure



Visual Analytics for :

1. ... Tumor Tissue Characterization and Organ at Risk Segmentation → *Research and Treatment Planning in RT*
2. ... Exploring Organ Variability for RT → *Research and Treatment Planning in RT*



## WHO 2018

18.1 M Cancer Cases

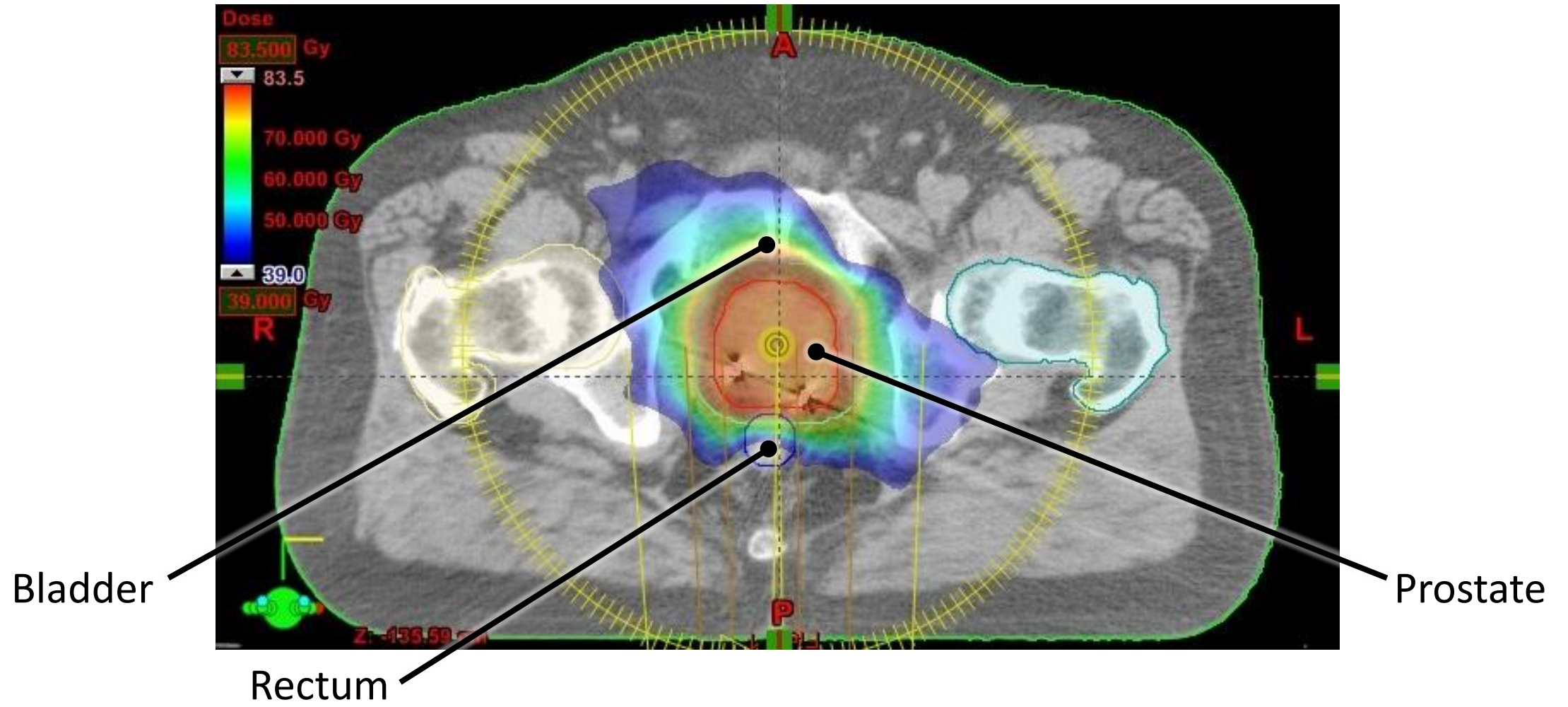
9.6 M Cancer Deaths



Prostate Cancer  
1 out of 6 men

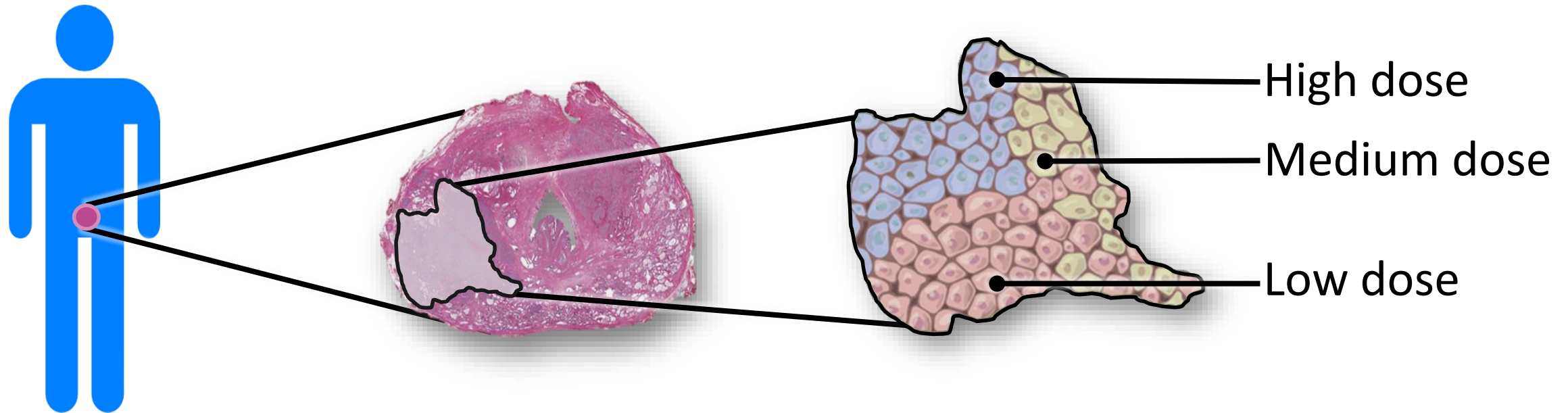


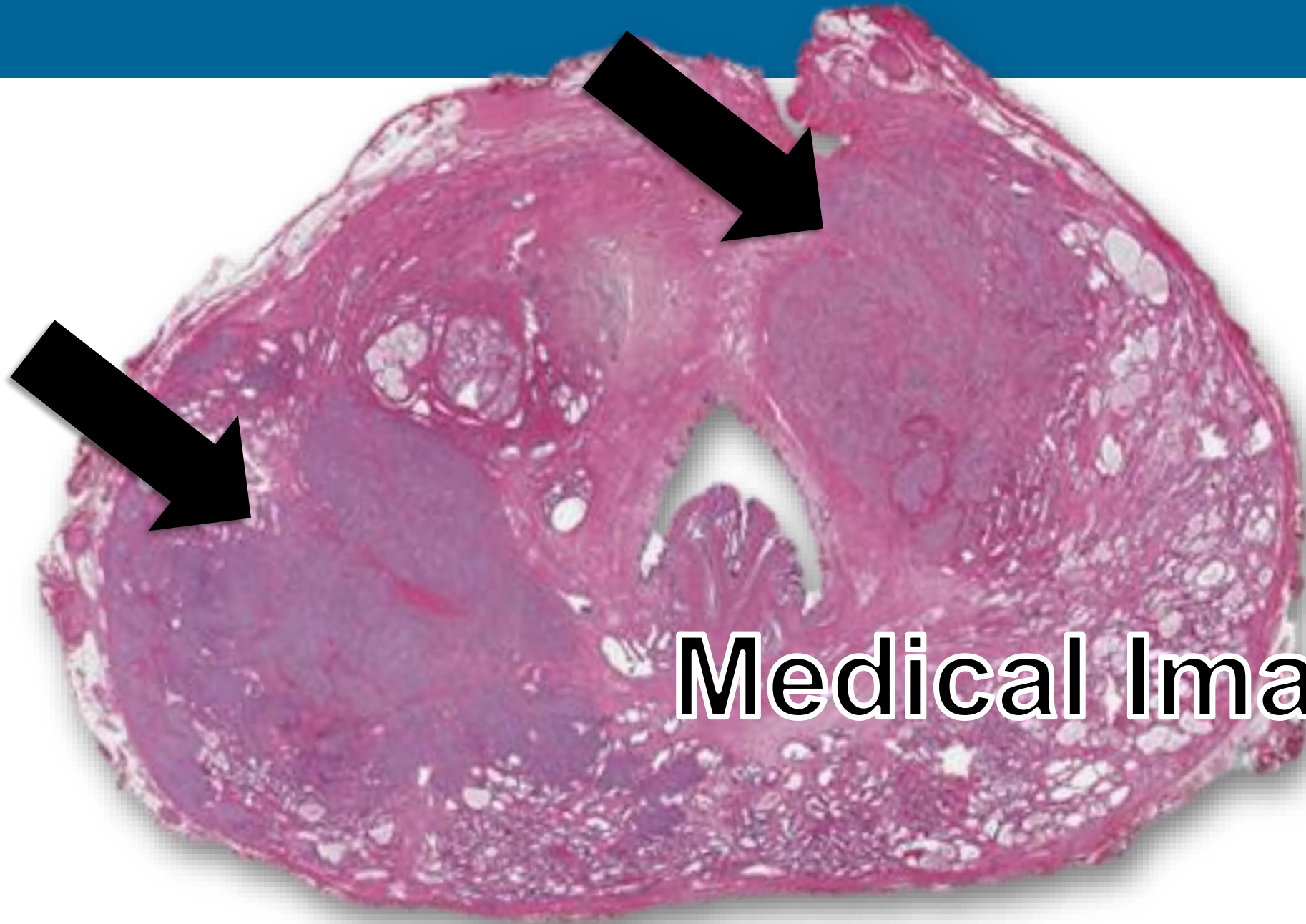
# 60% of patients receive radiotherapy treatment





# Tailoring the Dose to Tumor Characteristics





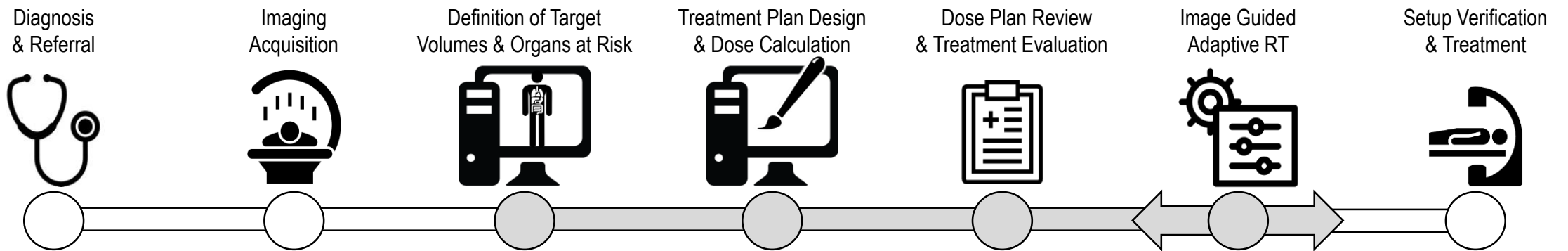
**Medical Imaging!**





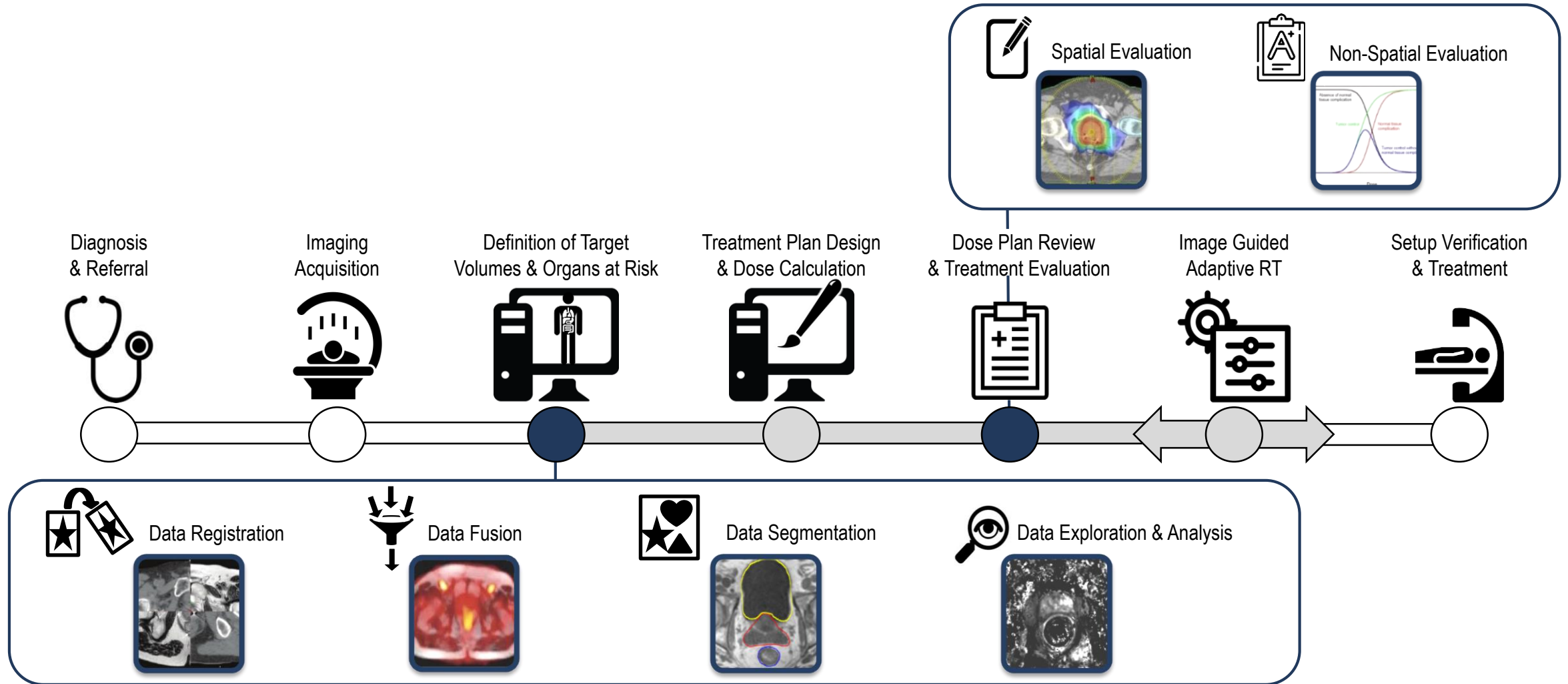
# RT Pipeline

[Schlachter, Raidou et al. 2019 STAR CGF]



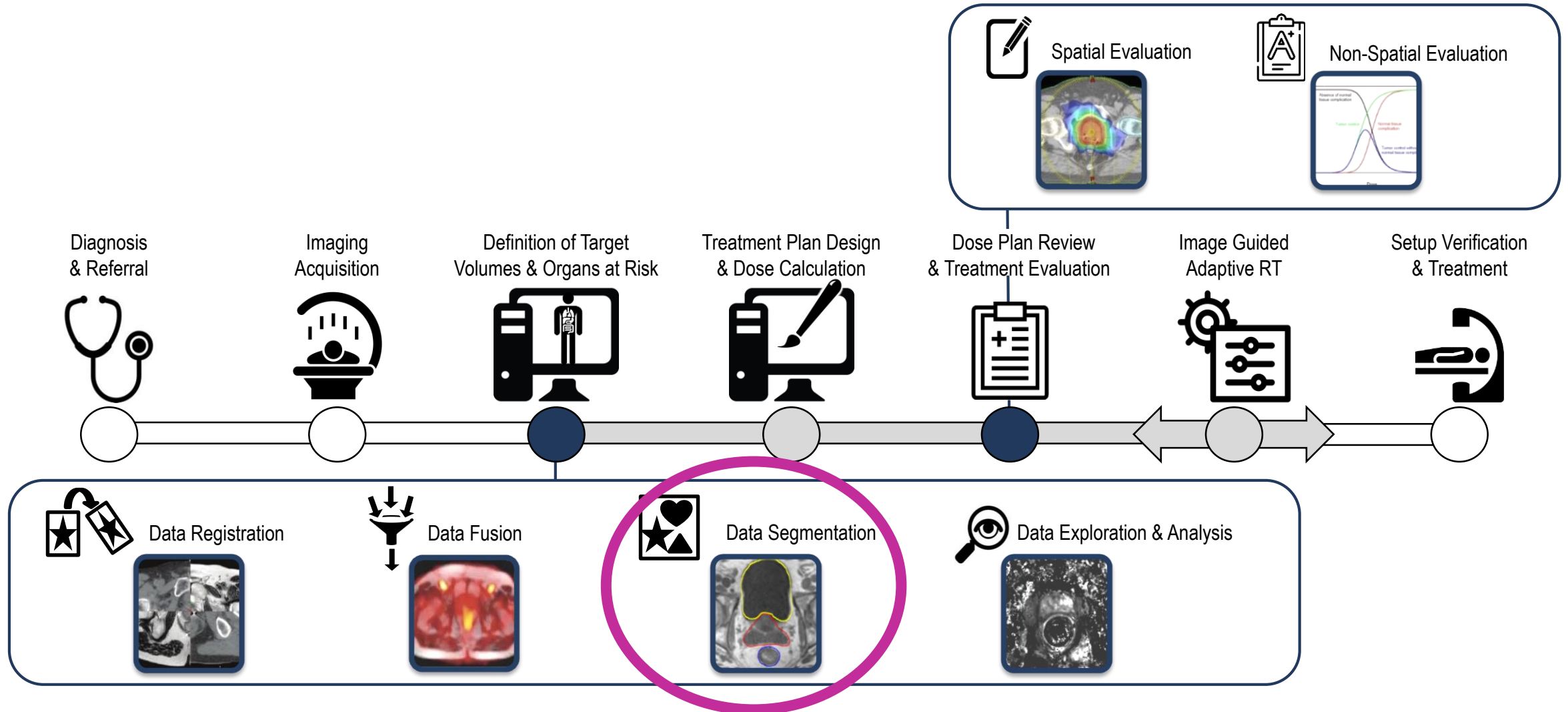
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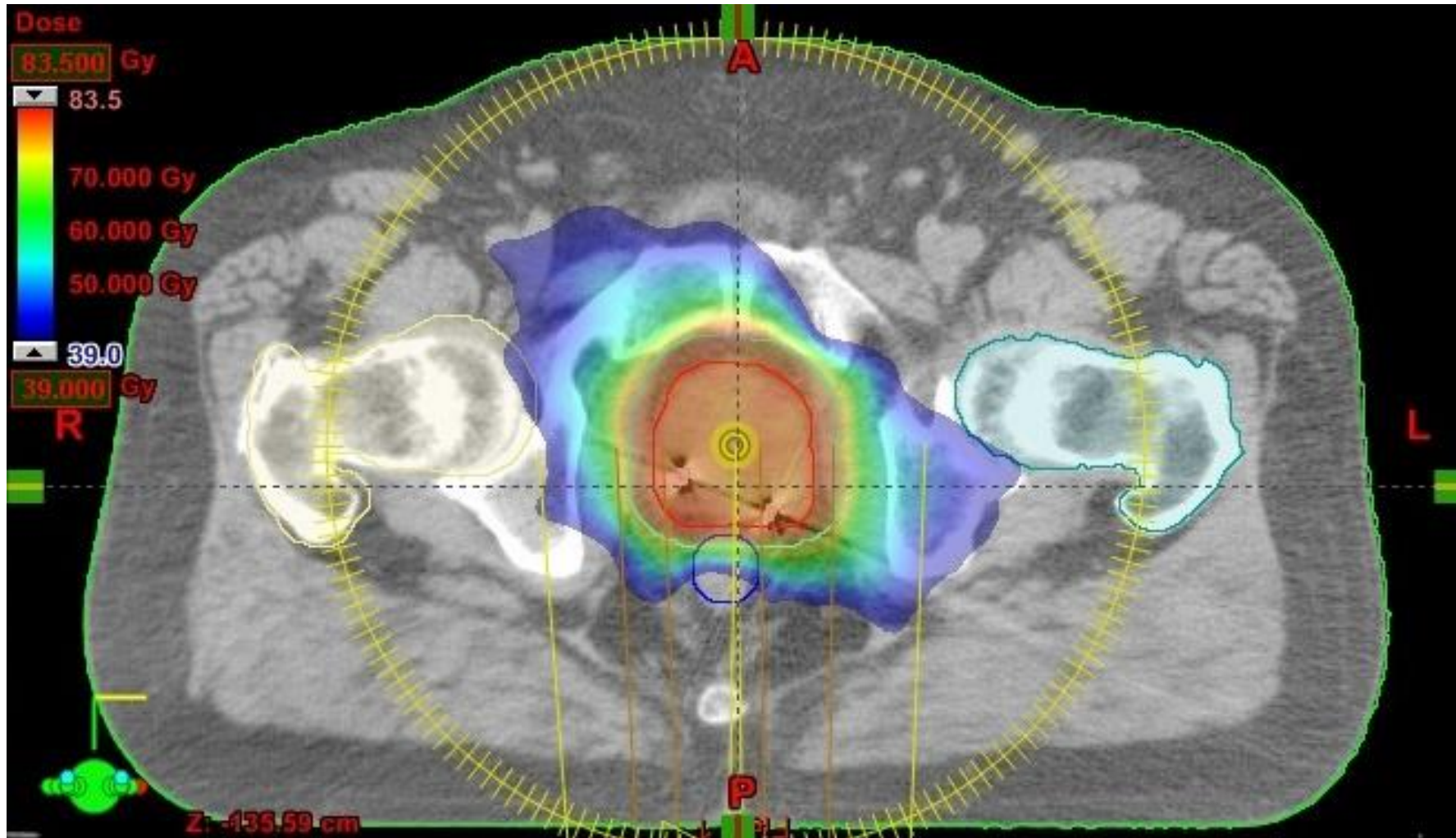


Visual Analytics for :

1. ... Tumor Tissue Characterization
2. and Organ at Risk Segmentation

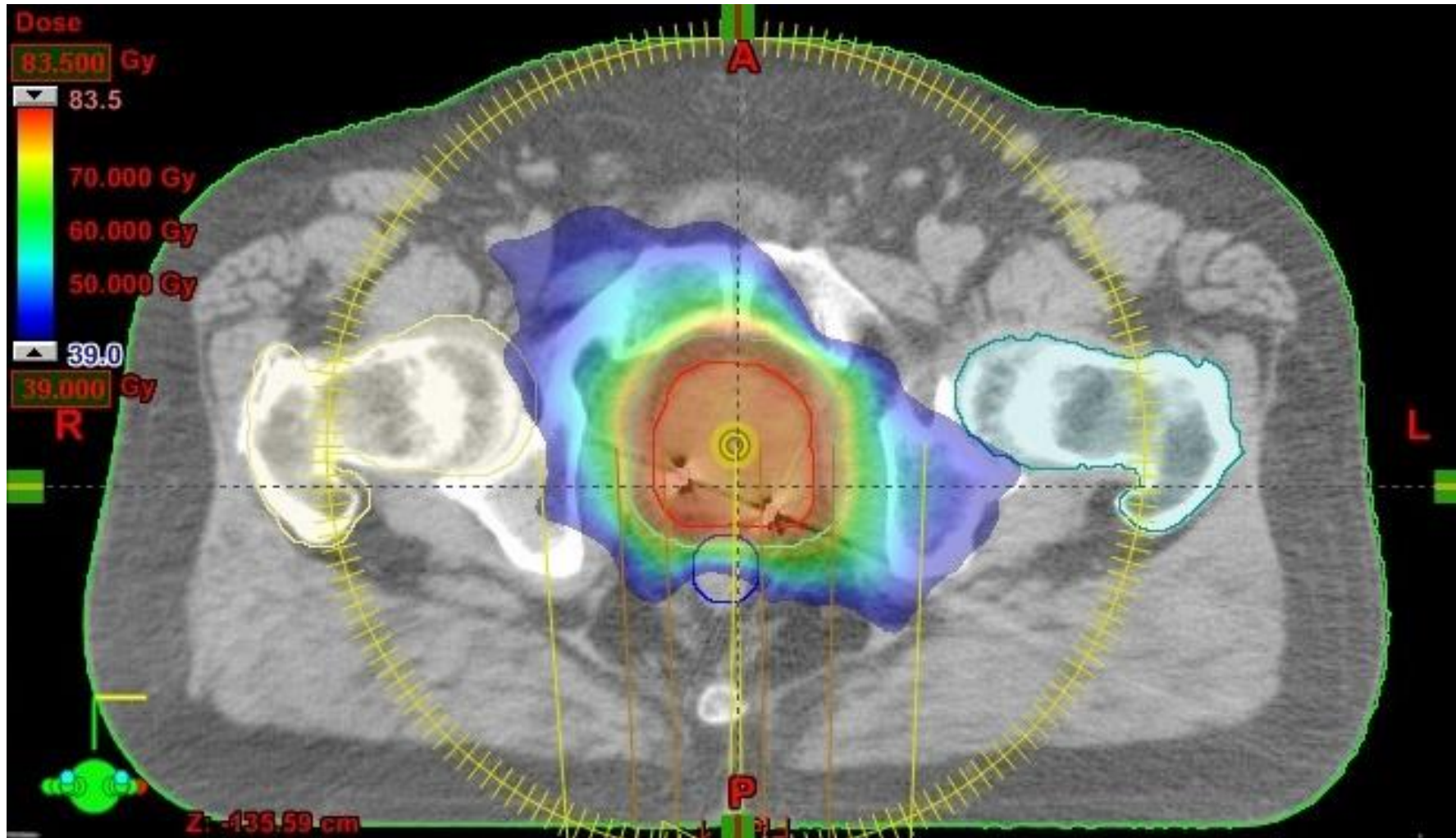


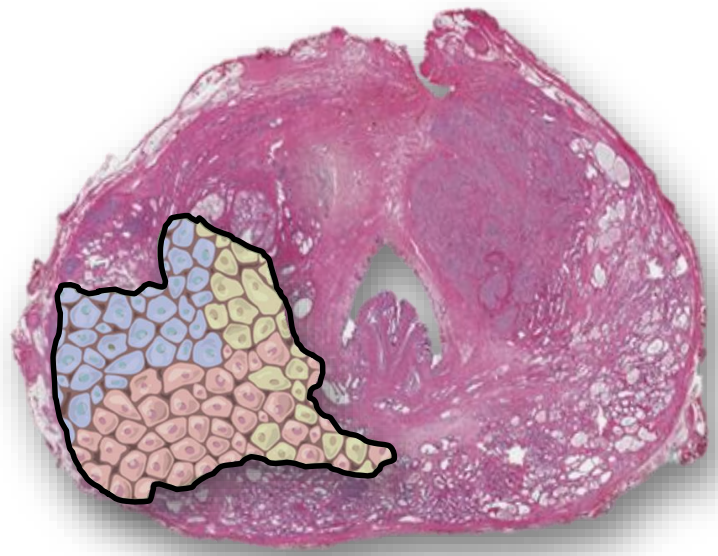
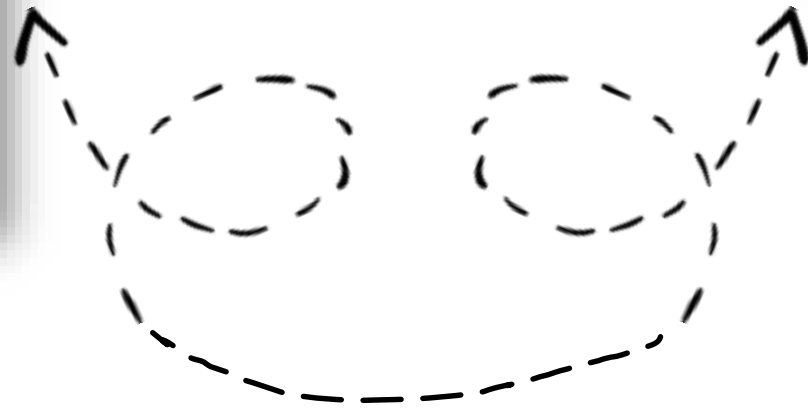
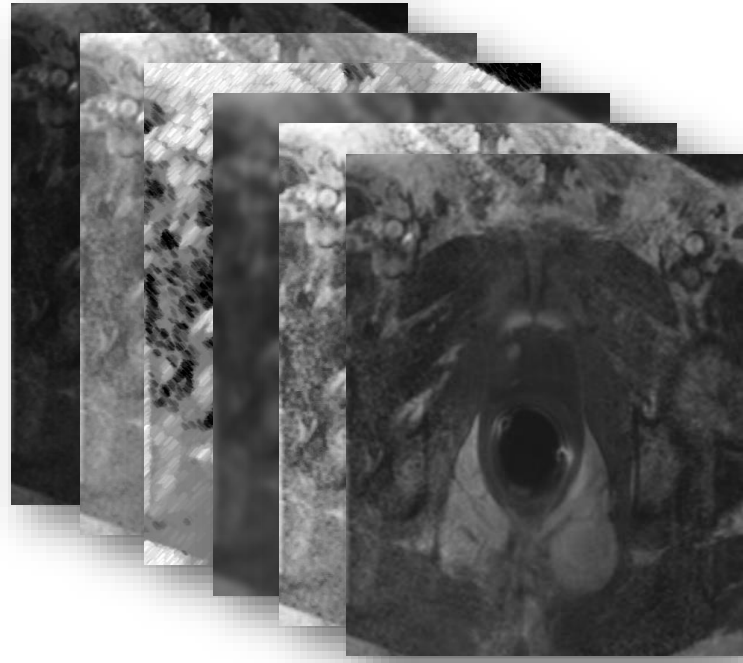
# Tumors vs. Healthy Organs (at Risk)

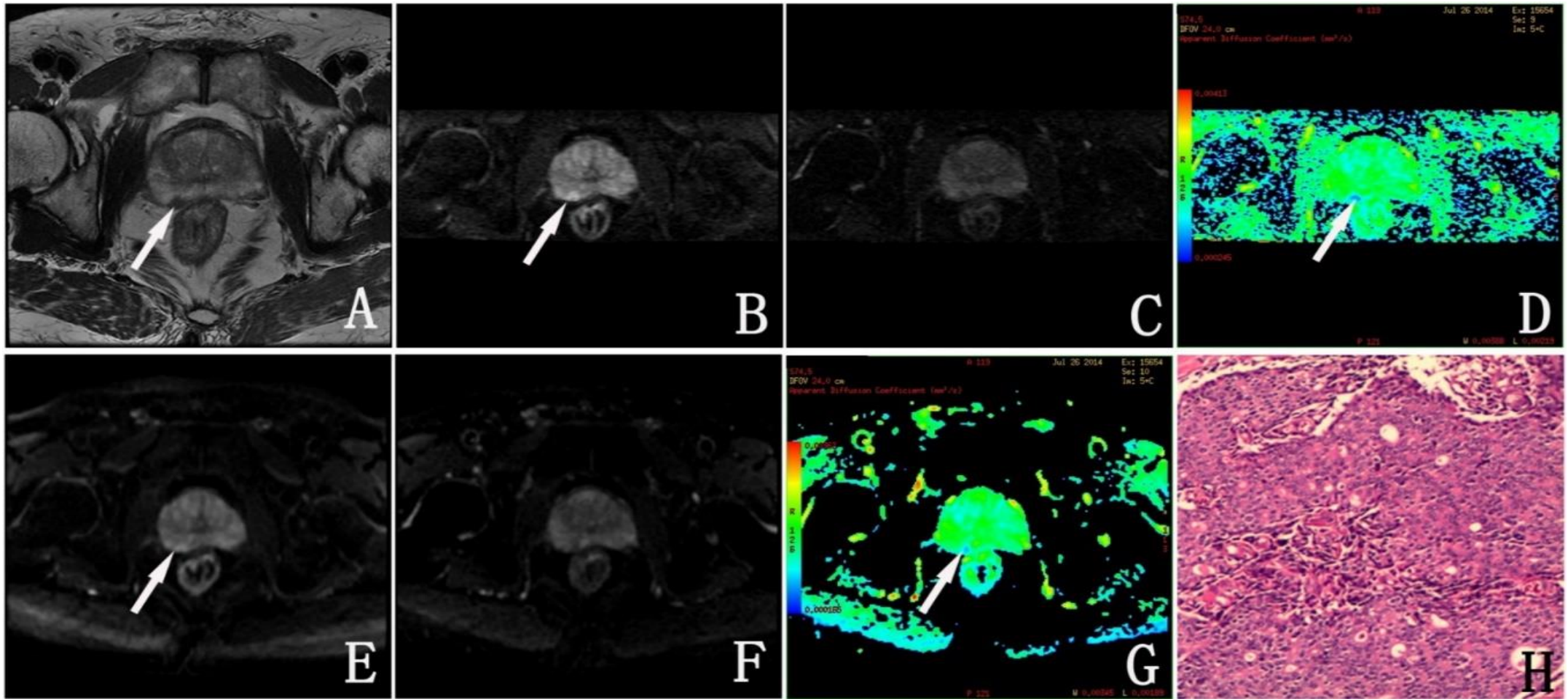




# Tumors vs. Healthy Organs (at Risk)



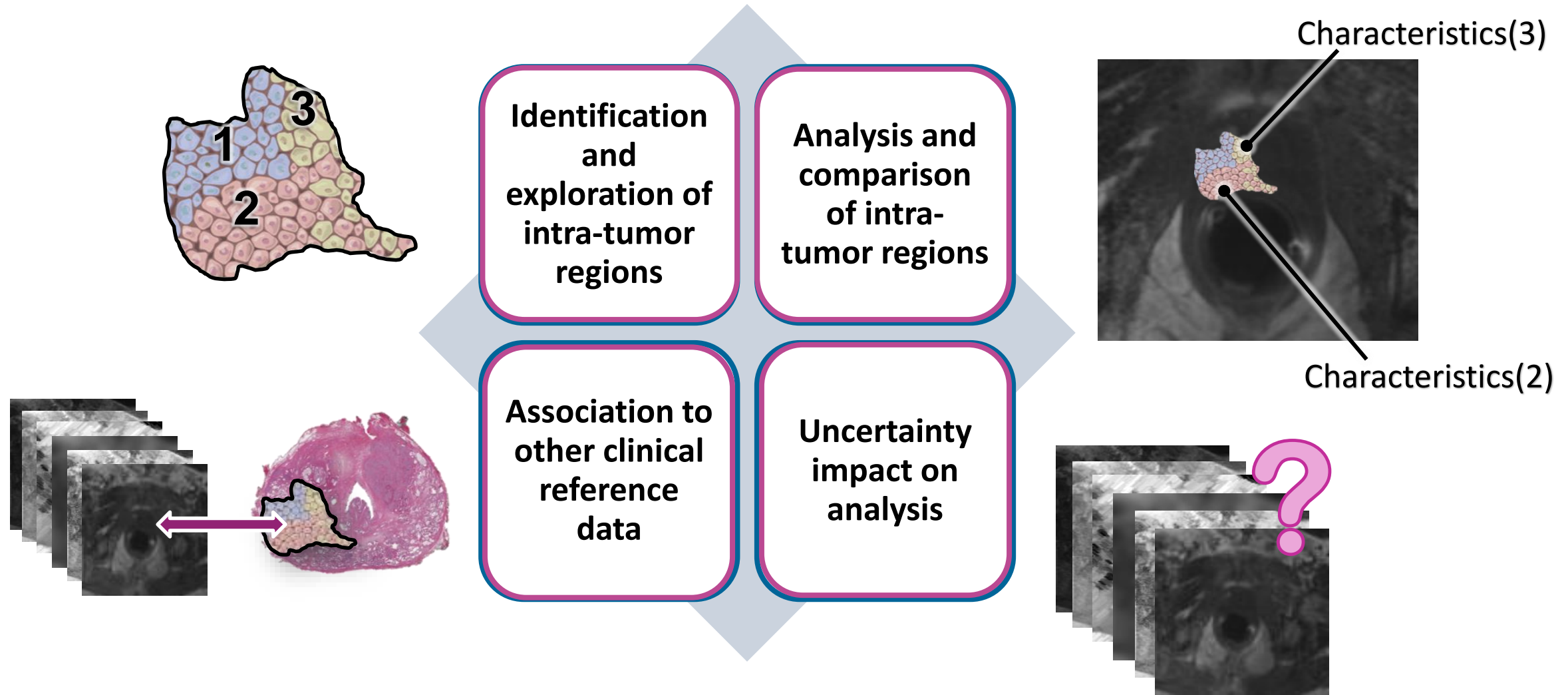




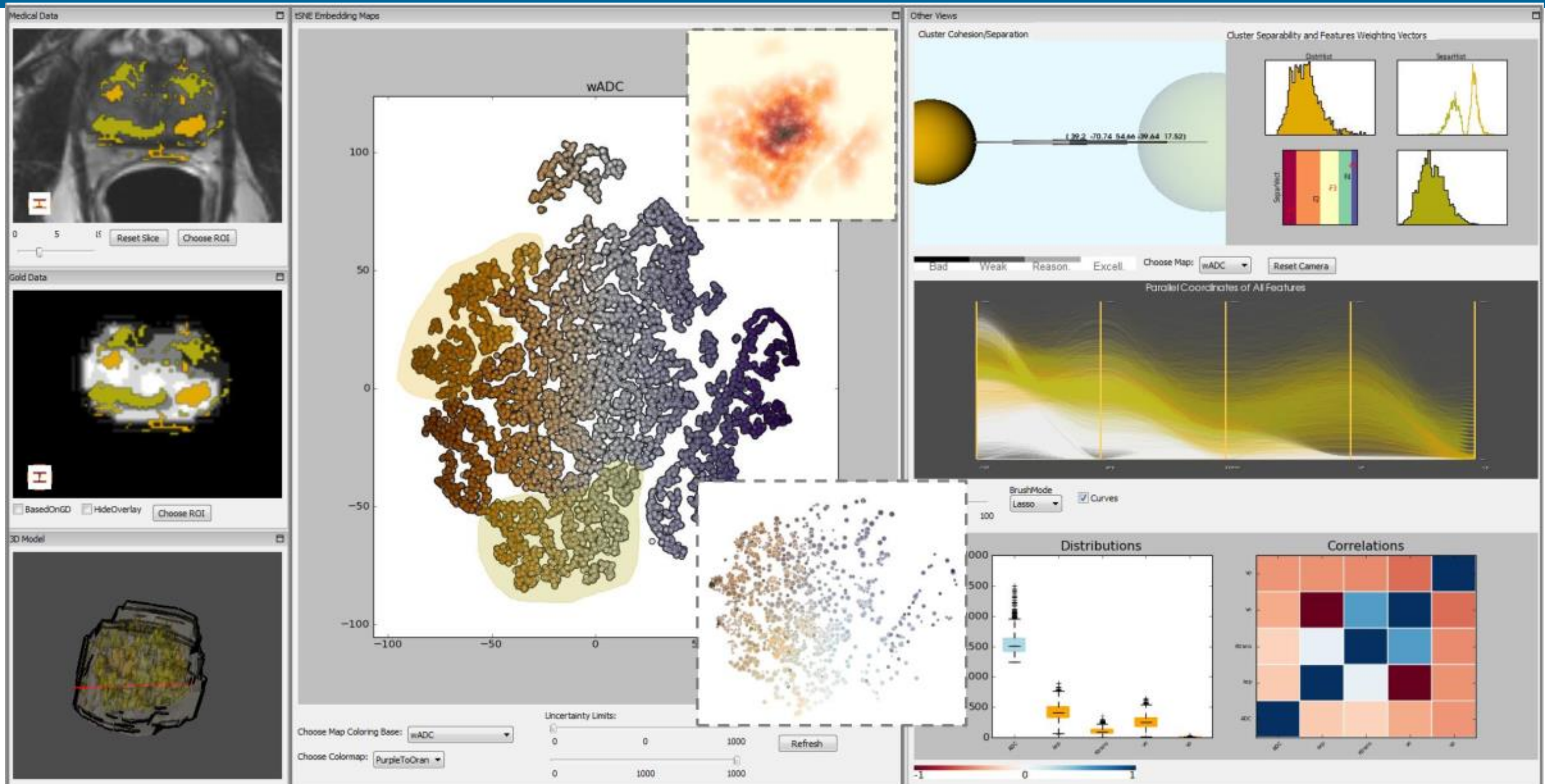
[Feng et al., ECR2015]







# Visual Analytics Solution

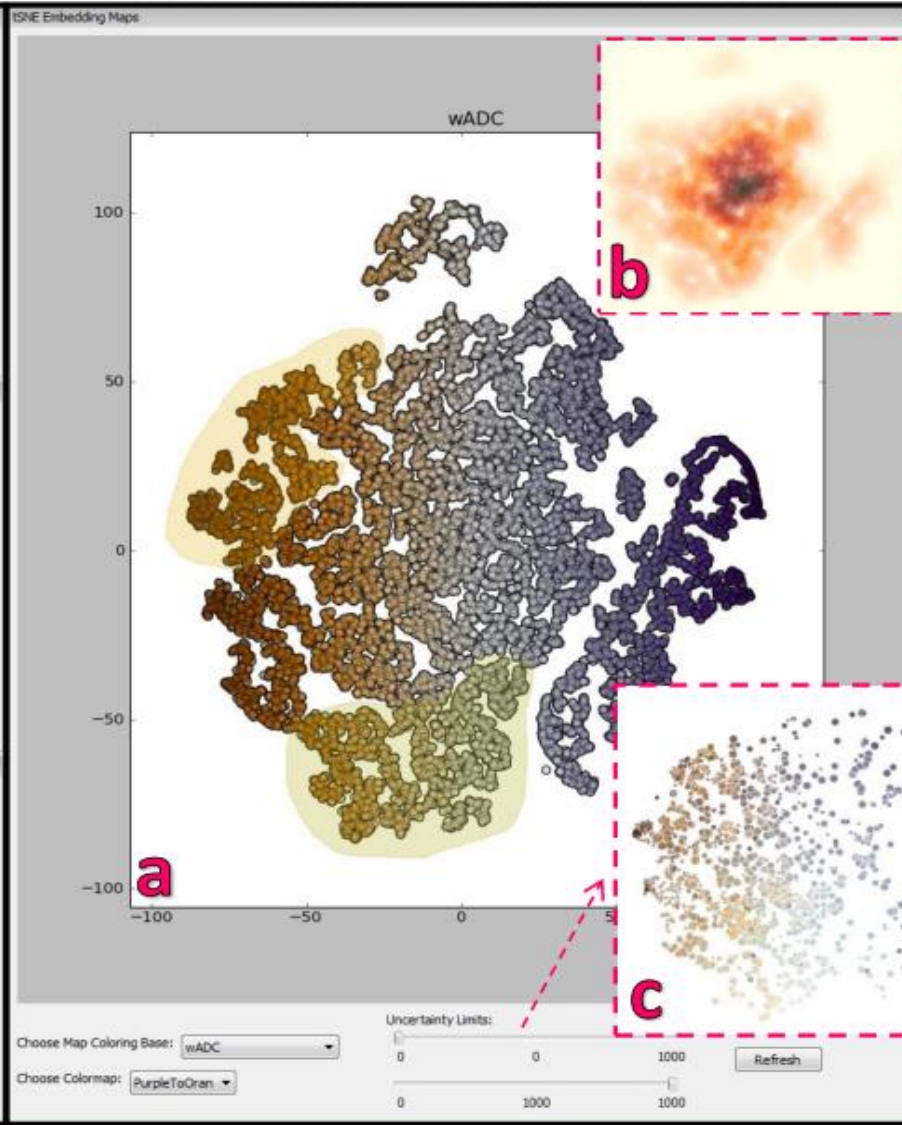


# 1. Identification and Exploration of Intra-tumor Regions

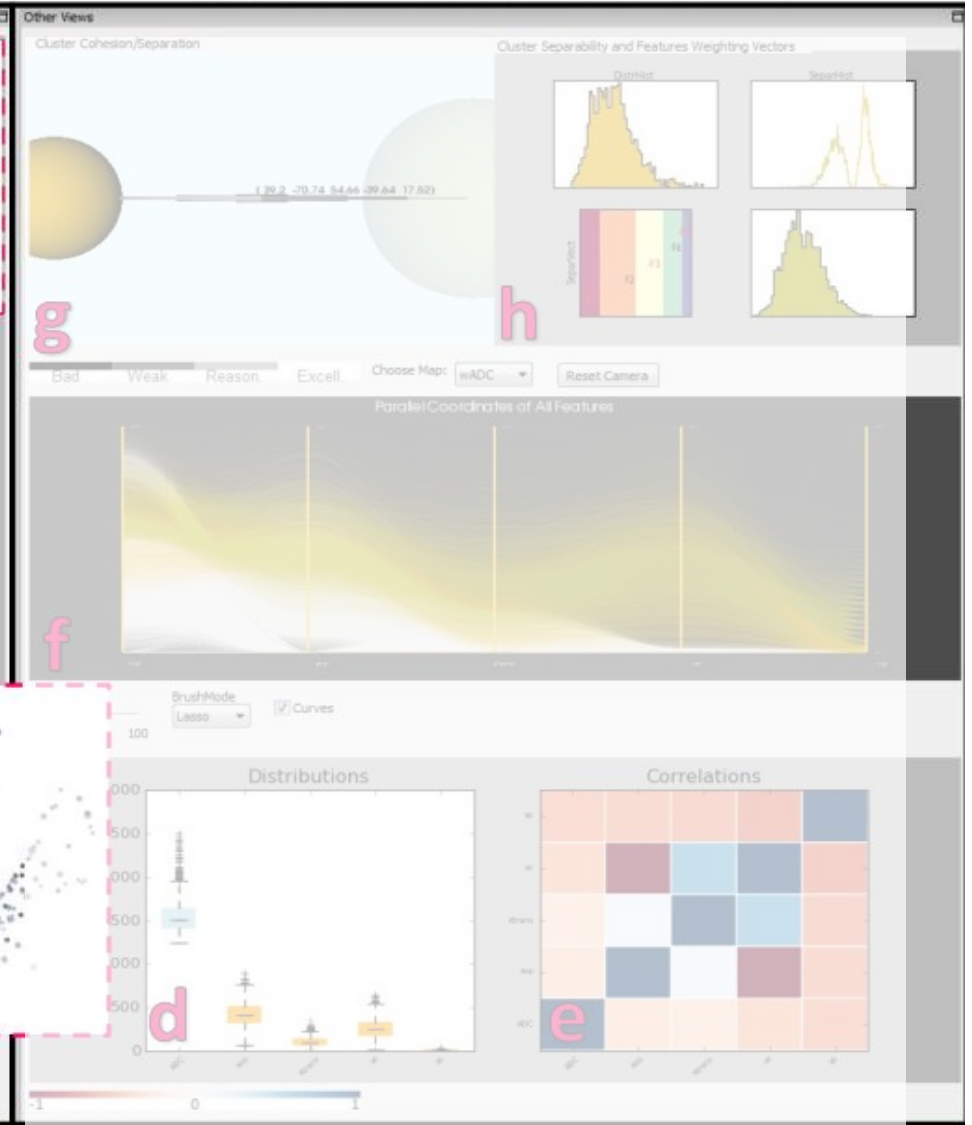
## ANAT. SPACE



## PROJECTION - FEATURE SPACE

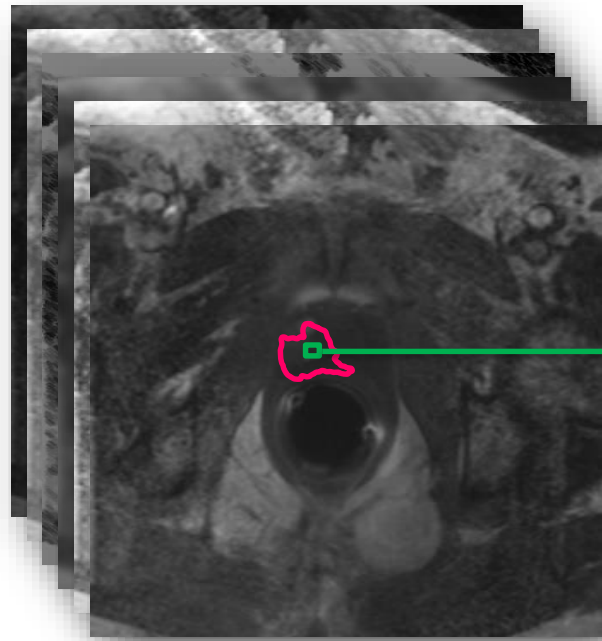


## CLUSTER ANALYSIS VIEW





# 1. Identification and Exploration of Intra-tumor Regions



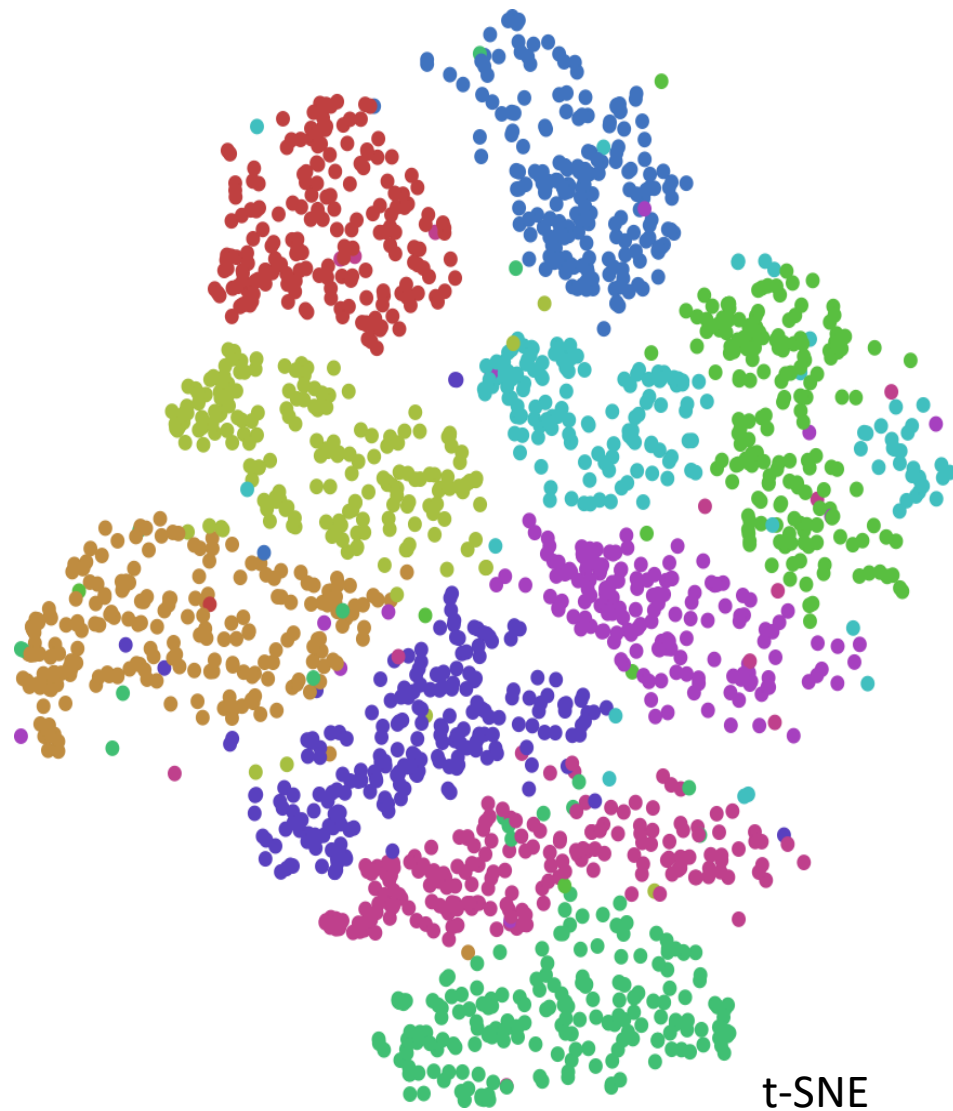
$$\mathbf{v} = \{ \underbrace{ttc_1, ttc_2, \dots, ttc_N}_{\text{Imaging-derived features per voxel}} \}$$

Imaging-derived features per voxel

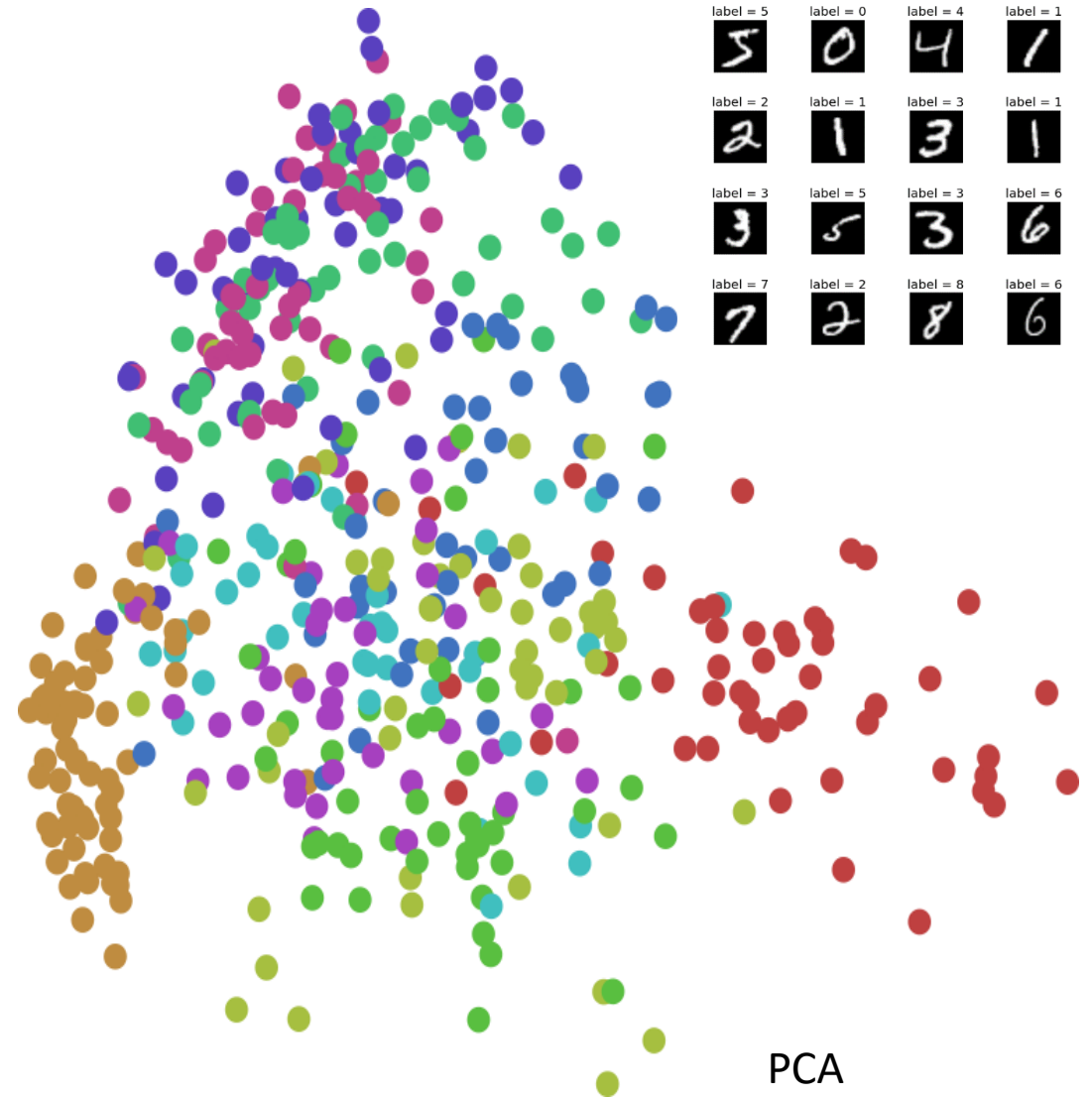
t-Distributed Stochastic Neighborhood Embedding (**tSNE**) - L. van der Maaten, 2008



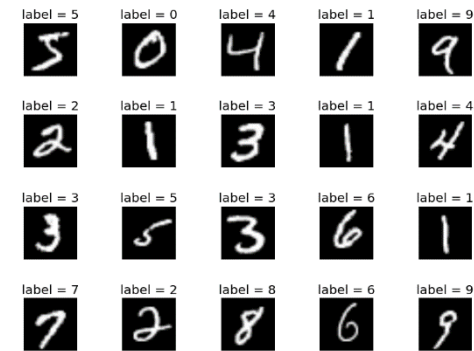
# PCA vs. t-SNE



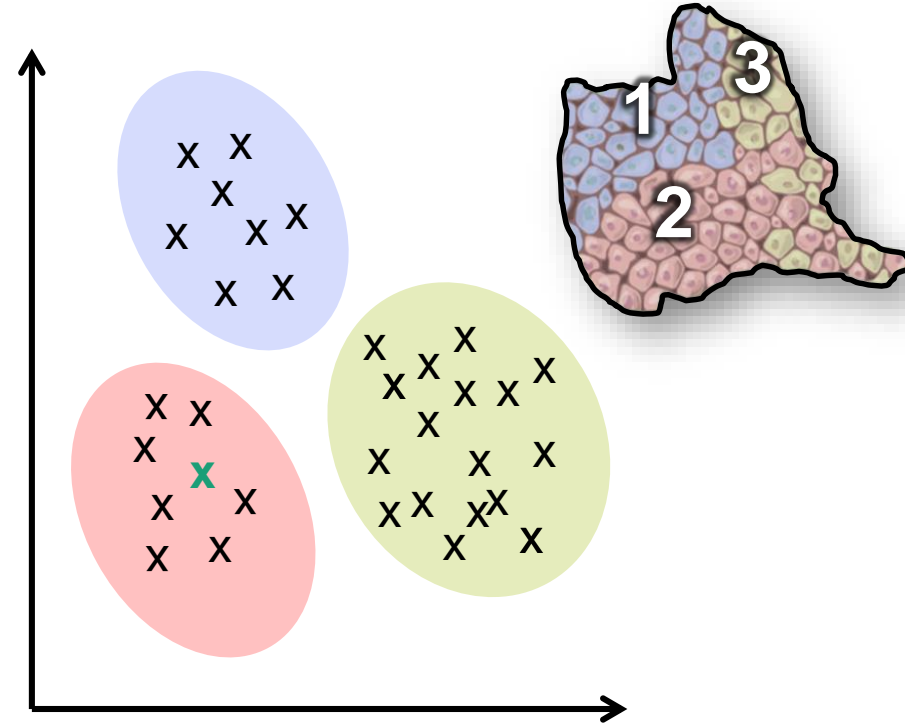
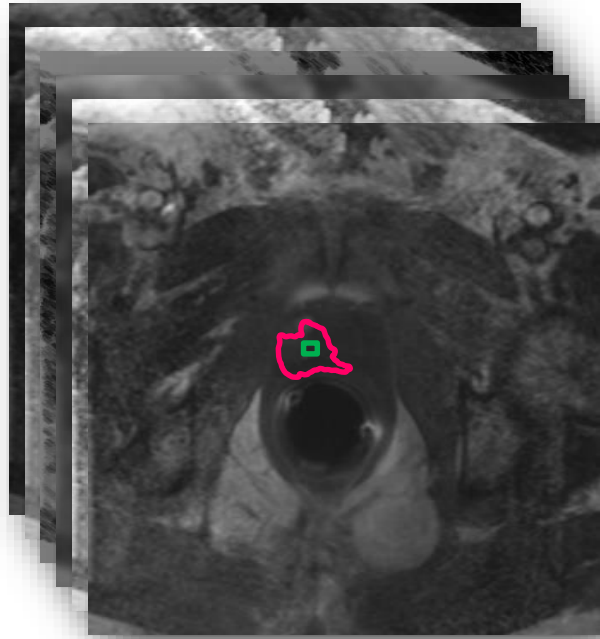
- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9



MNIST dataset example



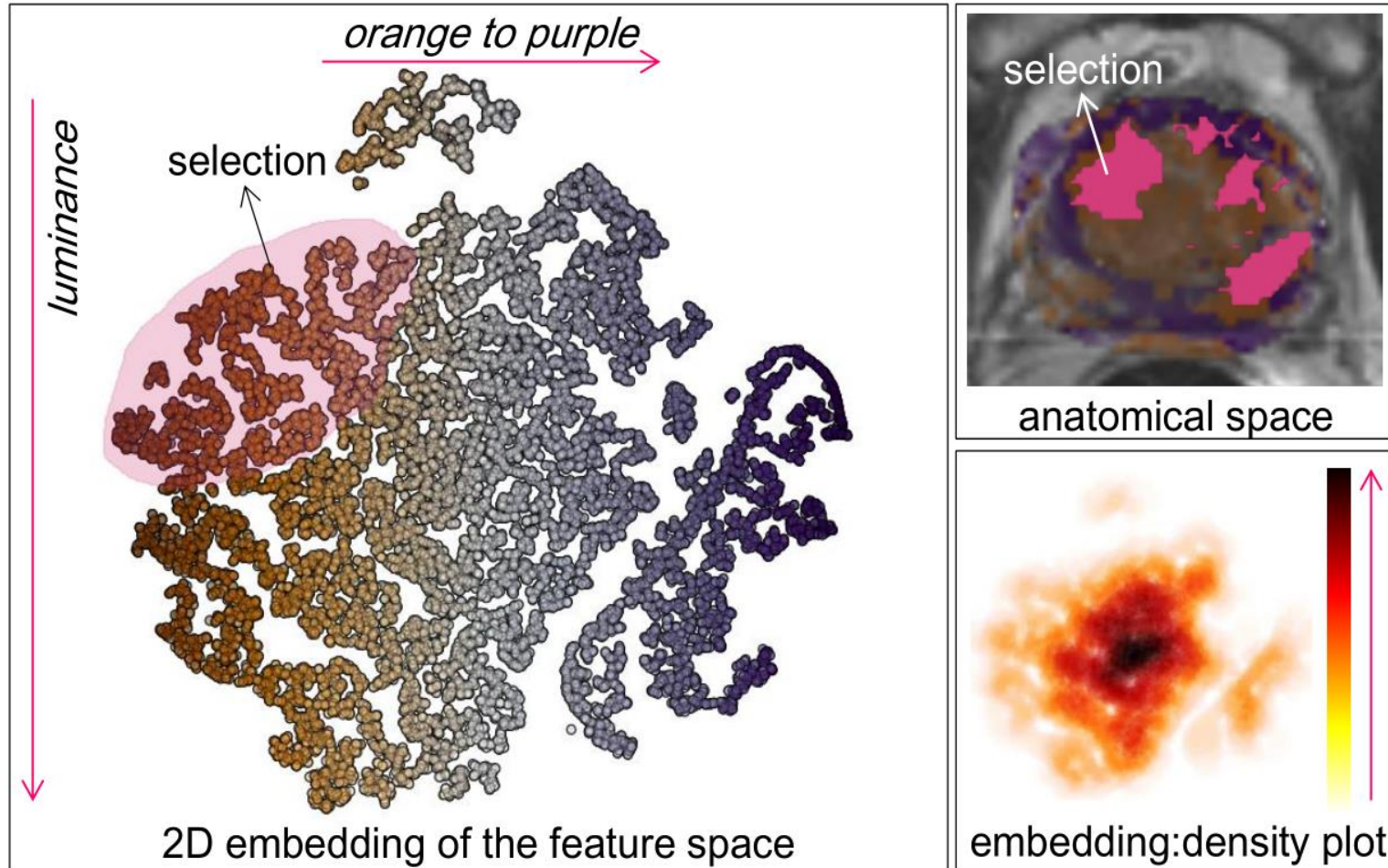
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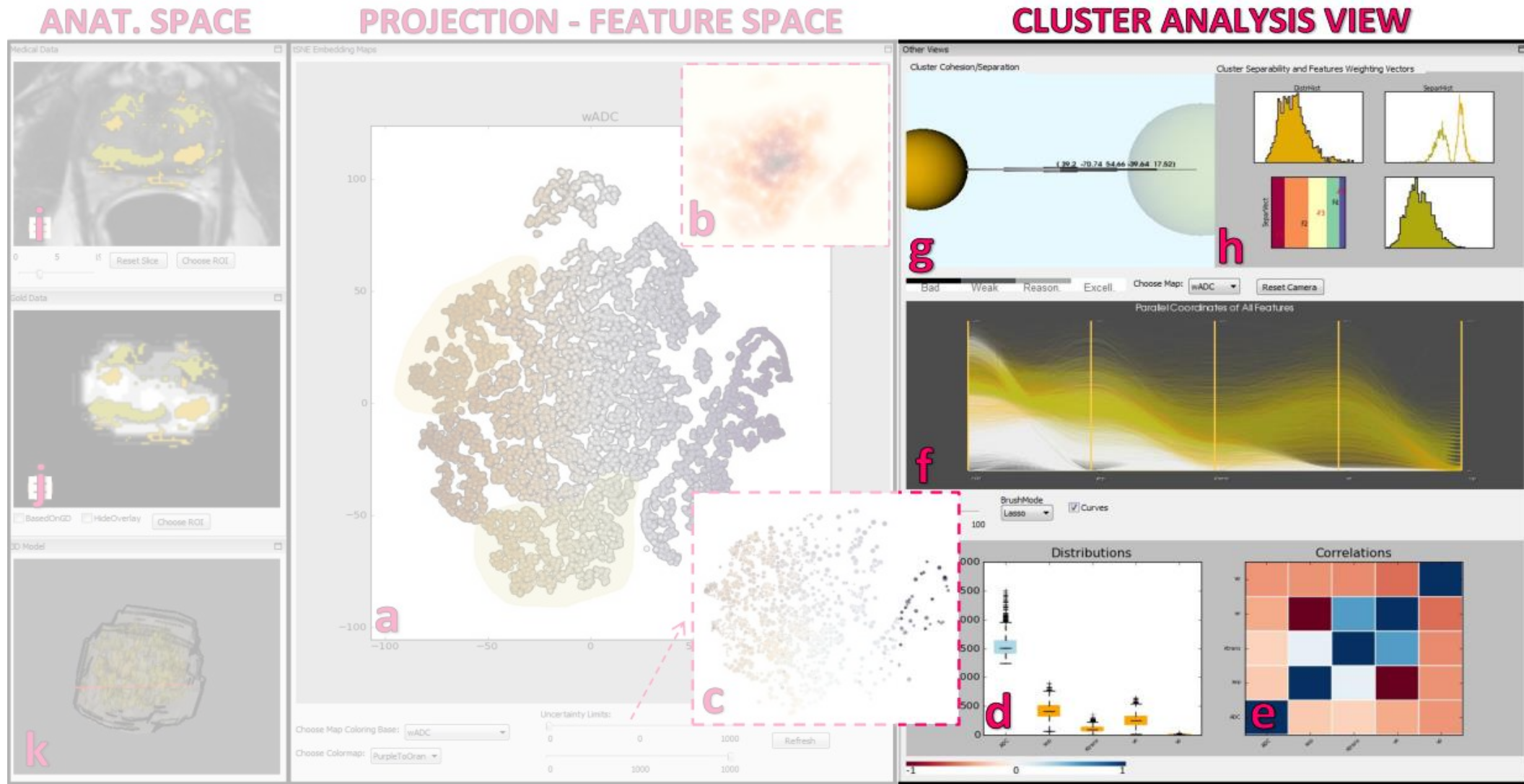


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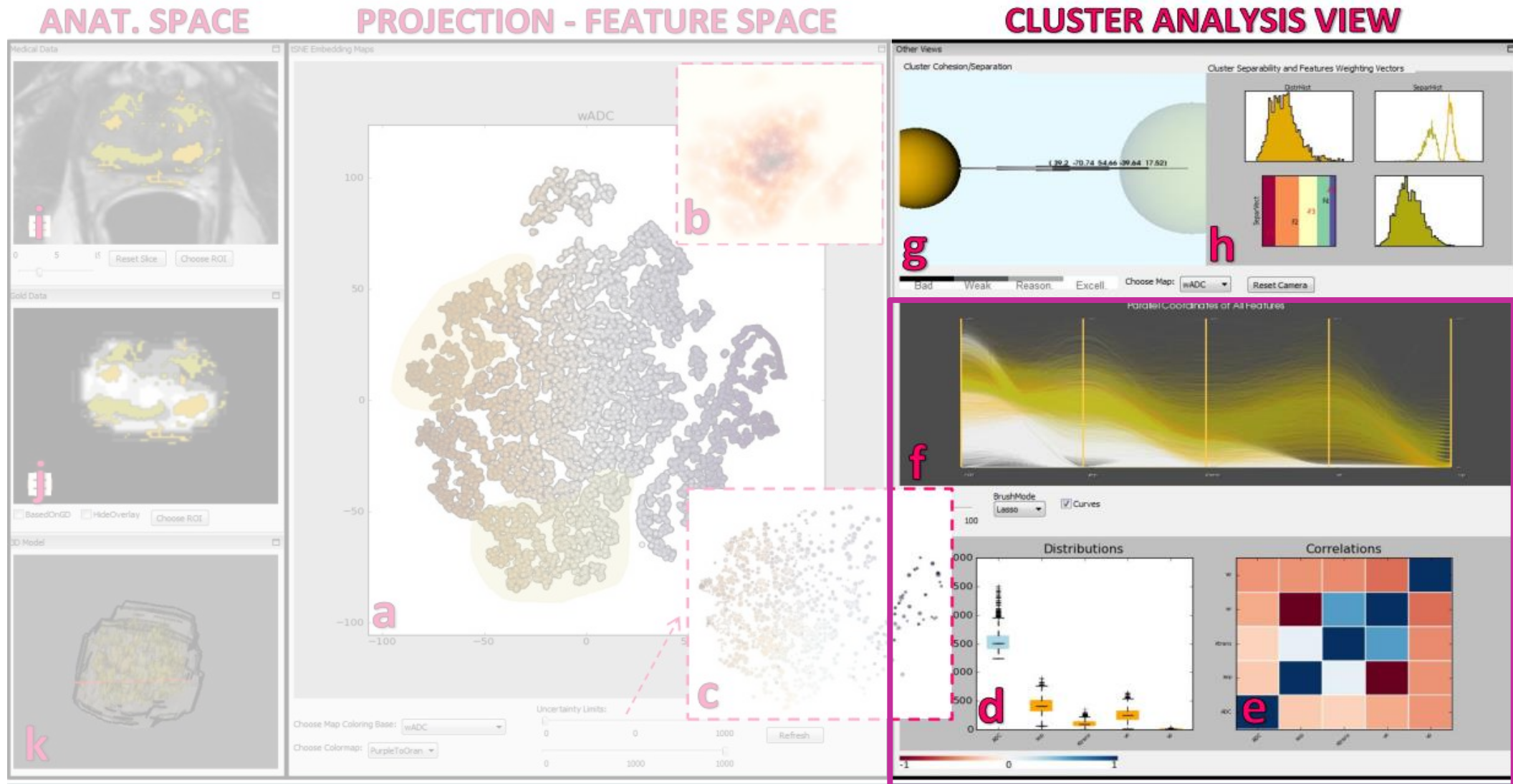


# 2. Analysis and Comparison of Intra-tumor Regions

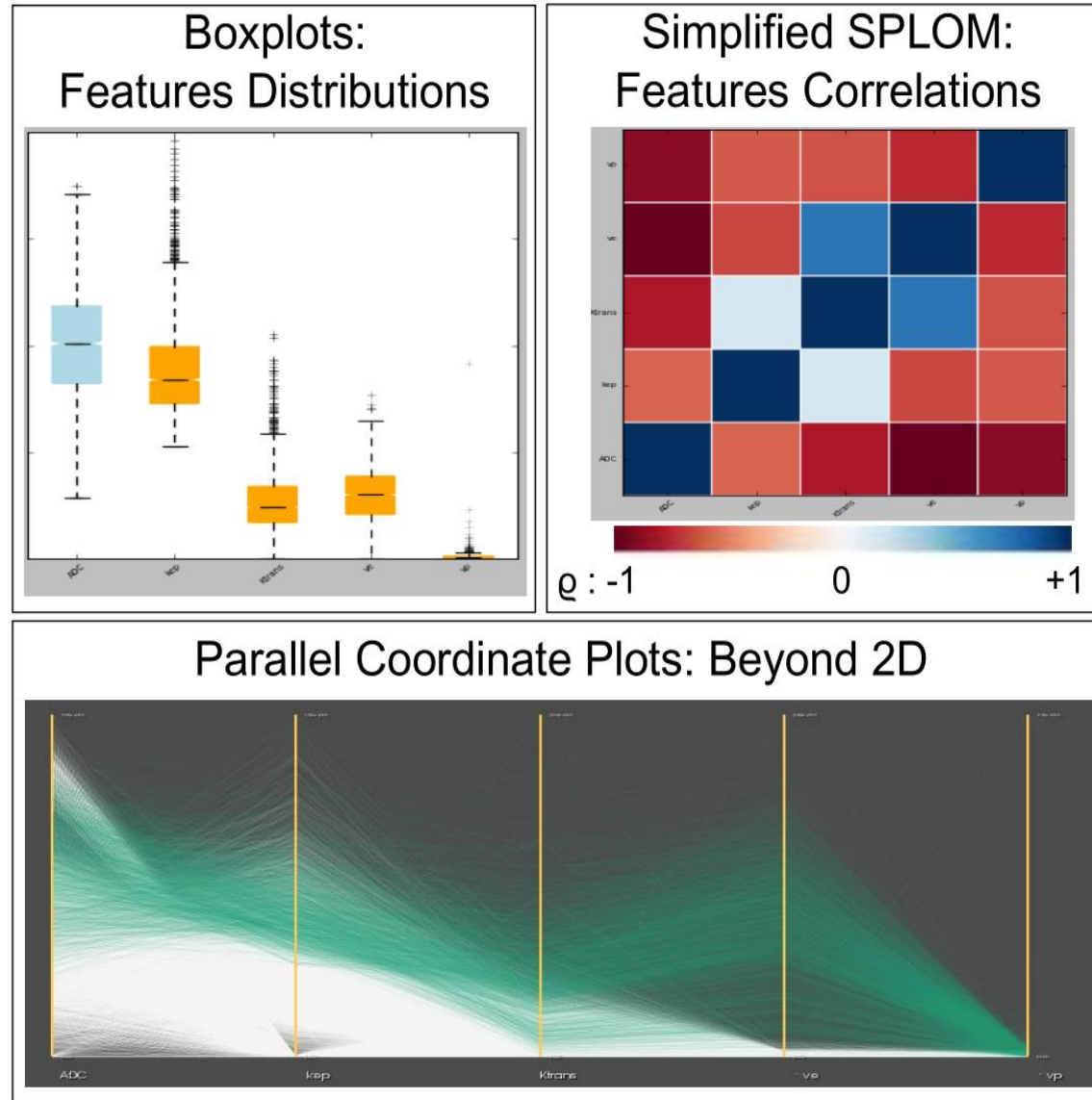




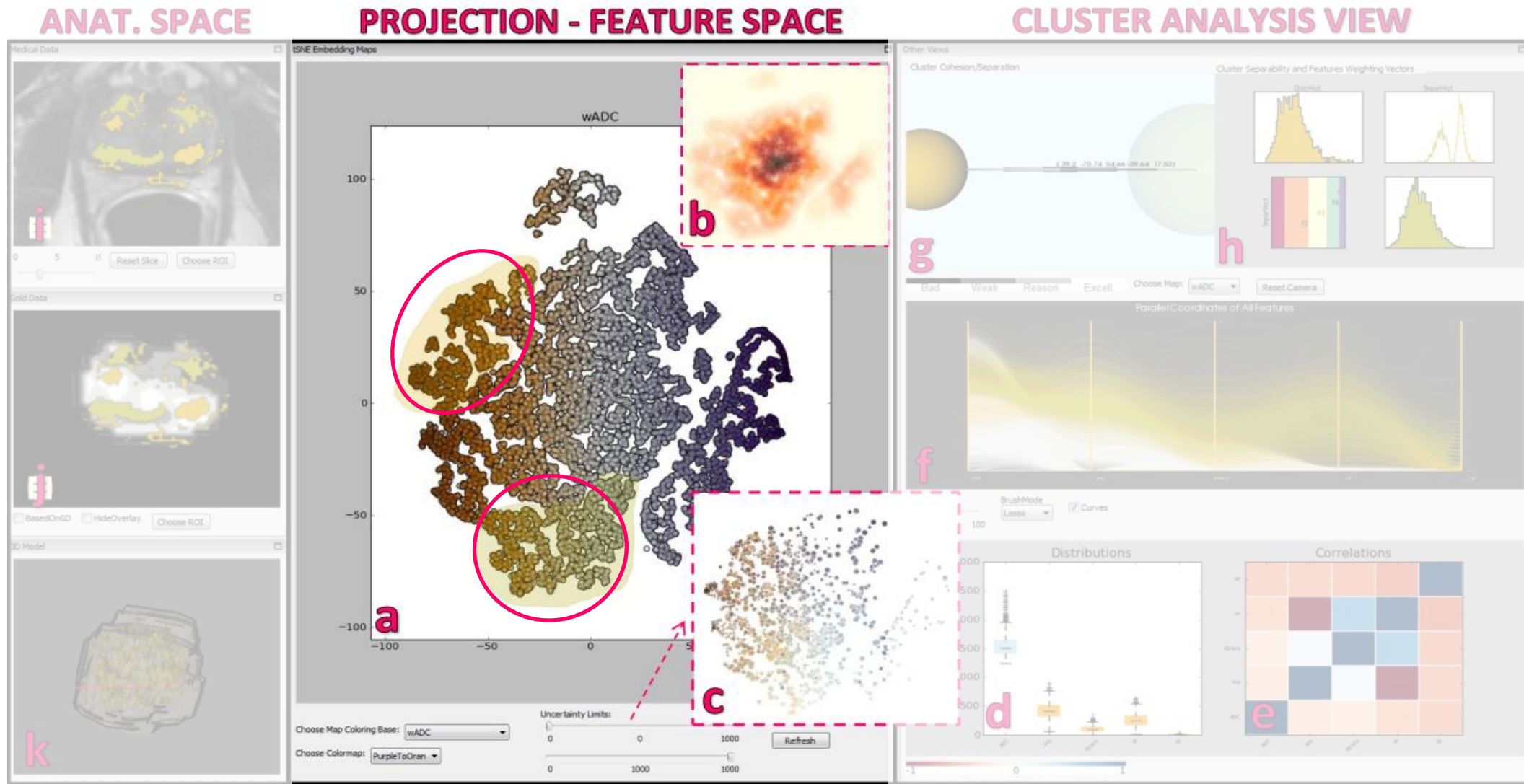
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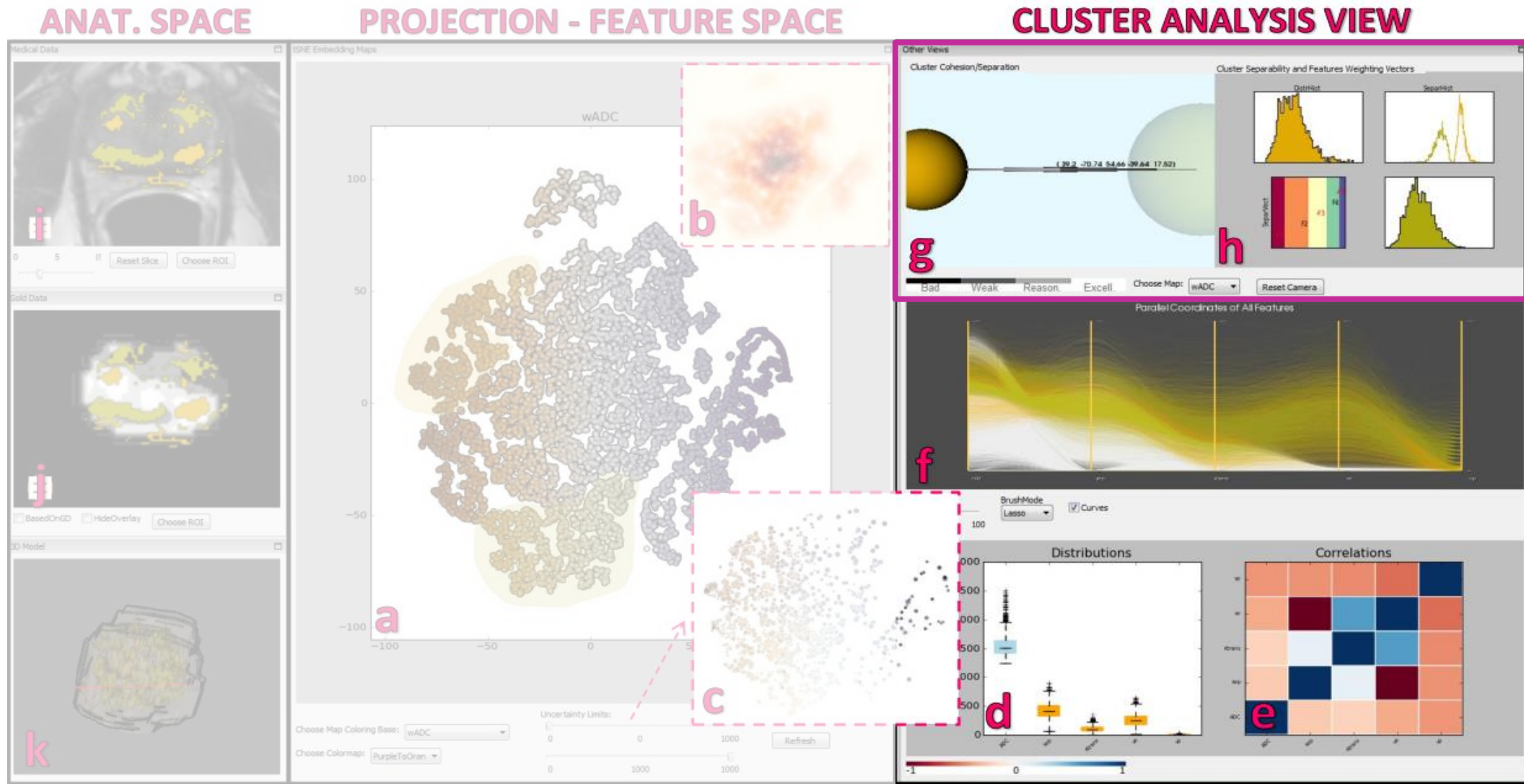


# 2. Analysis and Comparison of Intra-tumor Regions

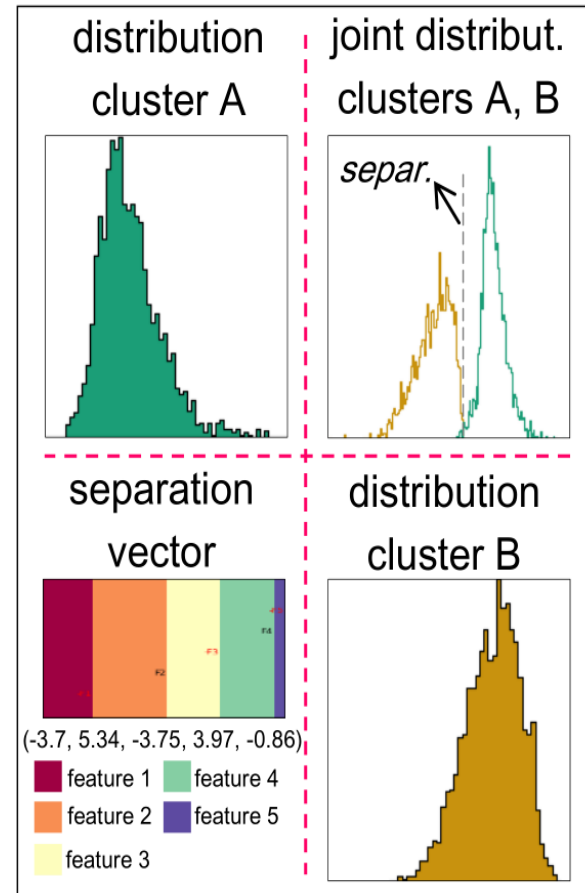
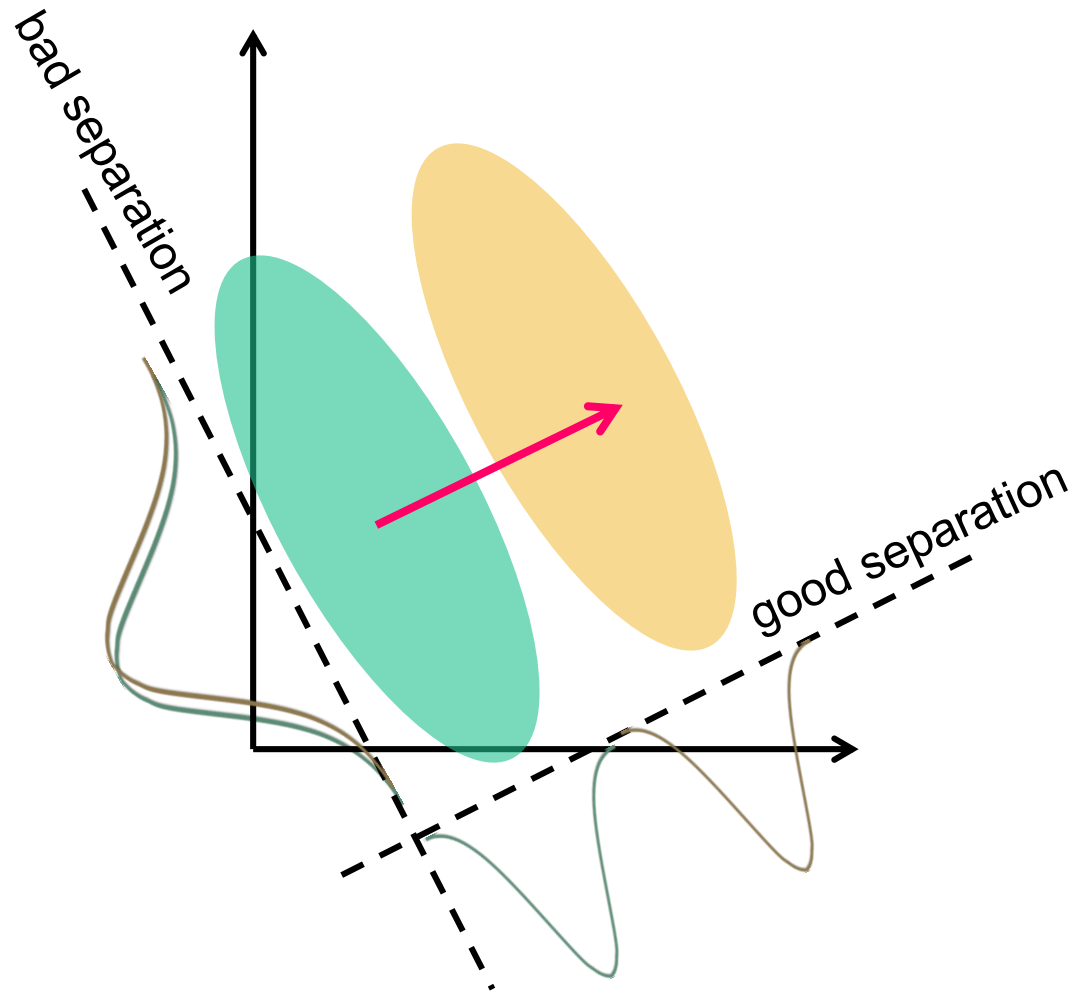




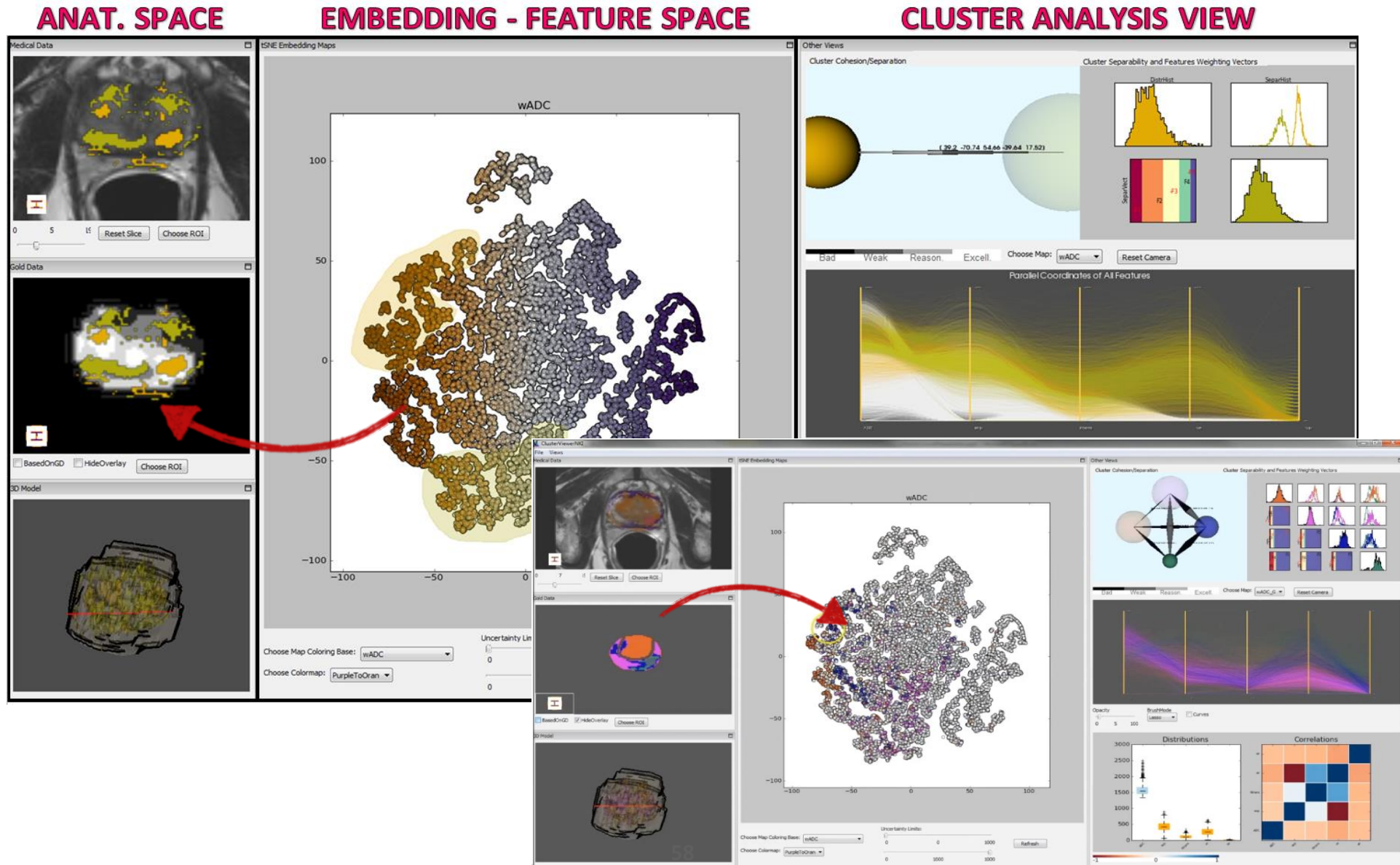
# 2. Analysis and Comparison of Intra-tumor Regions



# 2. Analysis and Comparison of Intra-tumor Regions

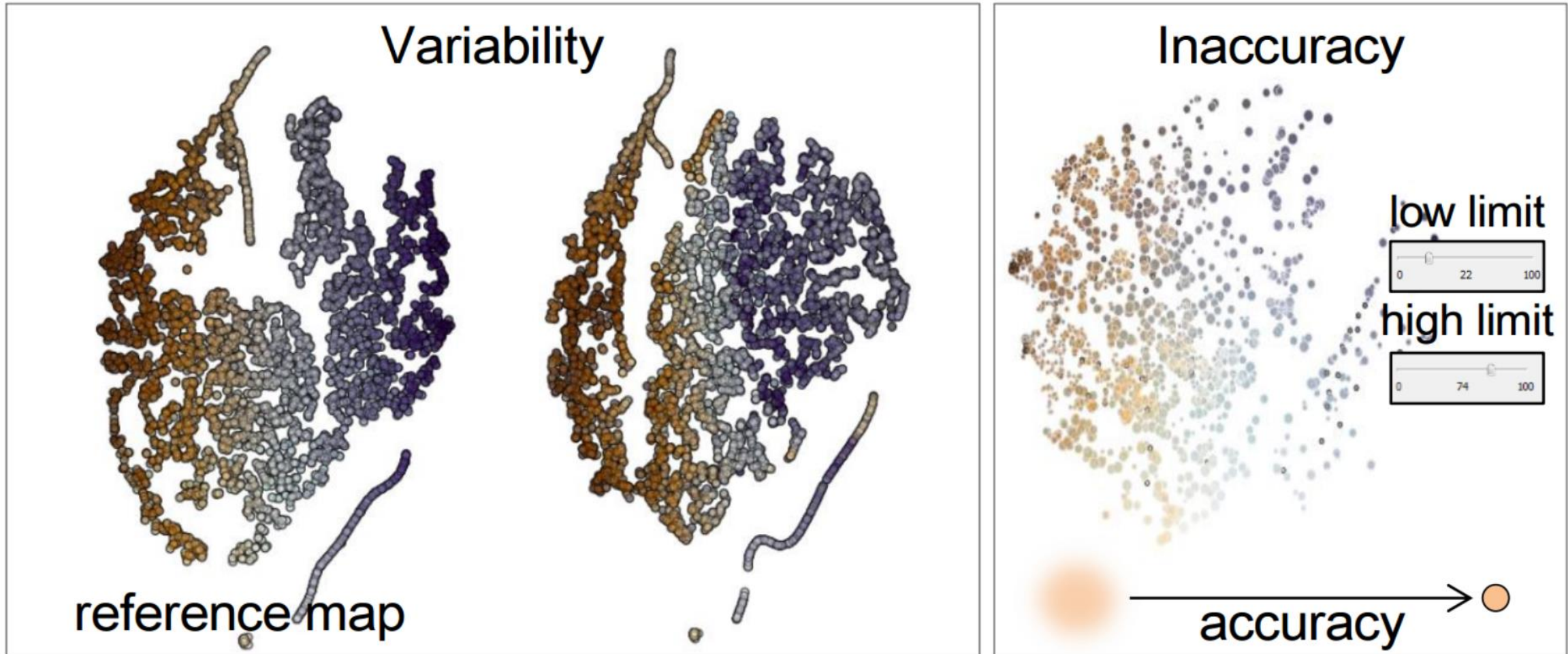


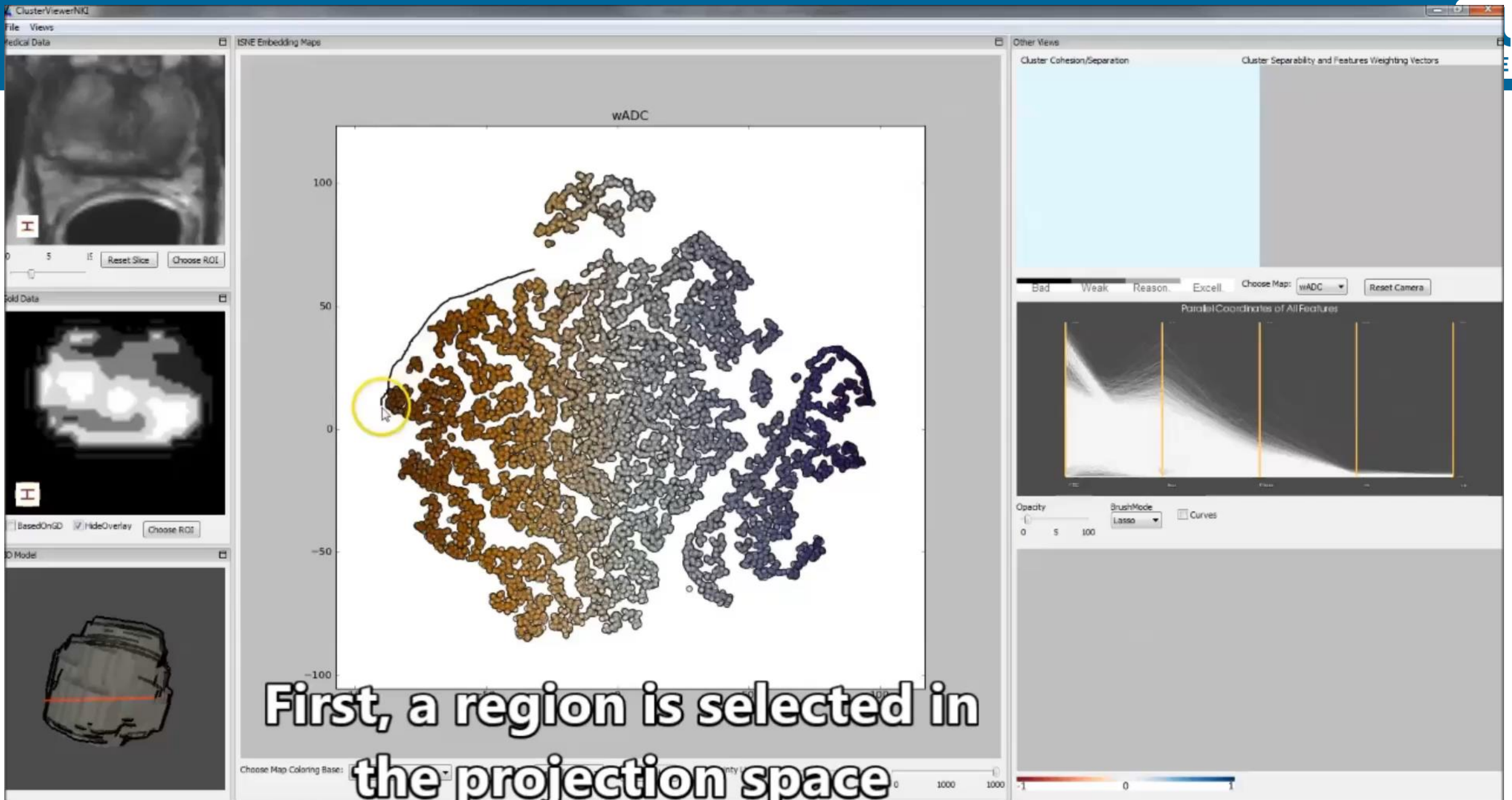
# 3. Association to clinical reference data





# 4. Effect of Variability/Inaccuracy

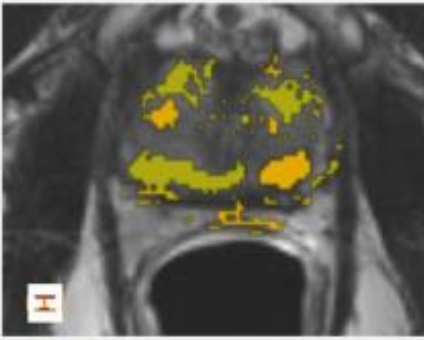




First, a region is selected in the projection space



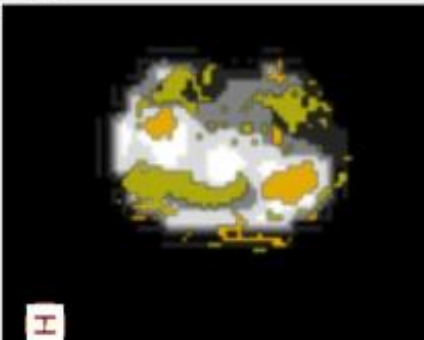
Medical Data



0 5 15

---

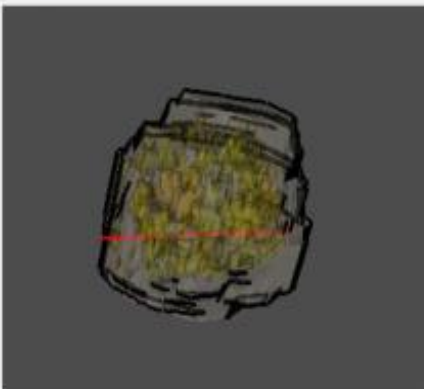
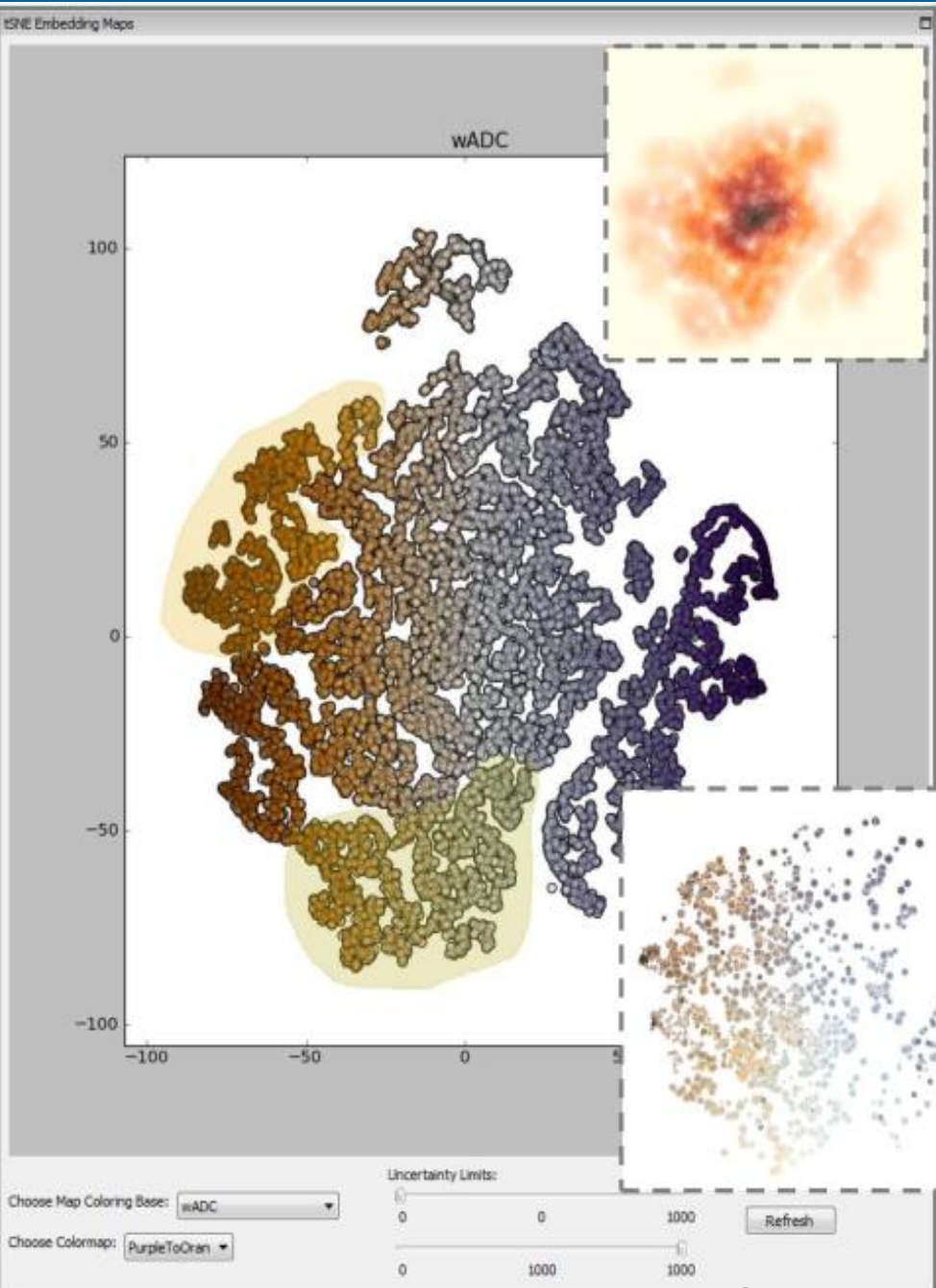
Gold Data



BasedOnGD  HideOverlay

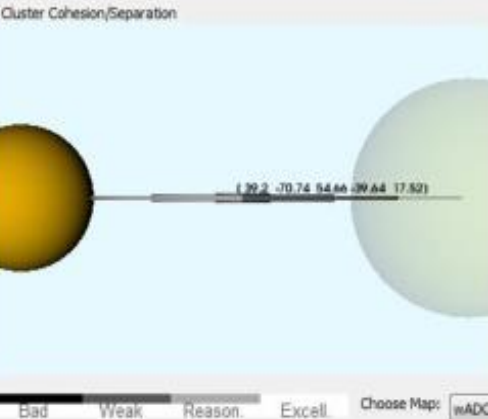
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3D Model

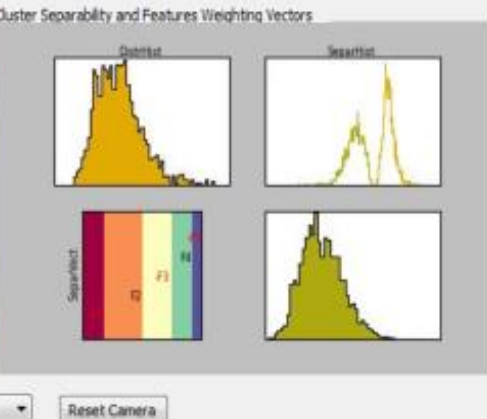



Other Views

Cluster Cohesion/Separation

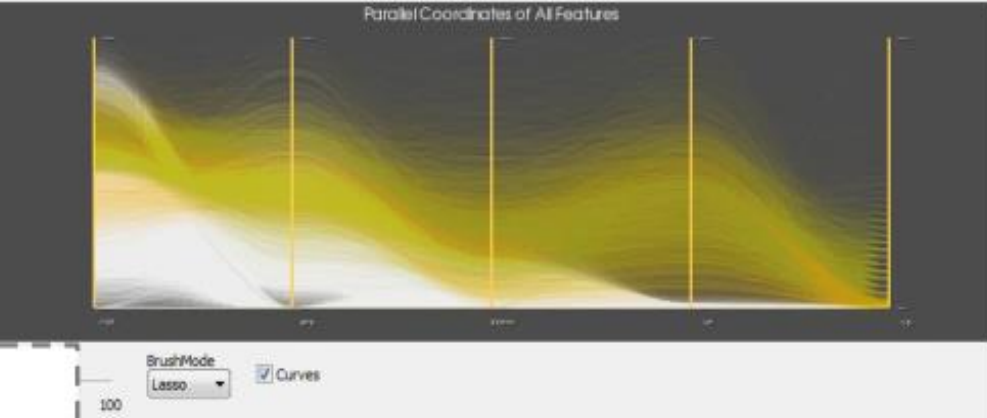


Cluster Separability and Features Weighting Vectors



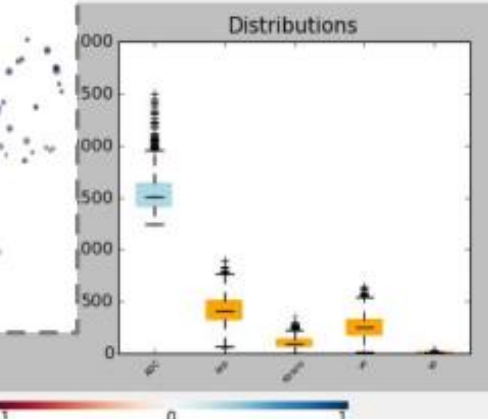
Bad Weak Reason Excell Choose Map:

Parallel Coordinates of All Features

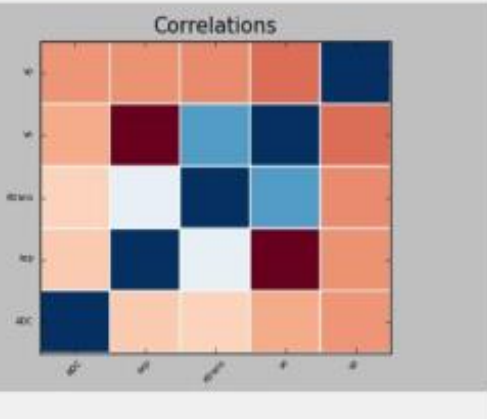


BrushMode:   Curves

Distributions



Correlations



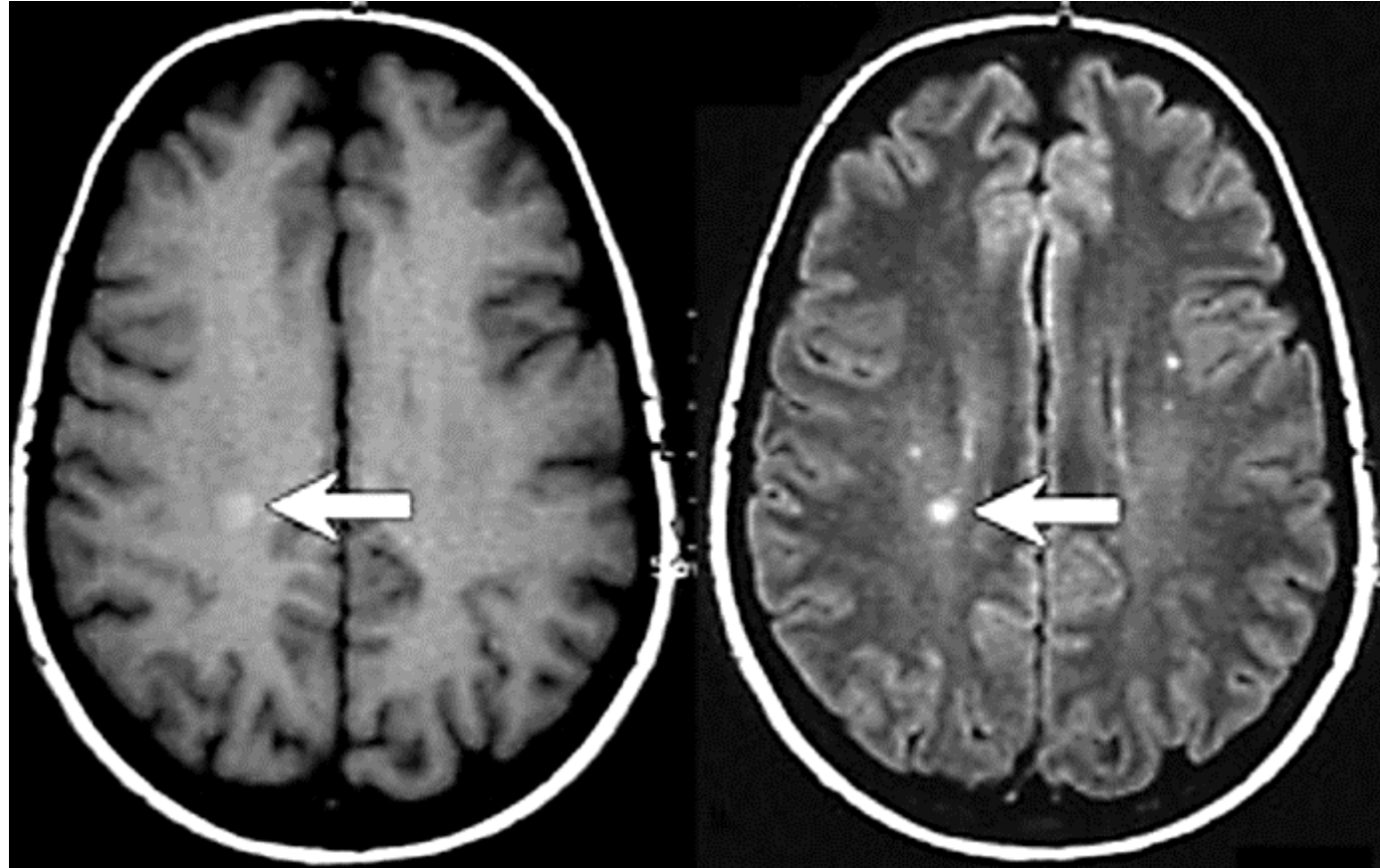
- Prostate Tumor Exploration
  - With Histopathological Data → Simple imaging features not enough for GS
  - With Risk Prediction Data → Current prediction models are sub-optimal
- Cervical Tumor Exploration
  - Validation of Different Models
- Lung Tumor Exploration
  - Evaluate the importance of multi-modal imaging in region detection
- Smart Feature Selection for Aiding the Design of Classifiers



- Prostate Tumor Exploration
  - With Histopathological Data → Simple imaging features not enough for GS
  - With Risk Prediction Data → Current prediction models are sub-optimal
- Cervical Tumor Exploration
  - Validation of Different Models
- Lung Tumor Exploration
  - Evaluate the importance of multi-modal imaging in region detection
- **Smart Feature Selection for Aiding the Design of Classifiers**



## White Matter Hyperintensities (WMH)

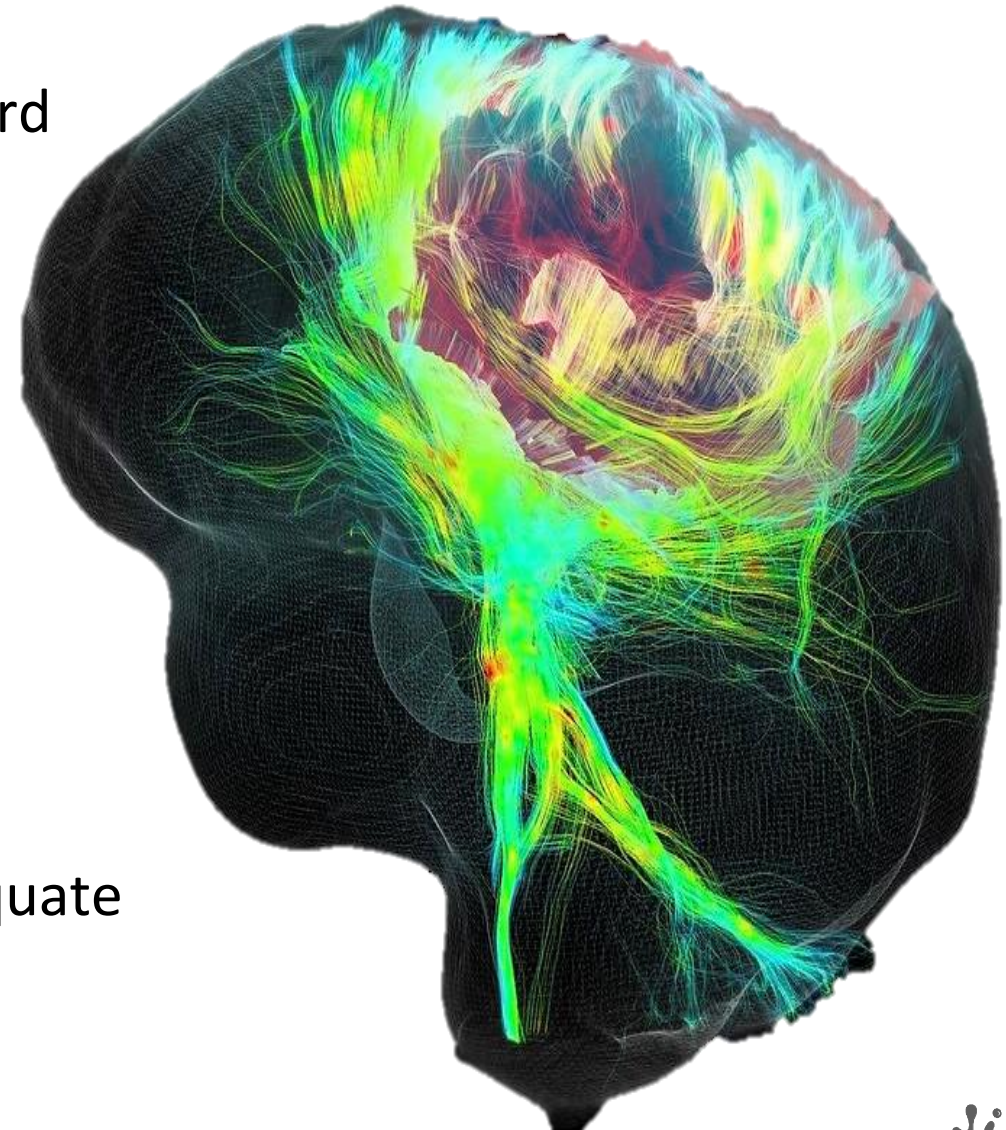


Segmentation for prognosis and disease monitoring





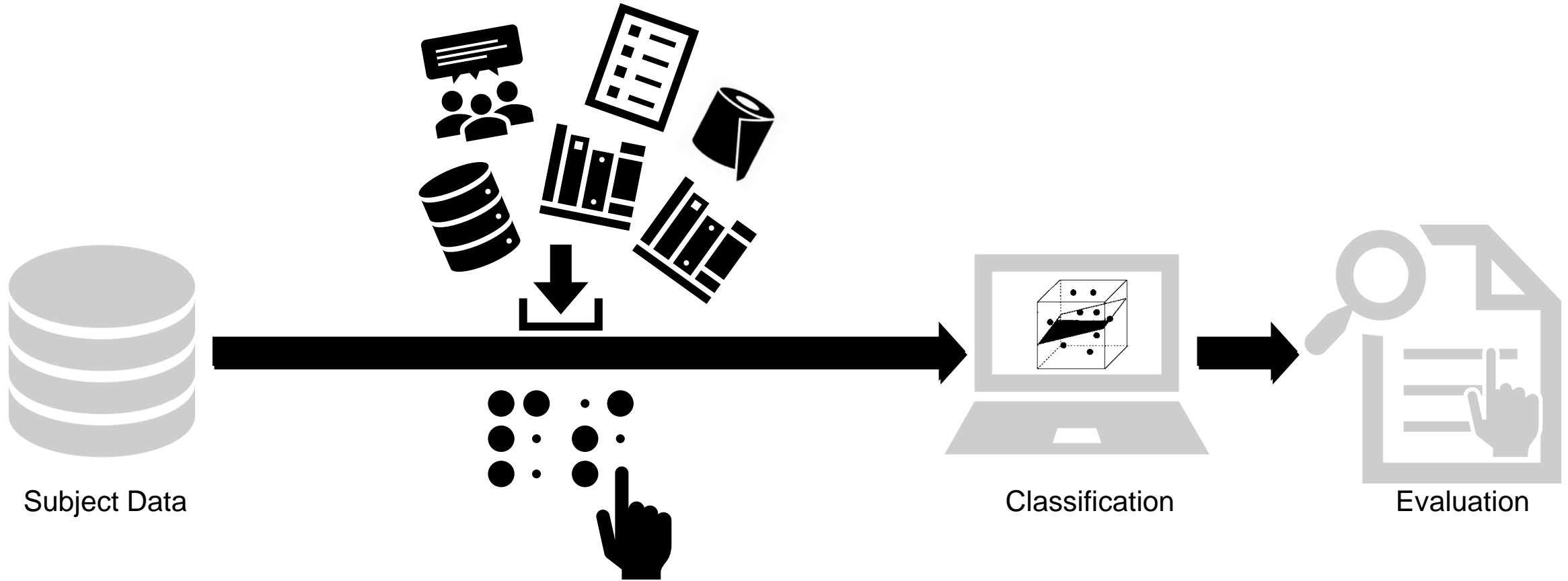
- Conventionally: T1 and T2.
- Diffusion MRI can provide additional features [Maillard 2013, Kuijf 2014]. Which features of all?
- Careful selection of features is more important than chosen classification algorithm [Sweeney 2014].
- Currently, this is a black box!
- A new pipeline, to aid the design of WMH classifiers.
- It provides new insight into the entire classification procedure, especially, in the identification of an adequate feature list, and the analysis of the outcome.



- 20 subjects of the MRBrainS13 challenge.
- Ground truth: manual delineations of WMH.
- 3T MR exam: T1-weighted, multi-slice FLAIR, multi-slice IR, single-shot EPI DTI sequence with 45 directions.
- Features: T1, FLAIR, IR, FA, MD, AD, RD, CL, CP, CS and the MNI152-normalized spatial coordinates [Kuijf 2014].

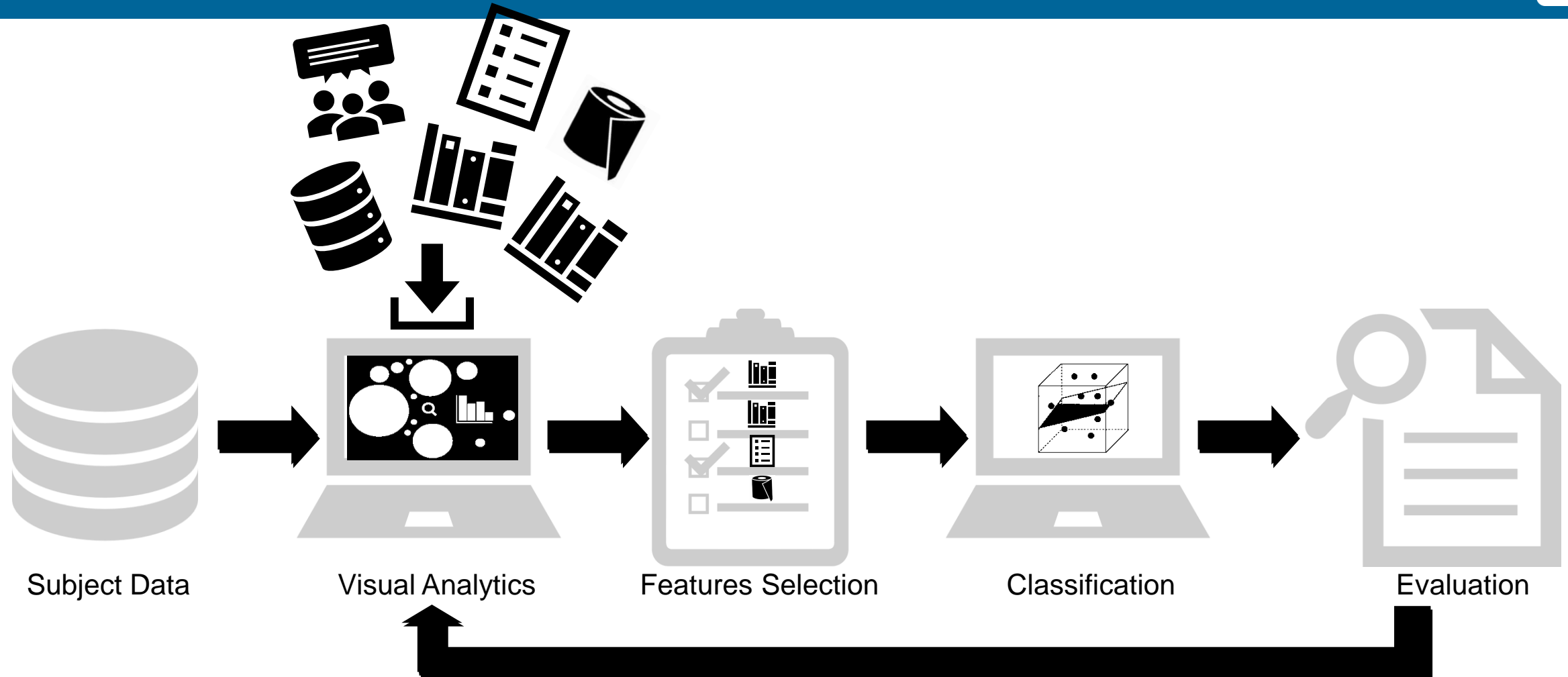


# Current Method

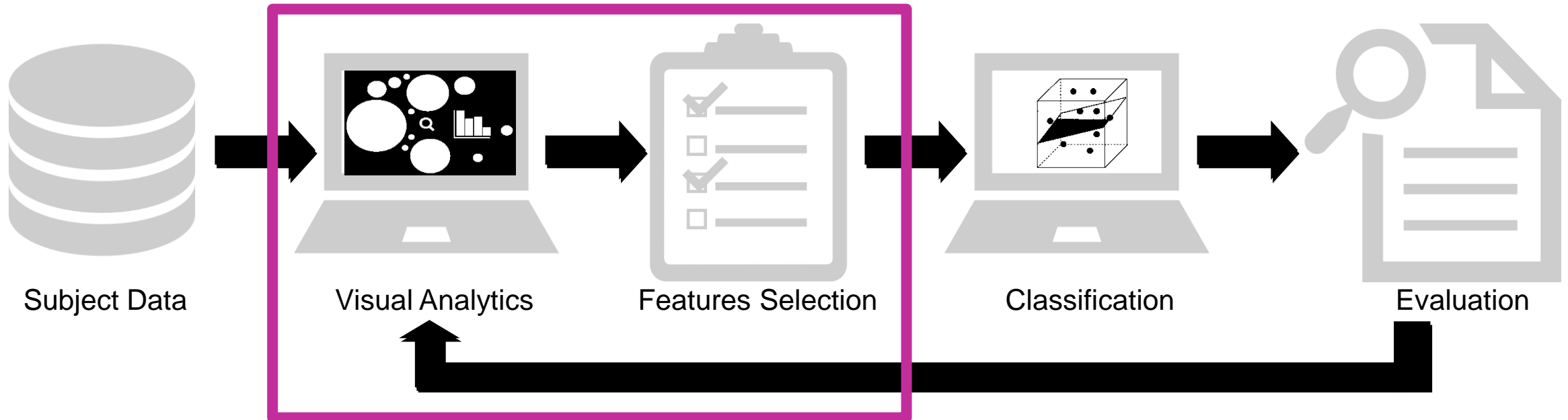




# Our Method

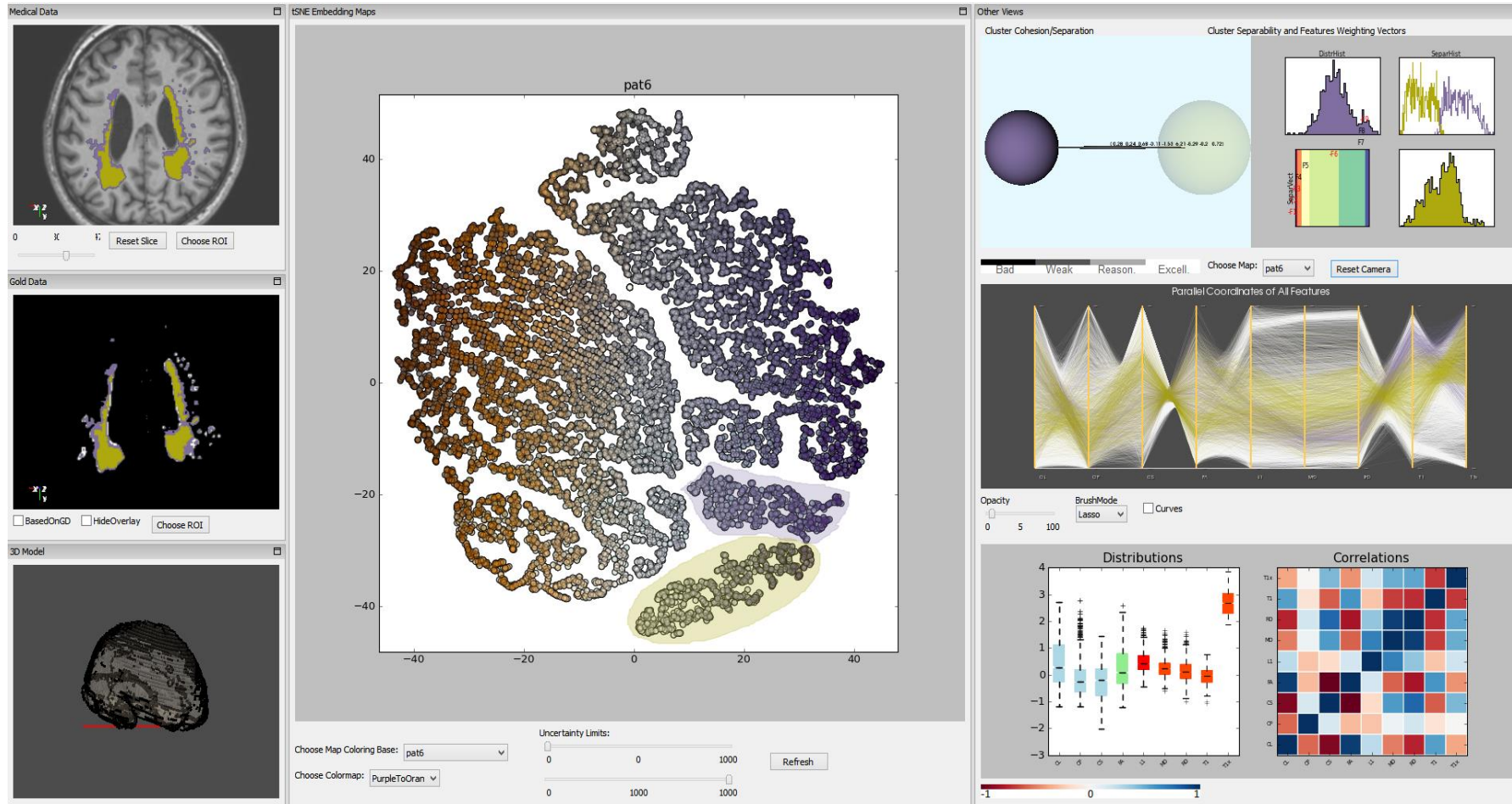


# Step-by-step Approach and Results



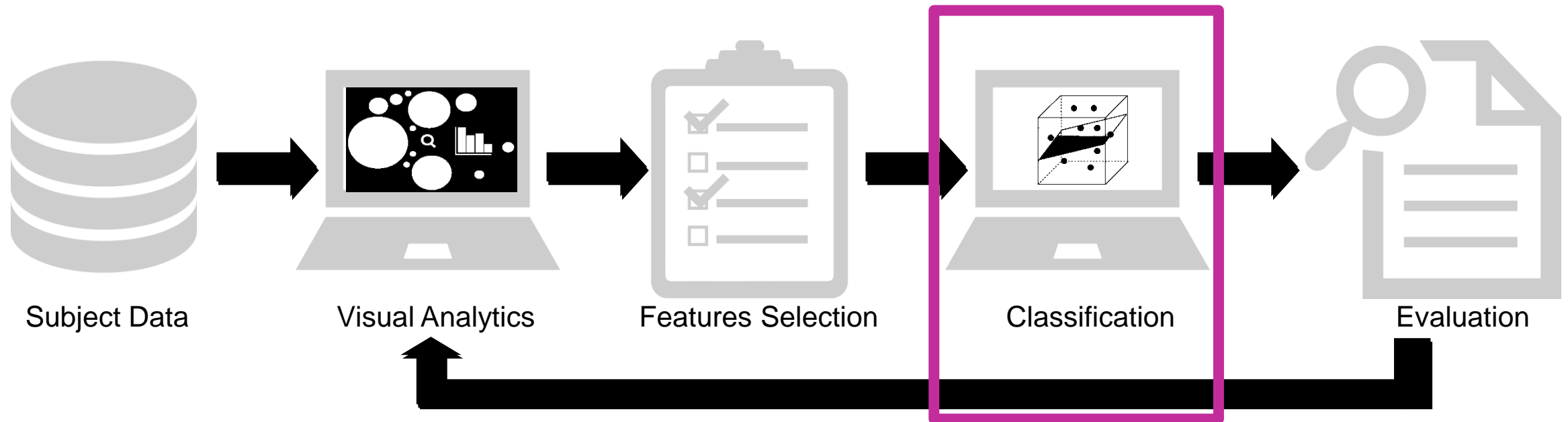
# Step-by-step Approach and Results

- Interactive exploration of the WMH structures and their intrinsic imaging-derived characteristics.
- Optimal set of features for the classifier is the combination of (T2-FLAIR, MD, RD, FA, Cs) + T1 & MNI152-normalized spatial coordinates → IR, AD, CL, CP out!



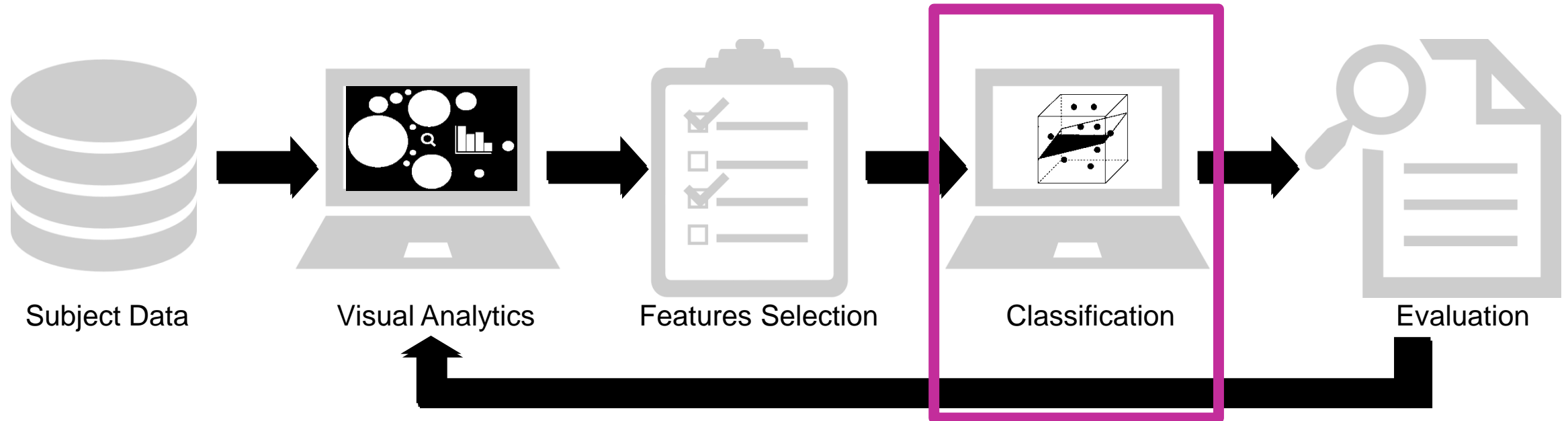
# Step-by-step Approach and Results

As proof-of-concept and for comparison to previous work:  
k-nearest-neighbor classifiers [Kuijf, 2014]  
( $k = 50, 75, \text{ or } 100$ , uniform or distance-based)

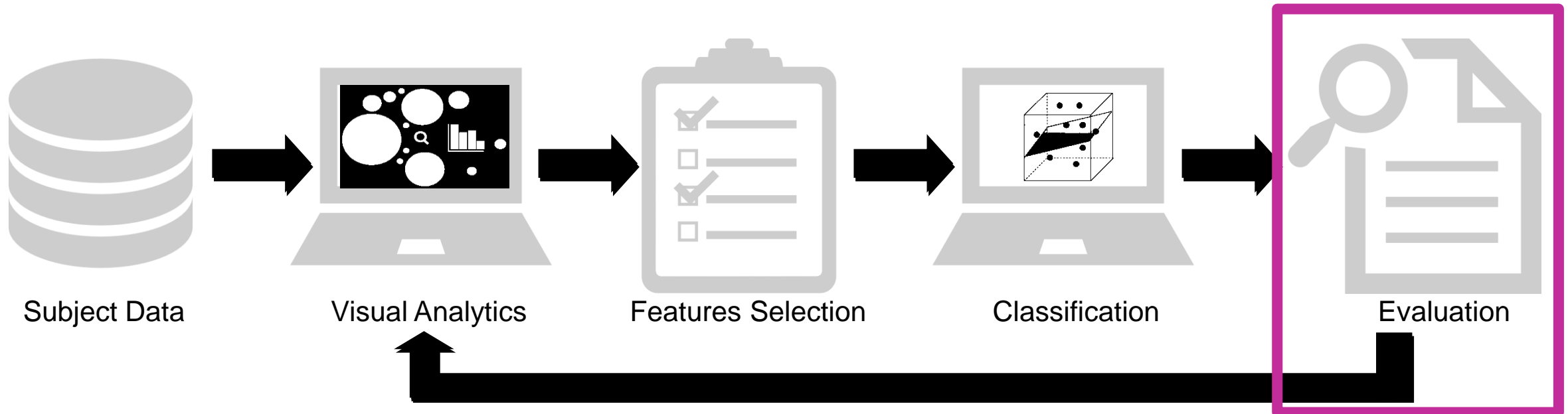


# Step-by-step Approach and Results

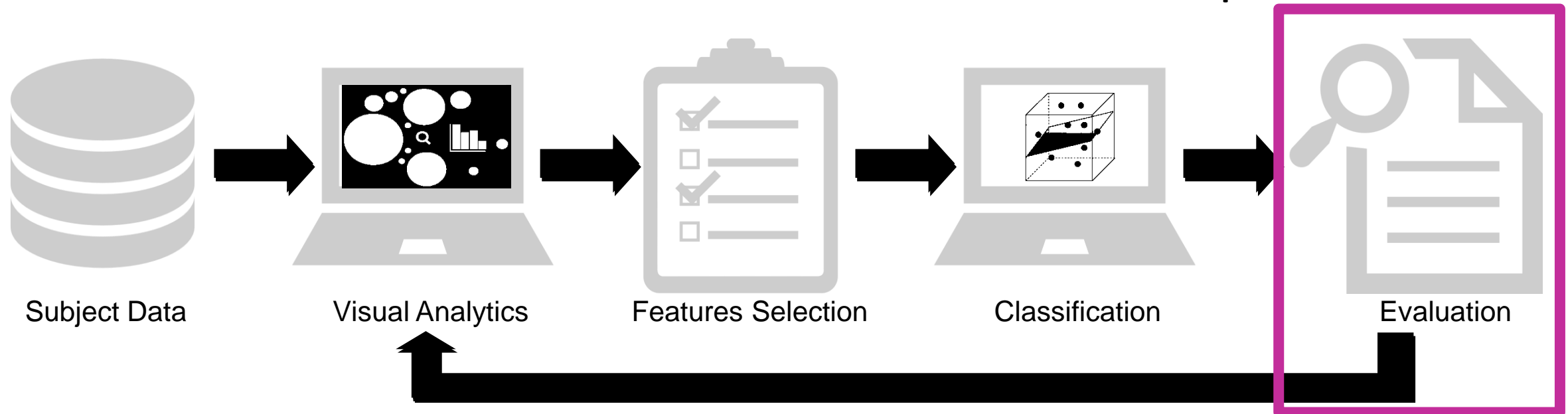
Comparable results with previous automated approaches  
Less features than in previous work  
(saving scanning and computational time)  
Smarter selection of features, not brute-force



- Again with the VA tool
- What was missed?
  - How the classifier works?
  - How can the classifier be improved?



- Core is always detected, periphery is missed – different TCs?
- Posterior WMHs more often missed.
- For different sized WMHs different features more important.

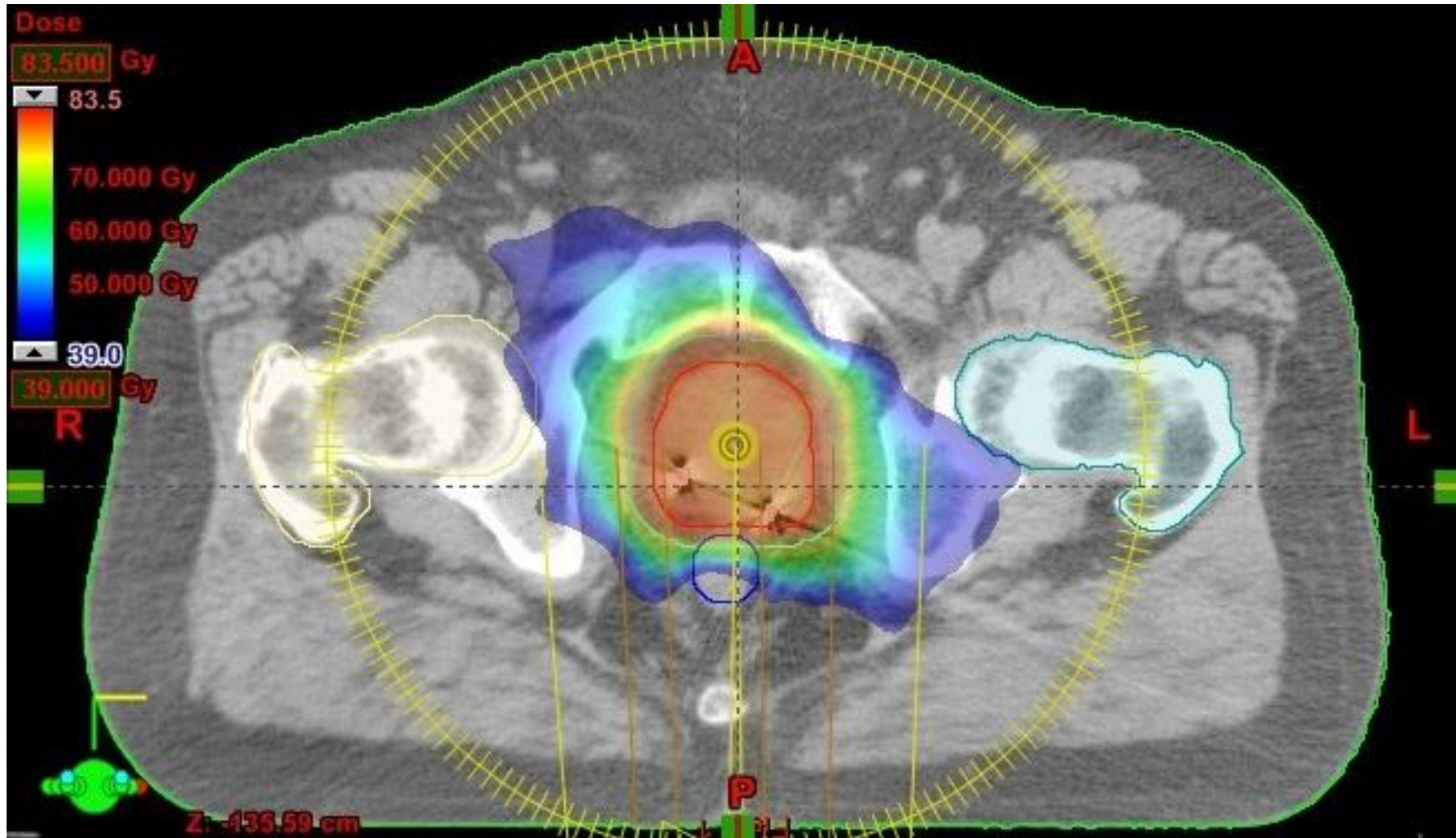


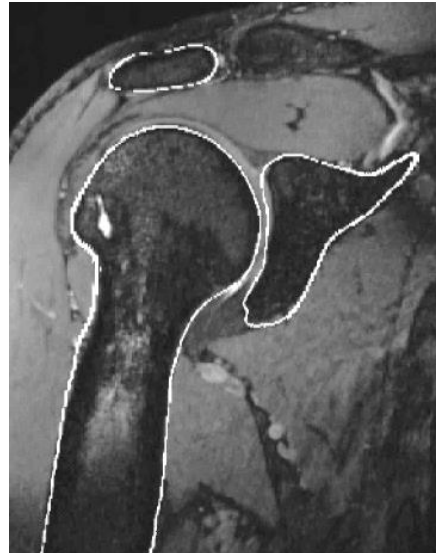
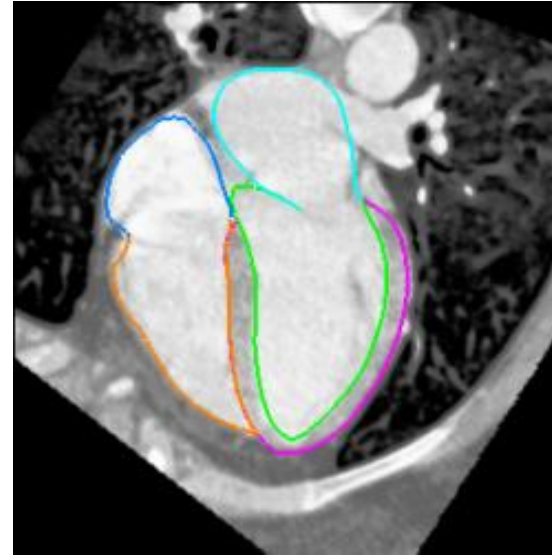
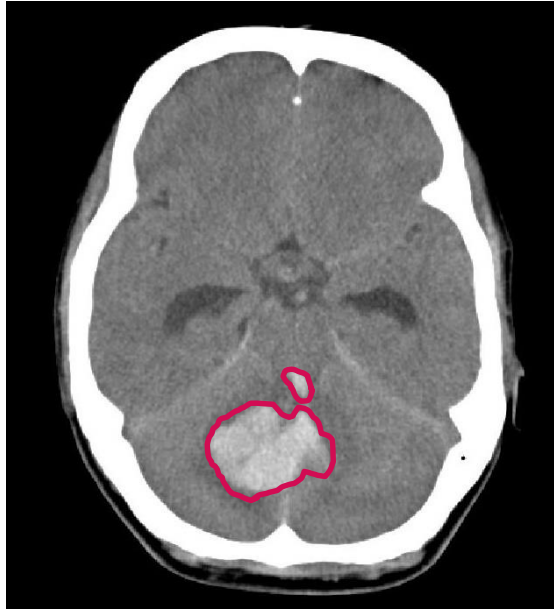


- Aiding the design of tissue classifiers in a “smart” way
- Understanding how features affect the result of the classifications
- Different parts of WMHs potentially require different features
- Better understanding of a complex problem



# Tumors vs. Healthy Organs (at Risk)





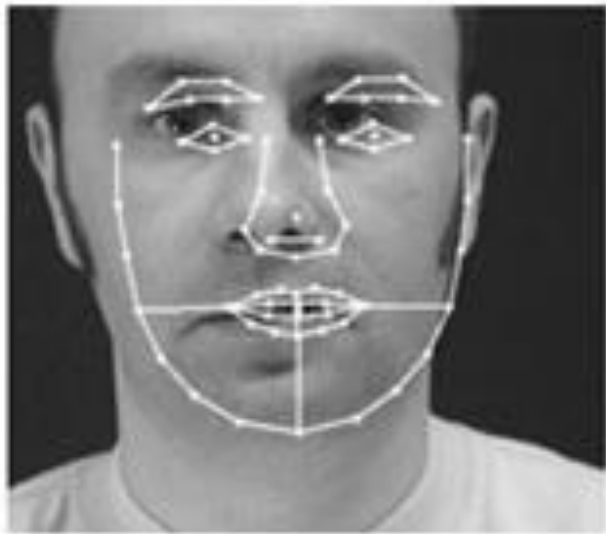
Manually

Semi-automatically

Automatically



# Active Shape Modeling



**Initial**



**After 5 it.s**



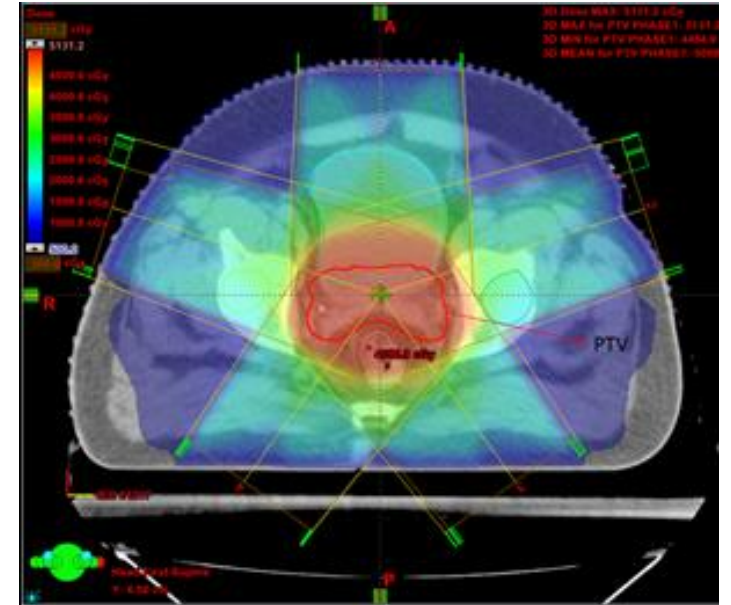
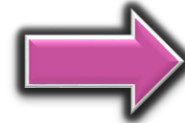
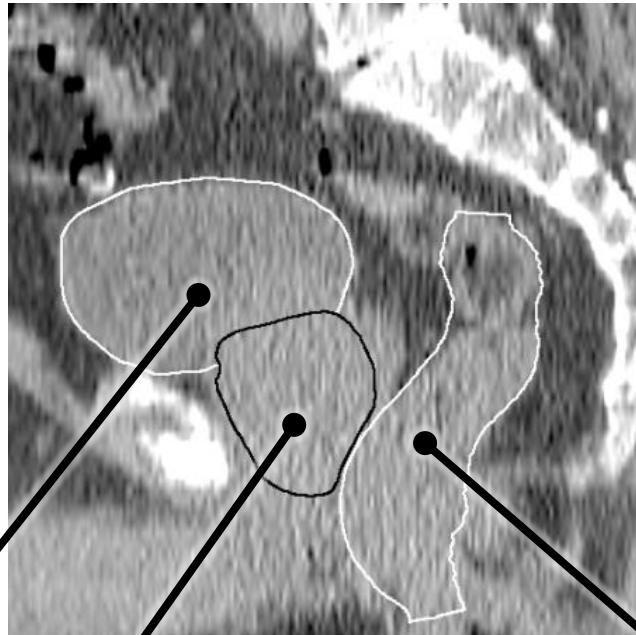
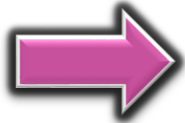
**10 it.s**



**Converged (18 it.s)**







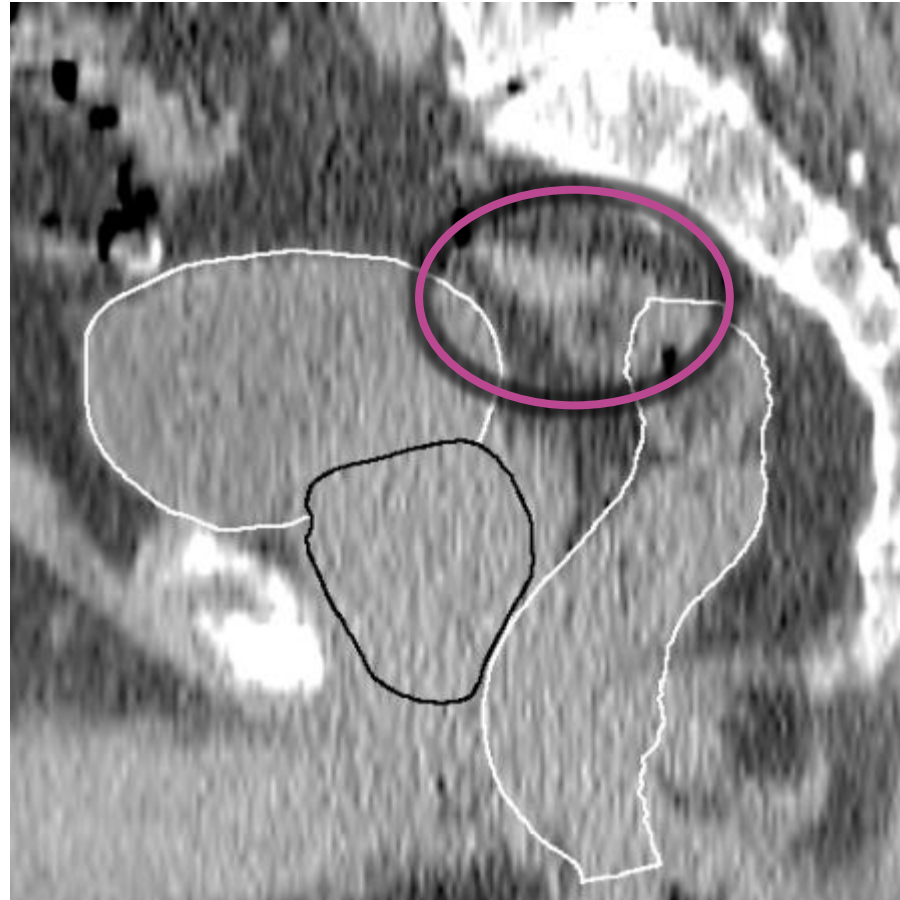
Bladder

Prostate

Rectum

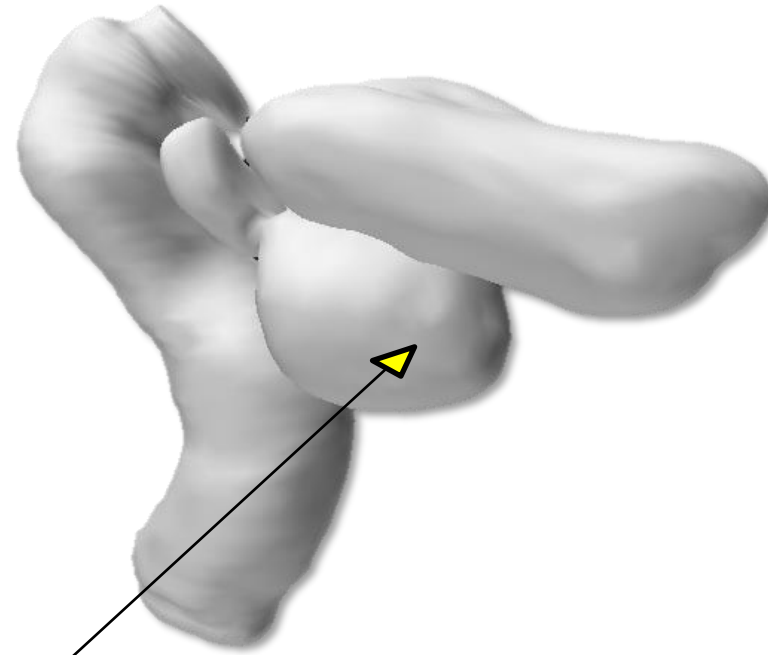
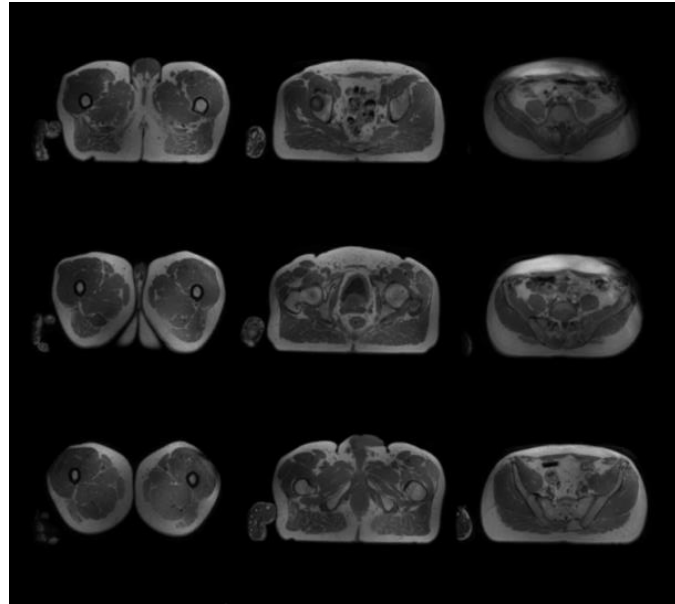


[Schadewaldt et al., 2013]



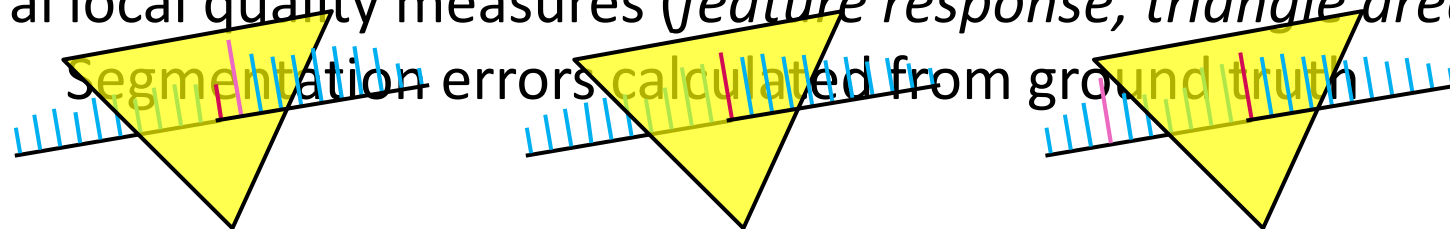
Why was it missed?  
How can it be improved?  
Awareness/prediction of inaccuracies?

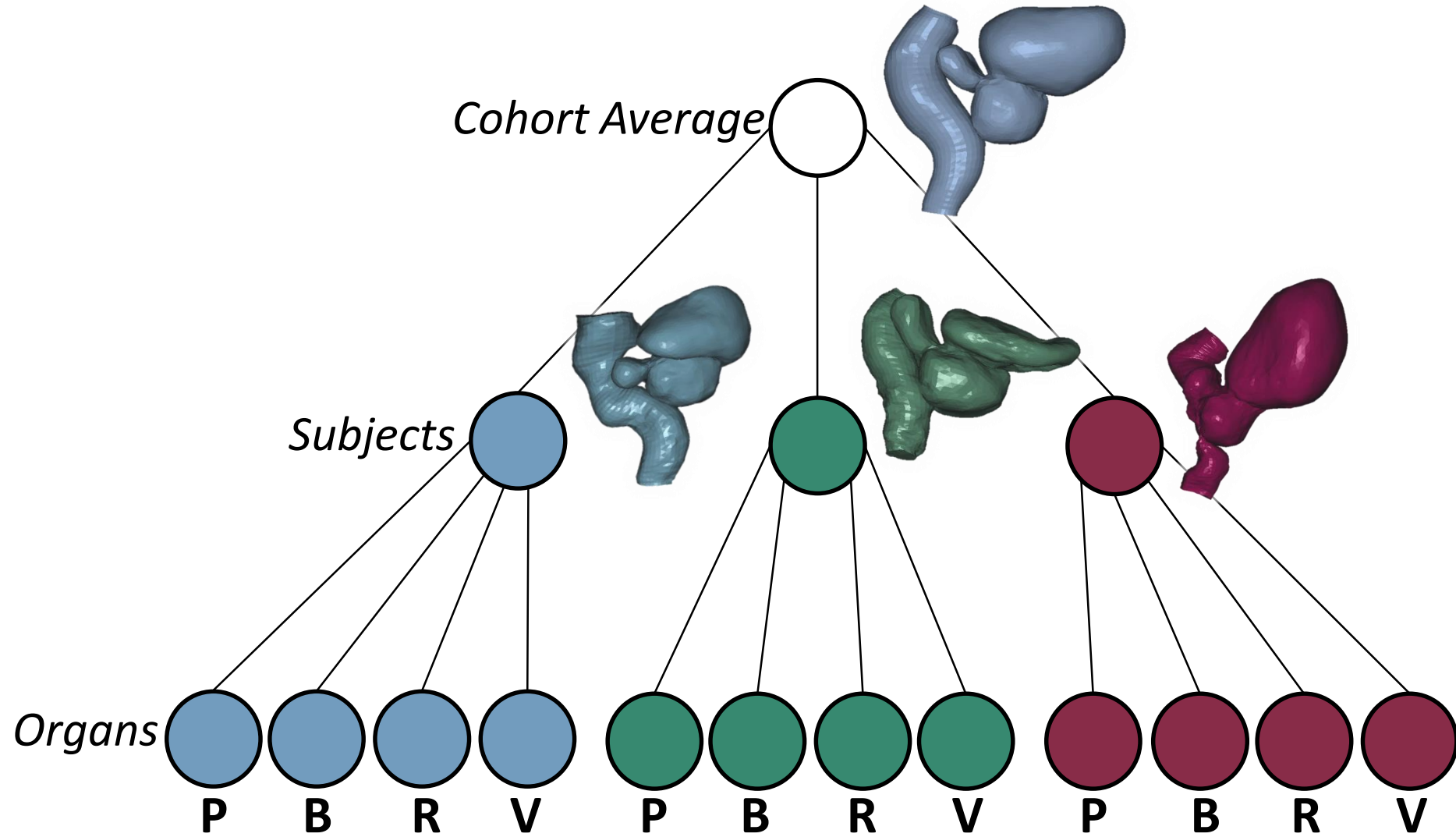




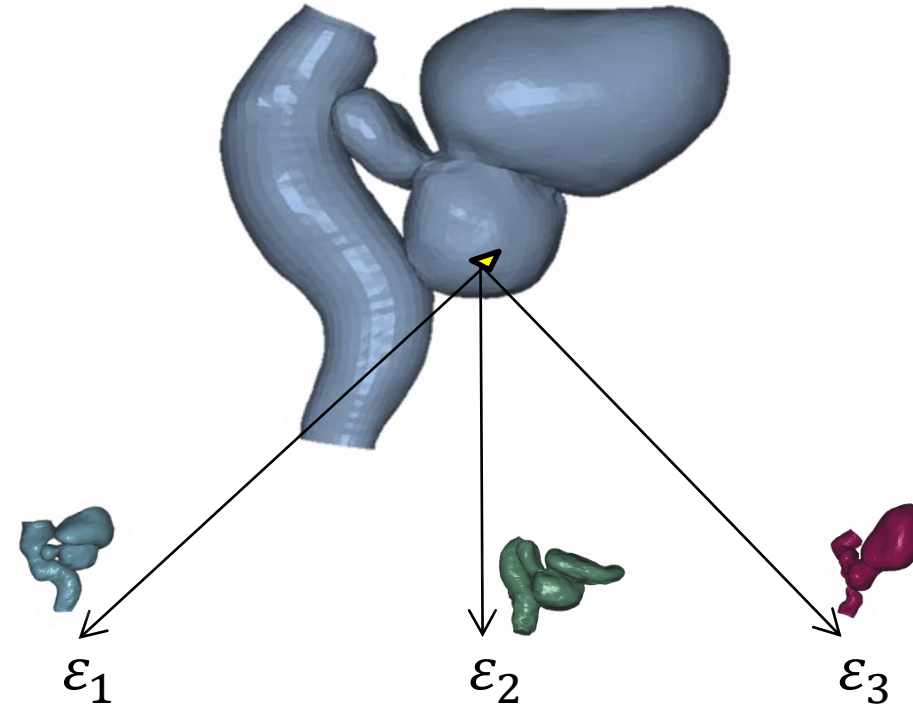
Feature Response Profile

Several local quality measures (*feature response, triangle area,...*)





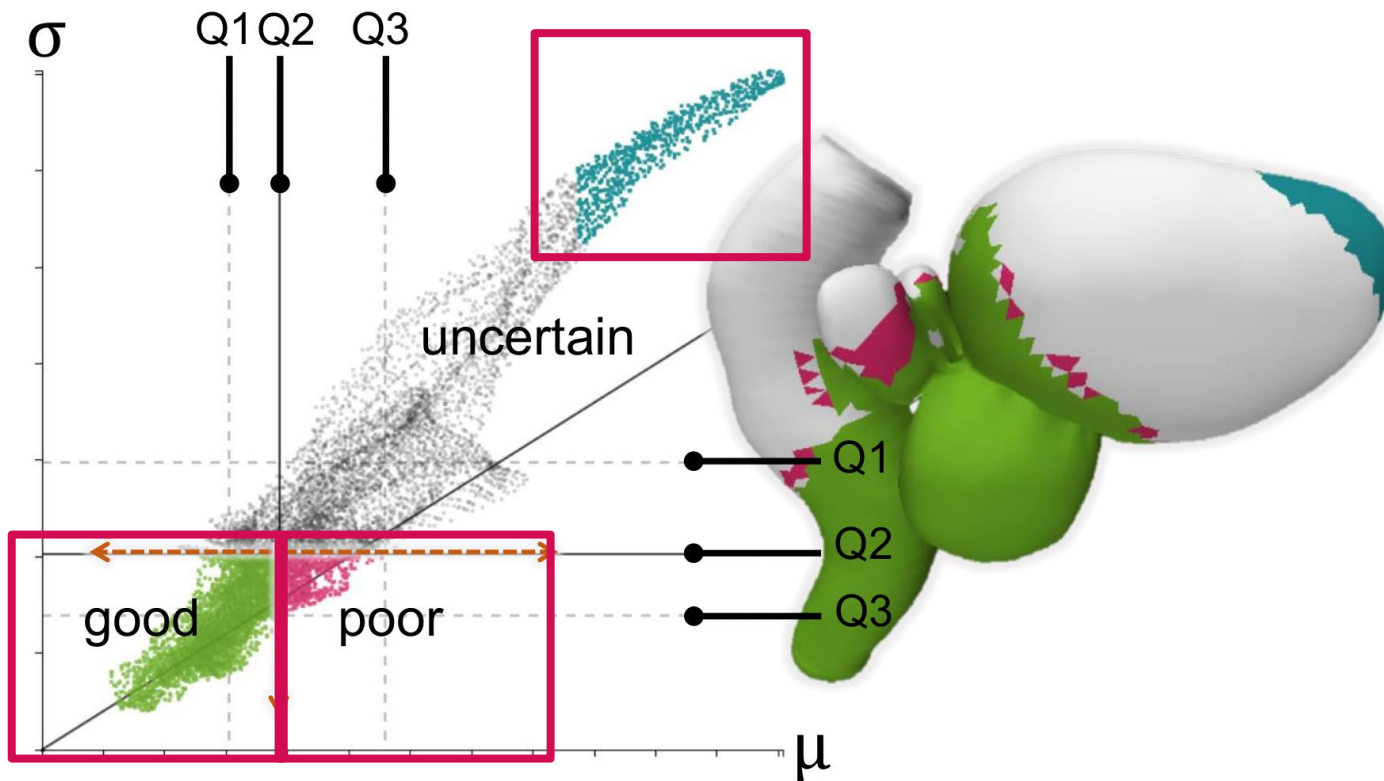
*Cohort Average Mesh*



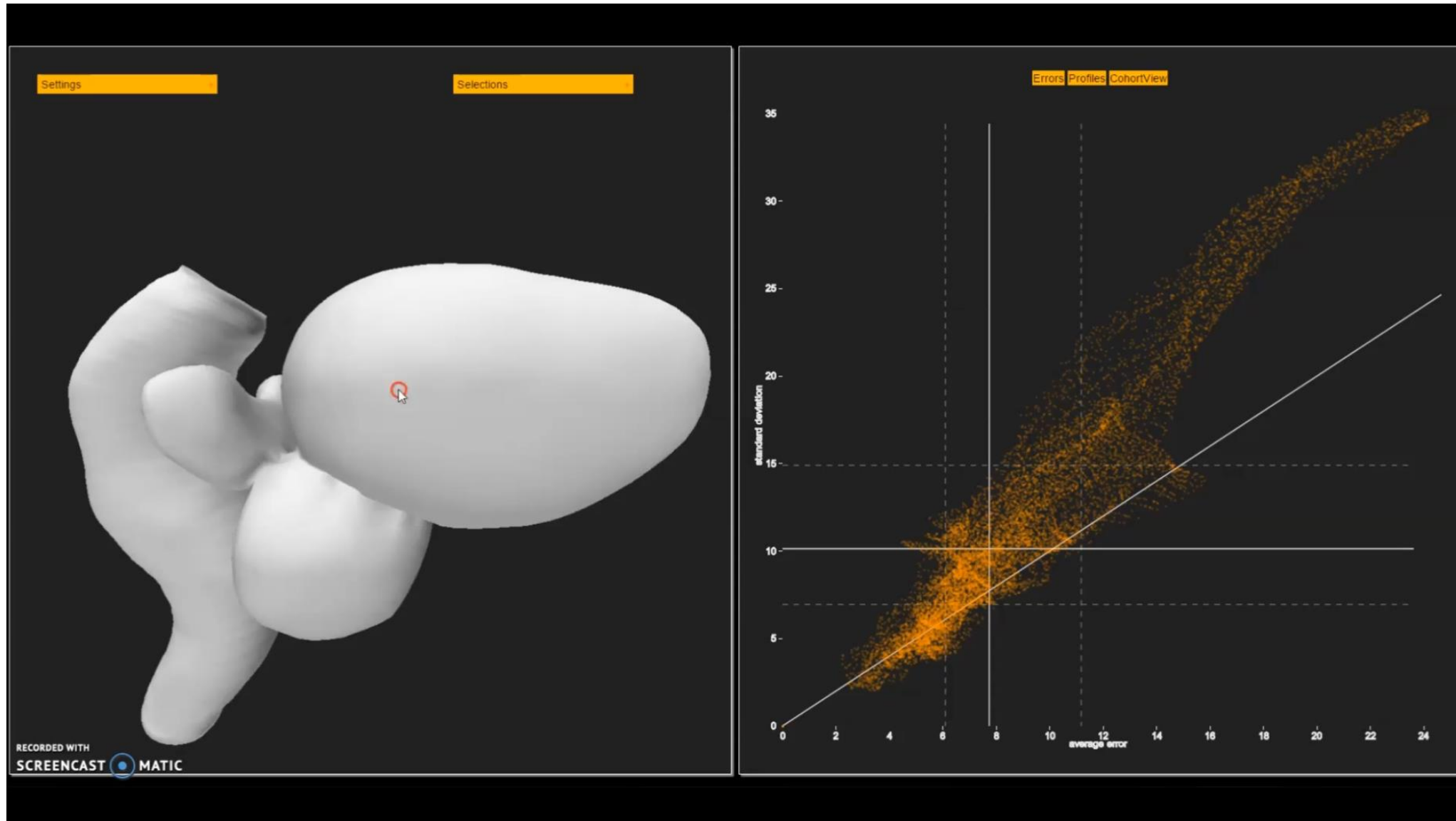
Triangle-to-triangle correspondence between subjects  $\rightarrow (\mu, \sigma)$



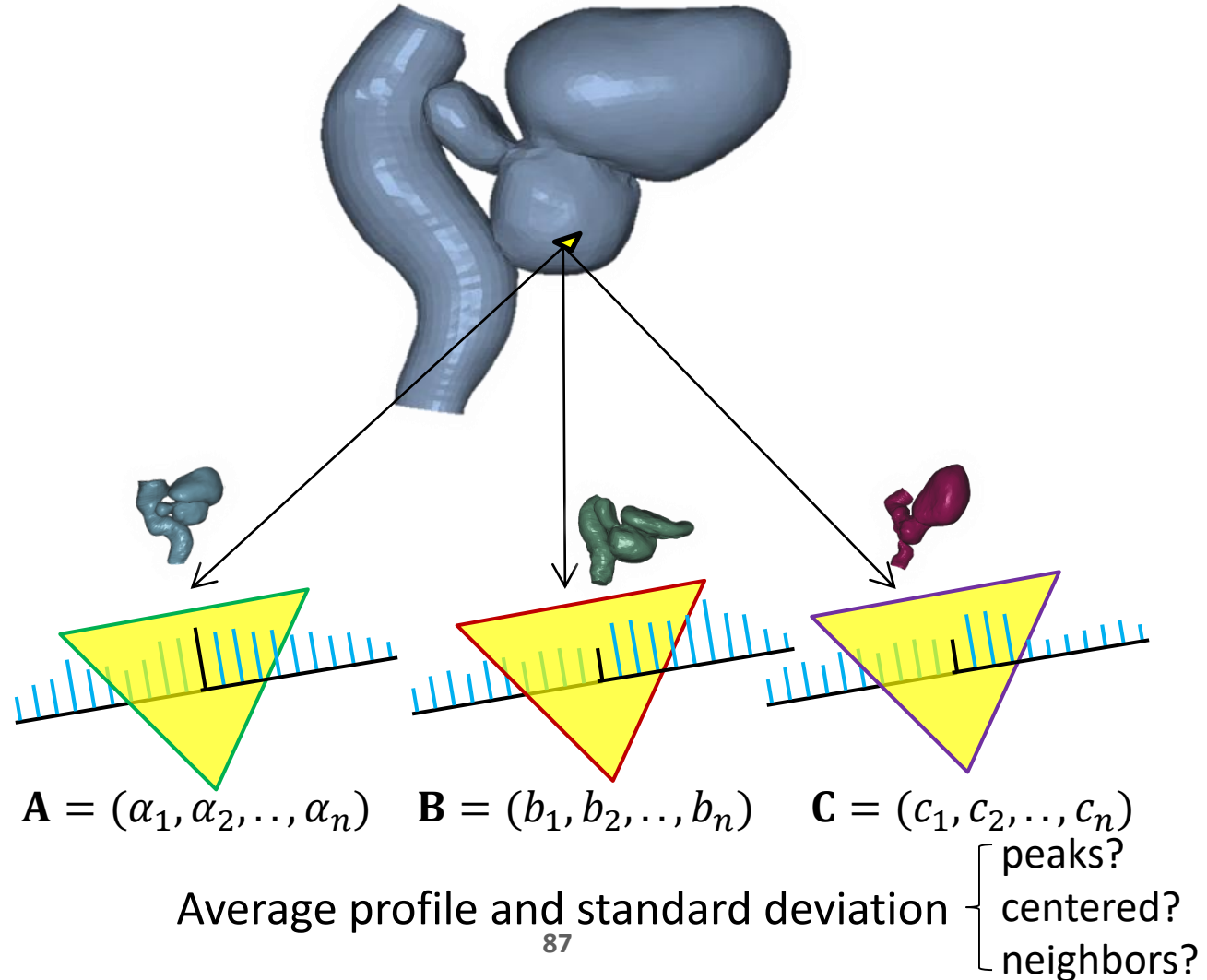




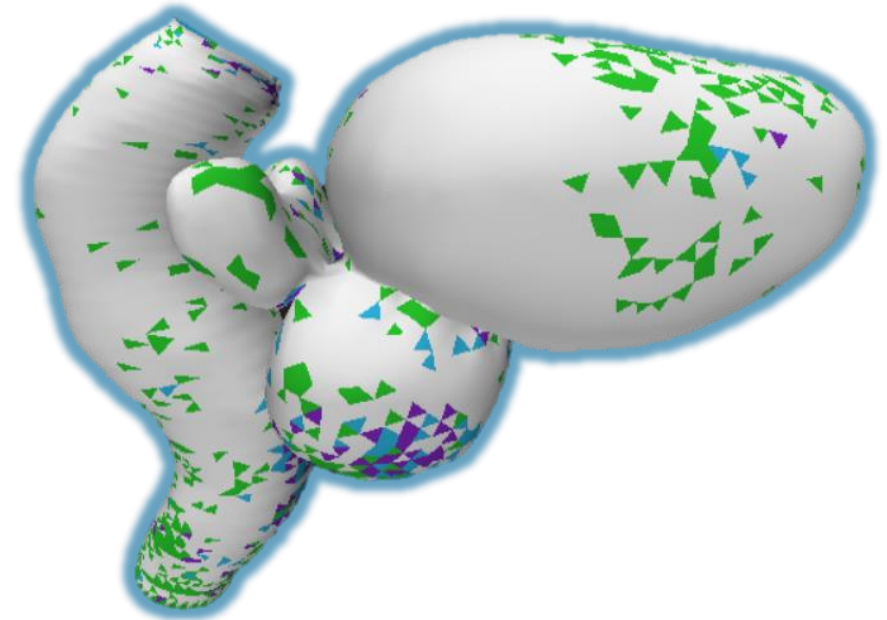
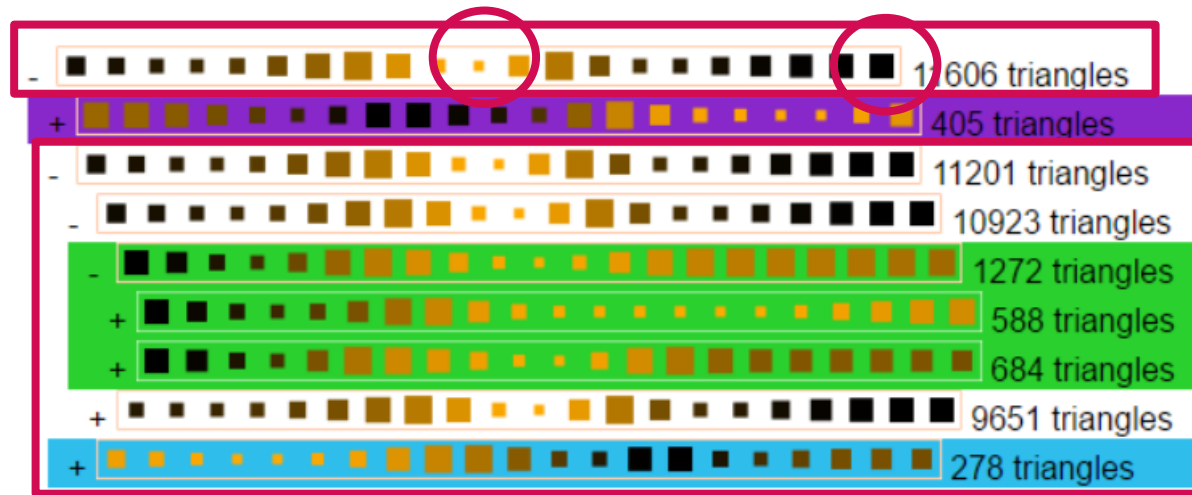
# Full Cohort Exploration and Analysis



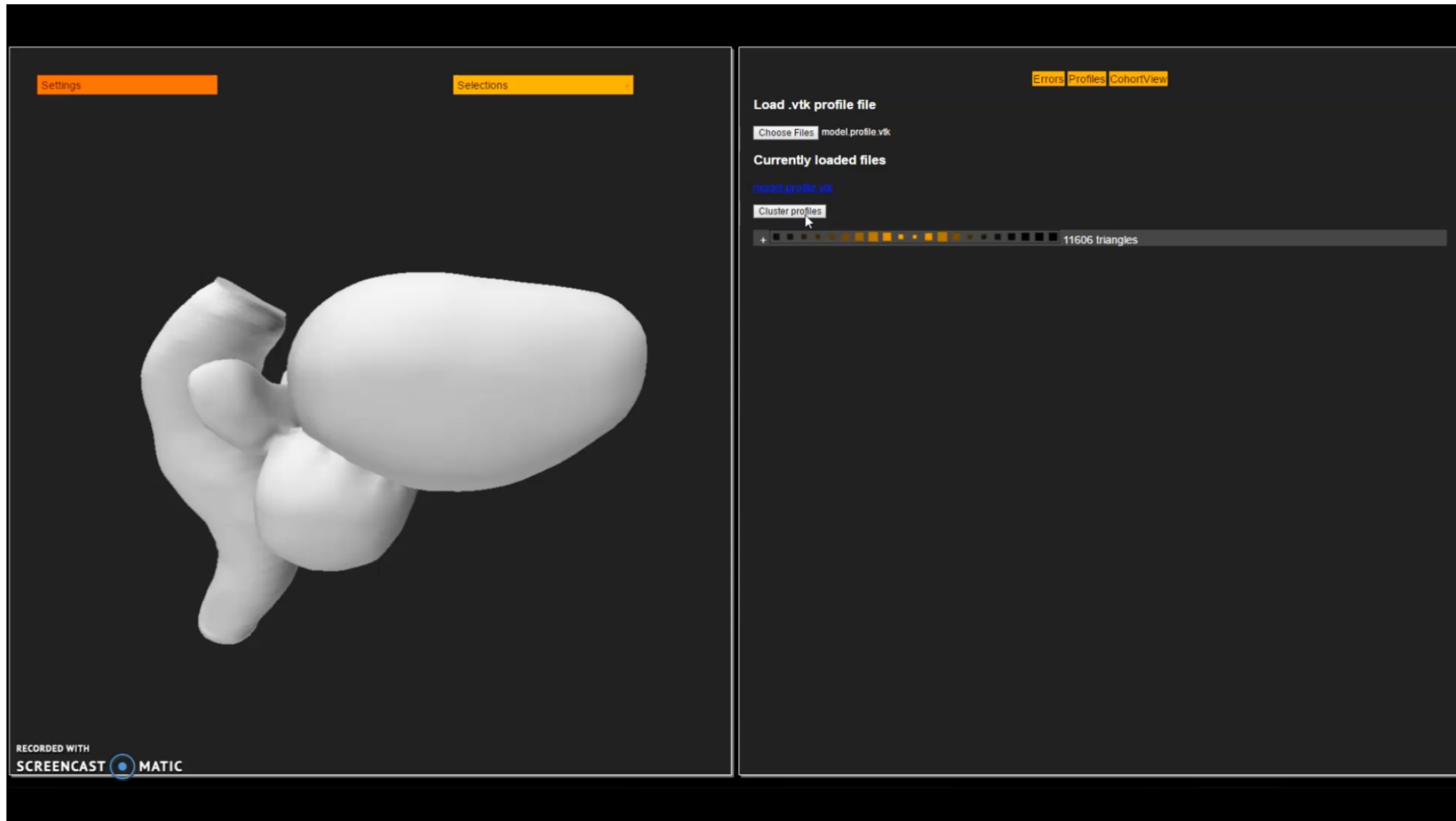
## Cohort Average Mesh



# Full Cohort Exploration and Analysis



# Full Cohort Exploration and Analysis



The screenshot displays a software interface for 3D visualization and analysis. On the left, a white 3D model of a biological structure is shown against a dark background. The interface includes several panels and controls:

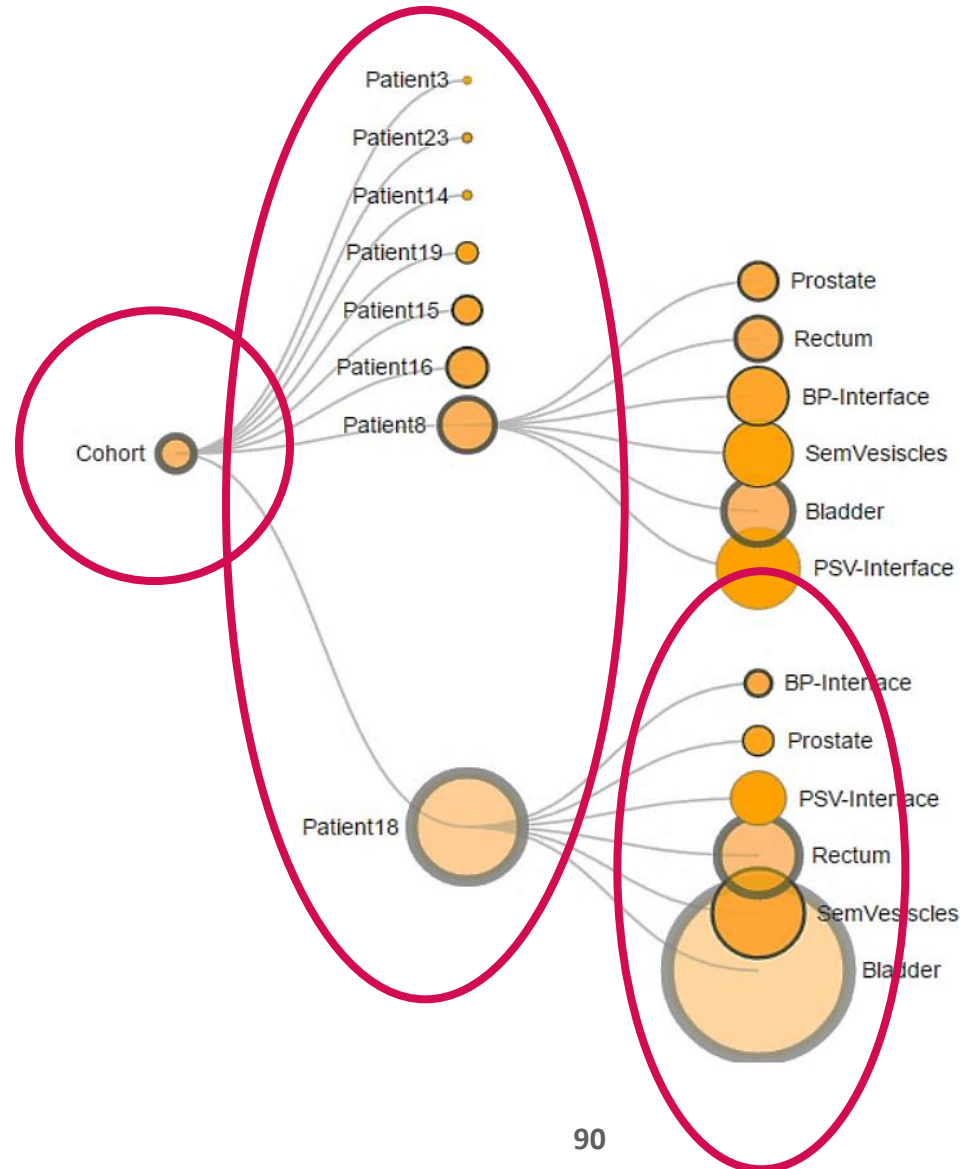
- Settings** and **Selections** tabs at the top left.
- Errors**, **Profiles**, and **CohortView** tabs at the top right.
- Load .vtk profile file** section with a **Choose Files** button and the filename `model.profile.vtk`.
- Currently loaded files** section showing `model.profile.vtk` and a **Cluster profiles** button.
- A horizontal bar representing a cluster profile, with a mouse cursor pointing to it and the text `11606 triangles` below it.

RECORDED WITH SCREENCAST MATIC

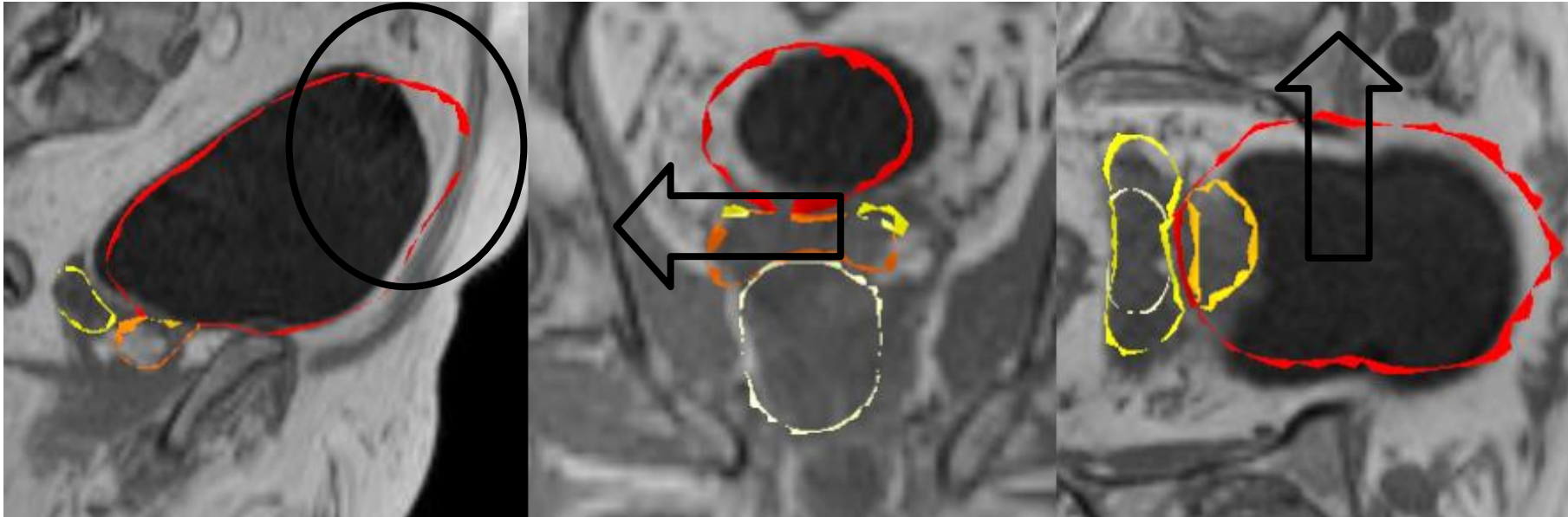




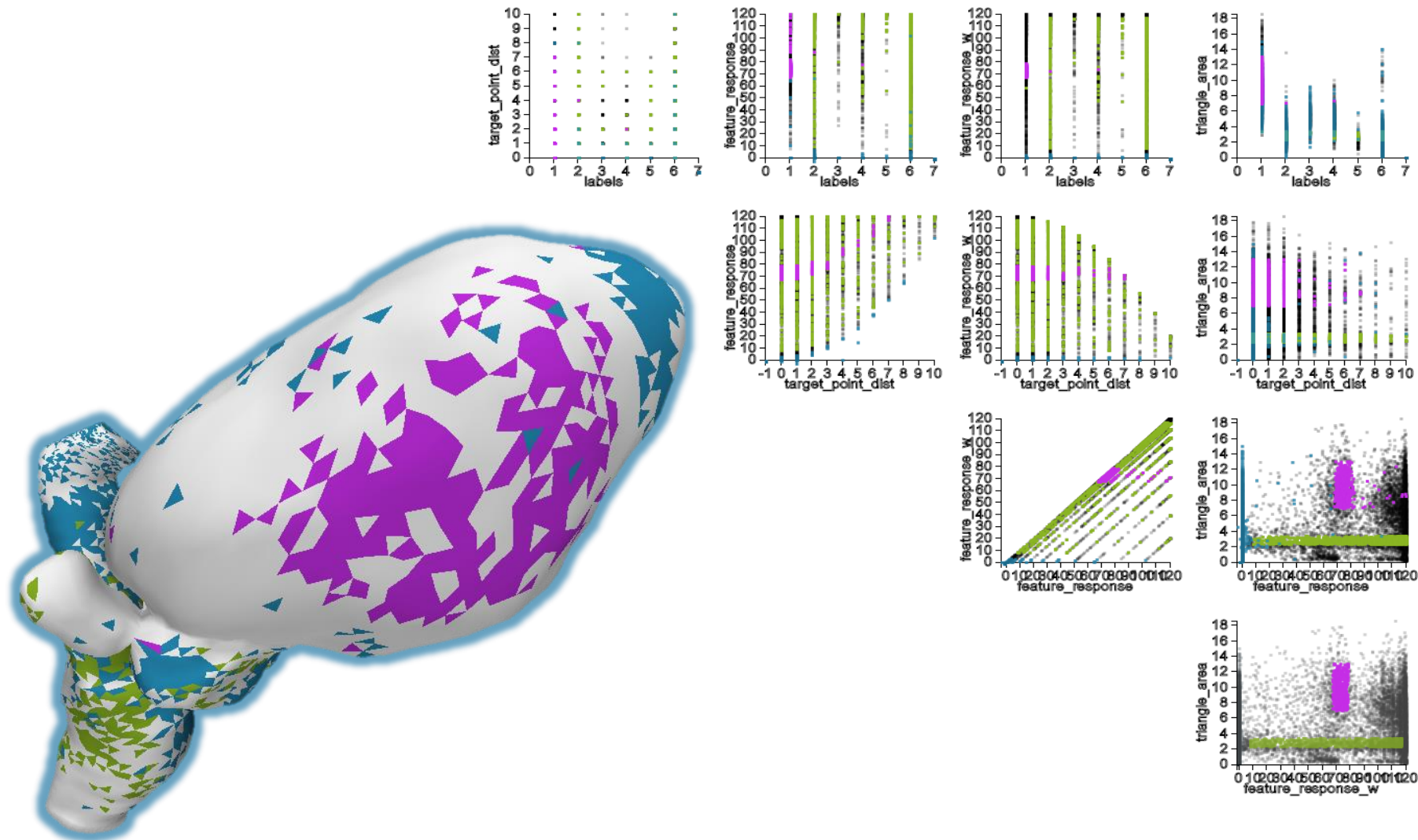
# Cohort Error Hierarchy Exploration



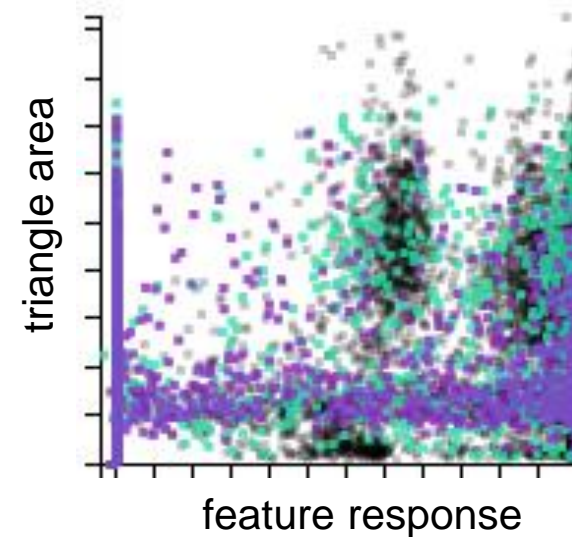
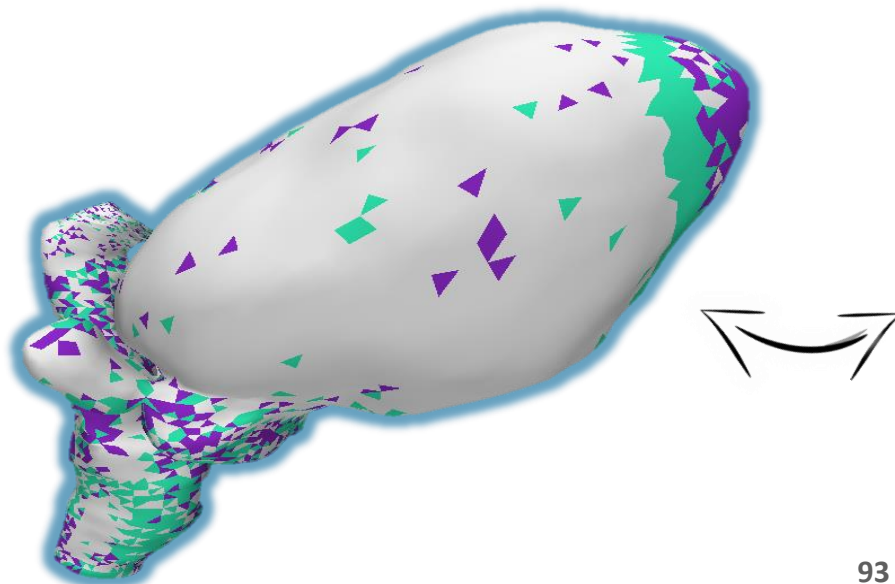
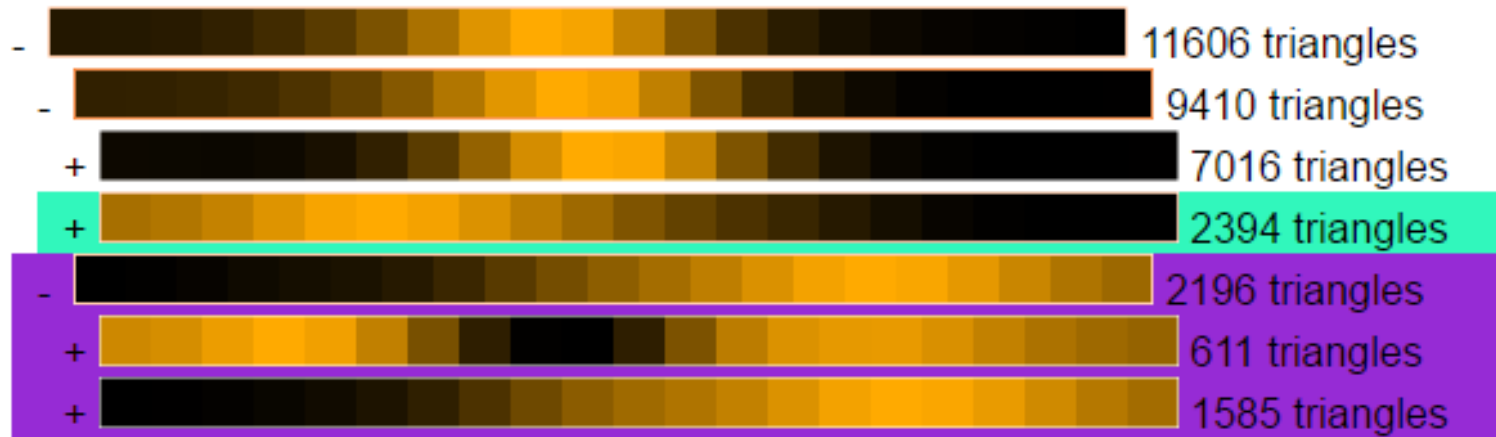
- Initial qualitative inspection w.r.t. imaging data



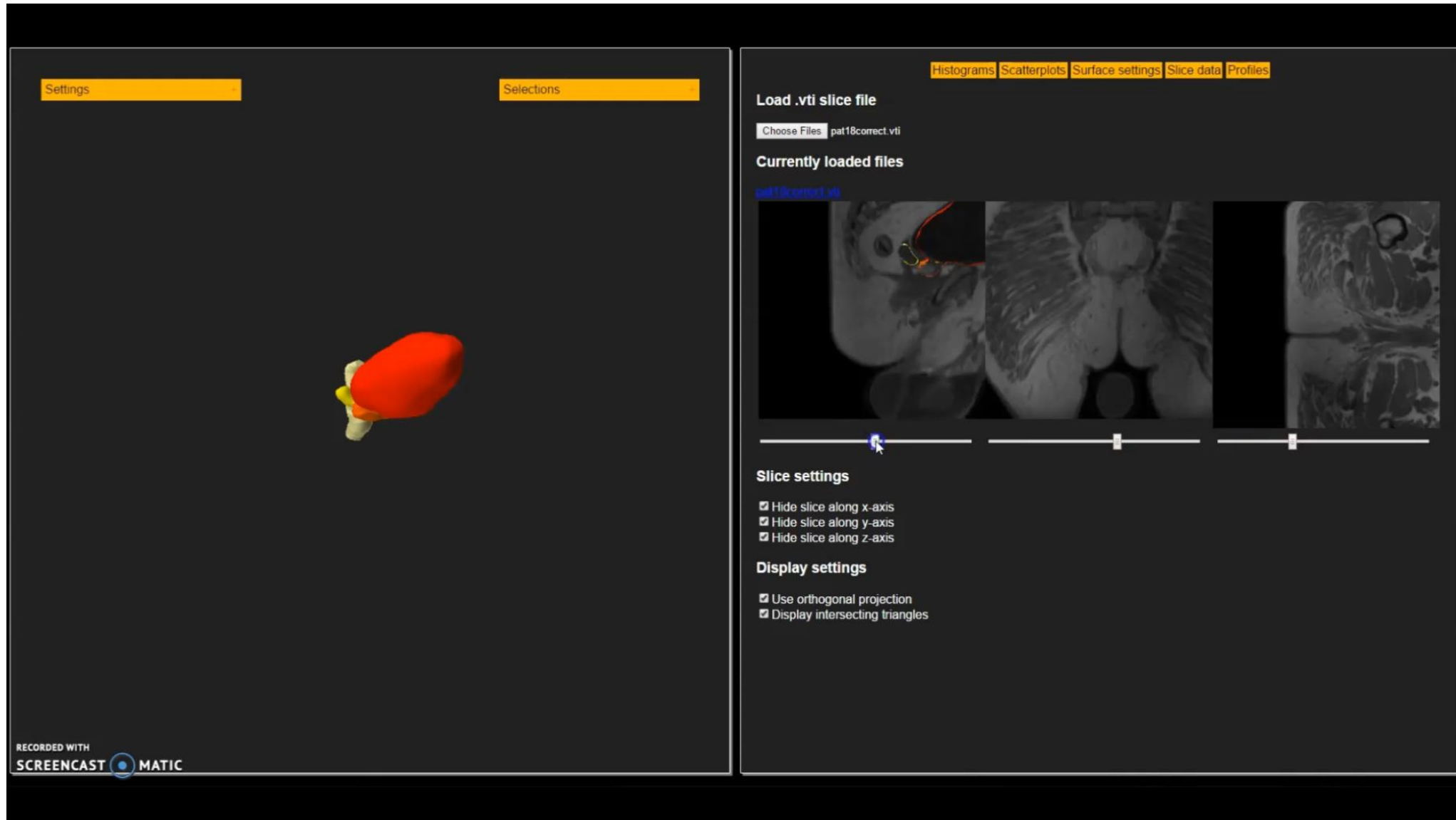
# Individual Subject Exploration and Analysis



# Individual Subject Exploration and Analysis



# Individual Subject Exploration and Analysis



Settings Selections

Load .vti slice file

Choose Files pat18correct.vti

Currently loaded files

pat18correct.vti

Slice settings

- Hide slice along x-axis
- Hide slice along y-axis
- Hide slice along z-axis

Display settings

- Use orthogonal projection
- Display intersecting triangles

RECORDED WITH SCREENCAST MATIC





- Visual tool for the exploration and assessment of the results and errors of automated segmentation processes.
- Better understanding of how the employed algorithm works.
- Going from an entire cohort to single cases.



# Comparative Visual Analysis of Pelvic Organ Segmentations

Oliver Reiter<sup>1</sup>, Marcel Breeuwer<sup>2;3</sup>, M. Eduard Gröller<sup>1;4</sup>, Renata G. Raidou<sup>1</sup>

<sup>1</sup>Institute of Visual Computing & Human-Centered Technology, TU Wien, Austria

<sup>2</sup>Eindhoven University of Technology, the Netherlands

<sup>3</sup>Philips Healthcare Best, the Netherlands

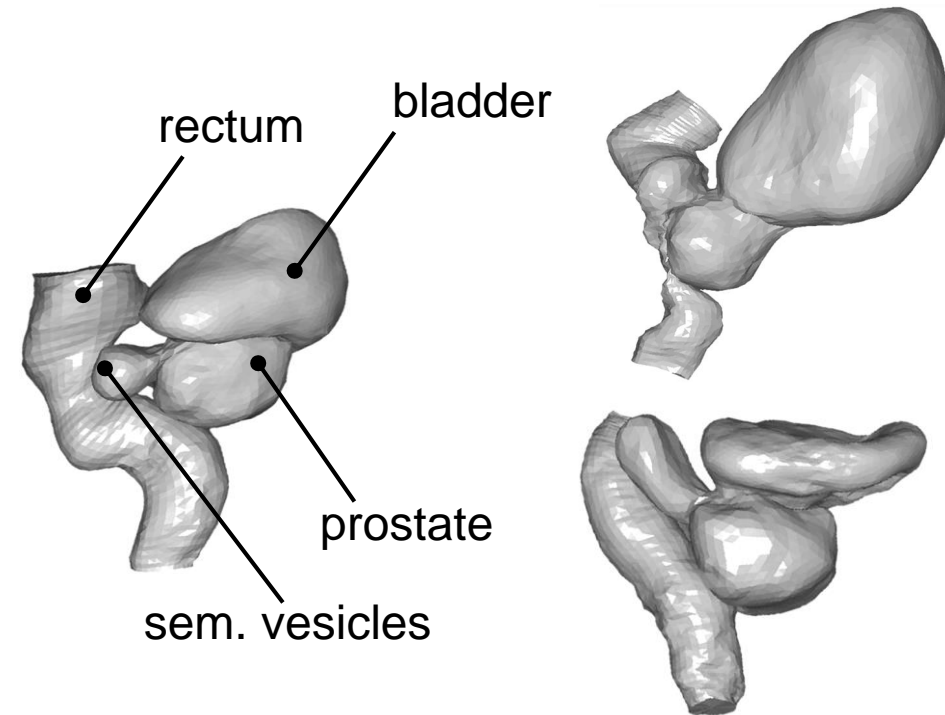
<sup>4</sup>VRVis Research Center, Austria



## Hypothesis: inaccuracy related to high variability of organs



Schadewaldt et al., 2013



*Anatomical Variability Across Patients*



A **web-based** framework for:

1. easy exploration and detailed analysis of pelvic organ **shape variability**
2. hypothesis generation w.r.t. the impact of shape variability on the **performance of segmentation** algorithms

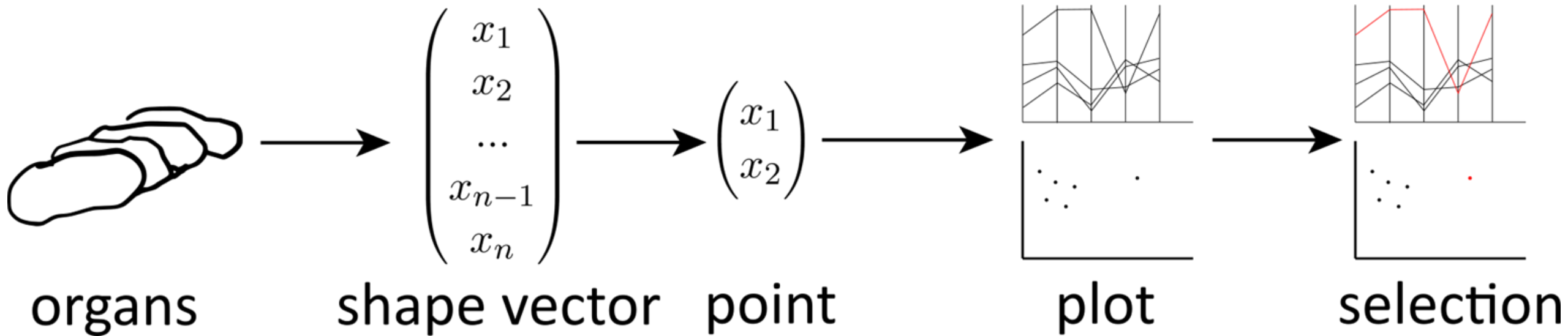
for each **individual** organ and for **all** organs at the same time.



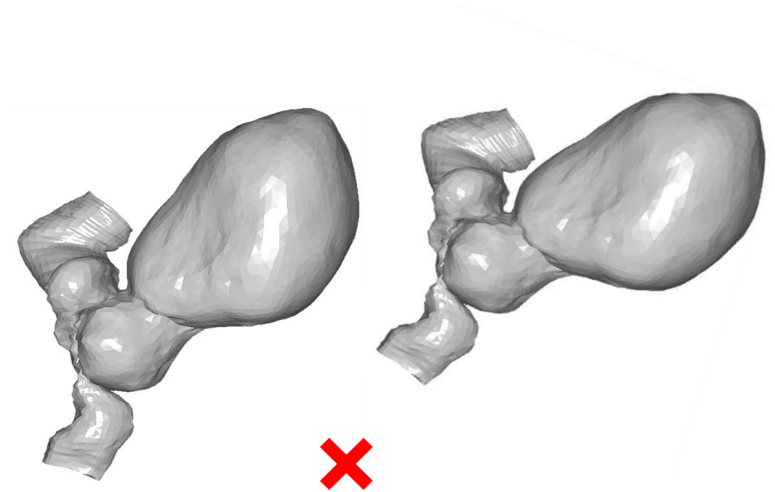
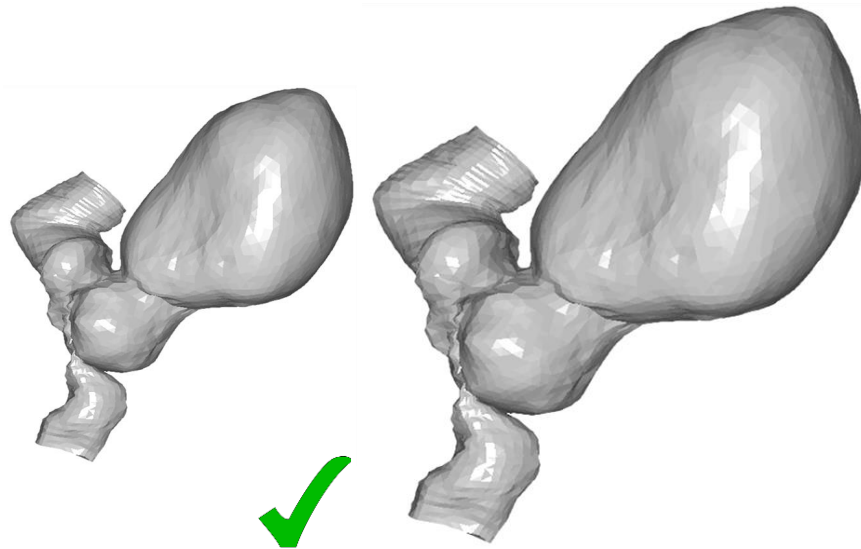
1. Quantification and Visualization of Organ Shape Variability
  - Per individual organ
  - Across all pelvic organs
  - Quantification requires adequate metrics
  
2. Comparative Visualization of Pelvic Organs
  - Across multiple patients
  - Multiple pelvic organs per patient
  - Organ interfaces







- Shape descriptors
  - Represent shapes as vectors
  - Translation/rotation/scale invariance
  
- In this work: no scale invariance, but translation/rotation

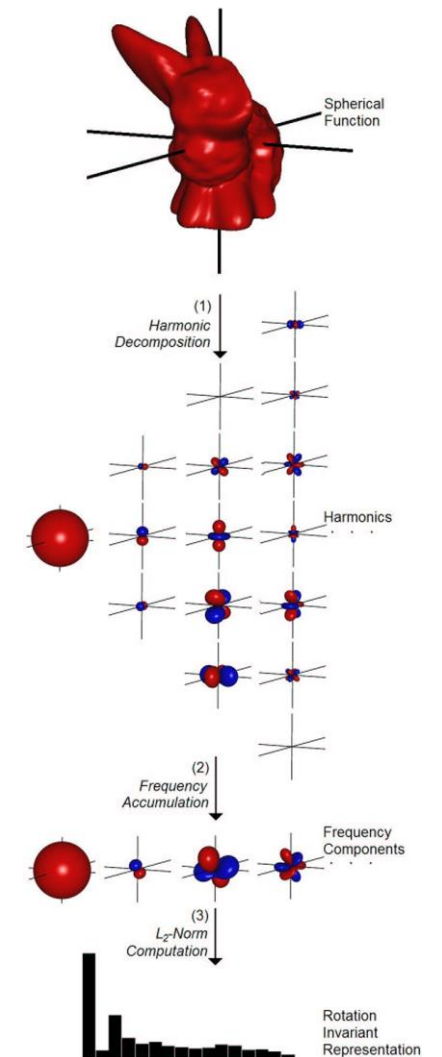


- Global feature based
- Graph based
- Zernike moments

[Zhang et al. **Survey of 3D Shape Descriptors**, 2004]



- Decompose spherical function into its harmonics
  - Accumulate based on the frequency
  - Compute L2 Norm
  - Rotation invariant for each frequency component
- 
- Result: Shape vector of frequencies



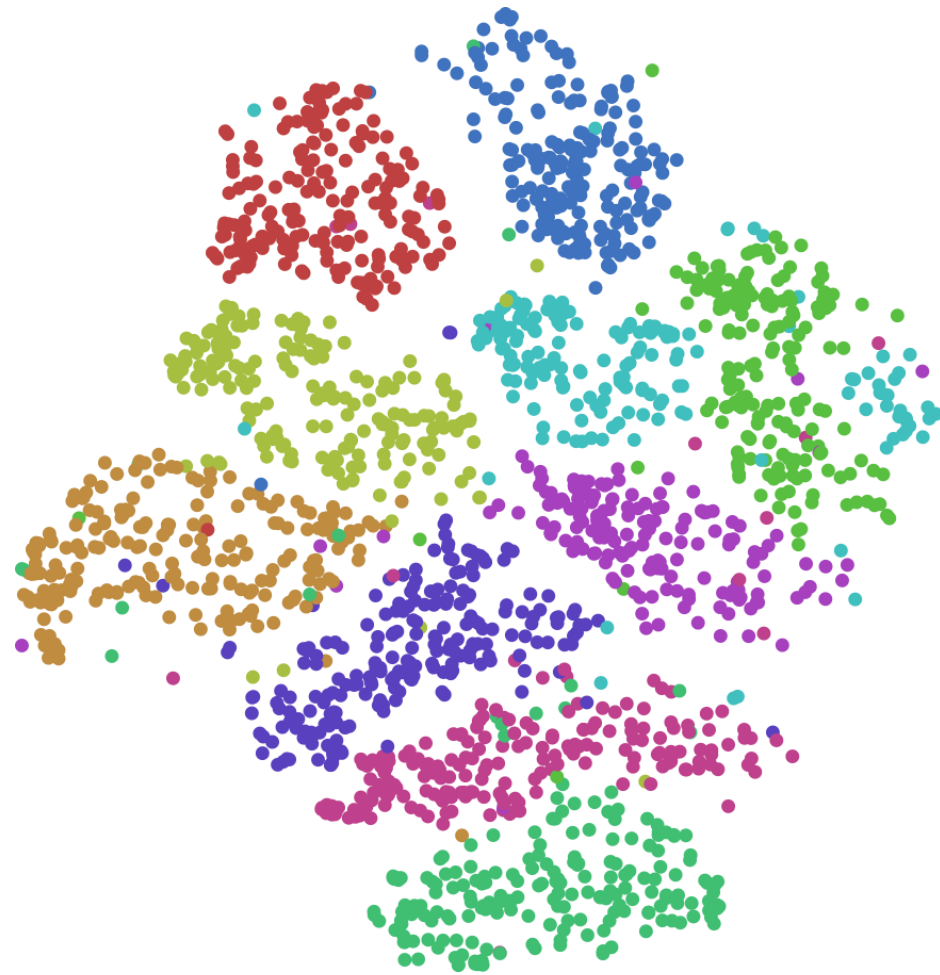
Kazhdan, Funkhouser and Rusinkiewicz, 2003



- Eight-dimensional shape description vector for each organ
- Dimensionality reduction necessary in order to visualize:
  - PCA for individual organ (within class visualization)
  - t-SNE for multiple organs (between class visualization)

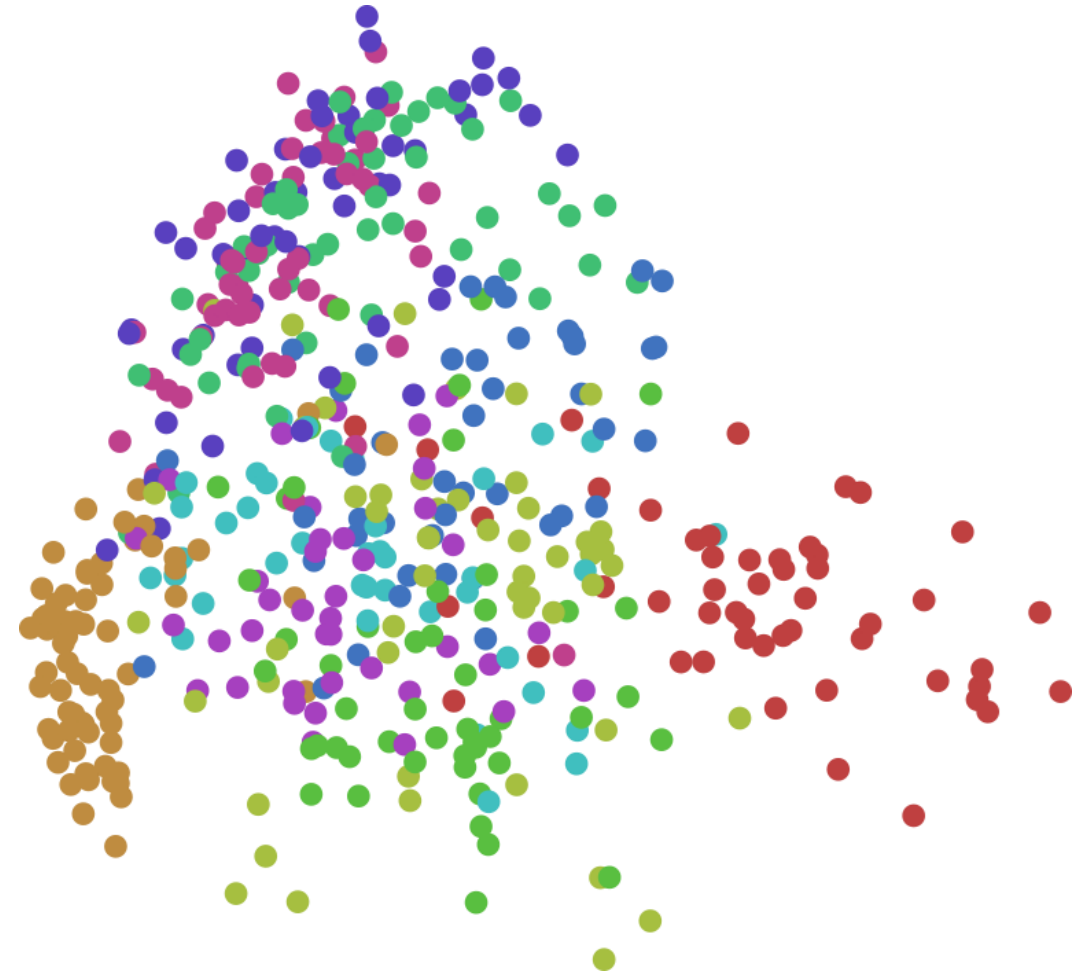


# Dimensionality Reduction - MNIST Dataset



t-SNE

- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9

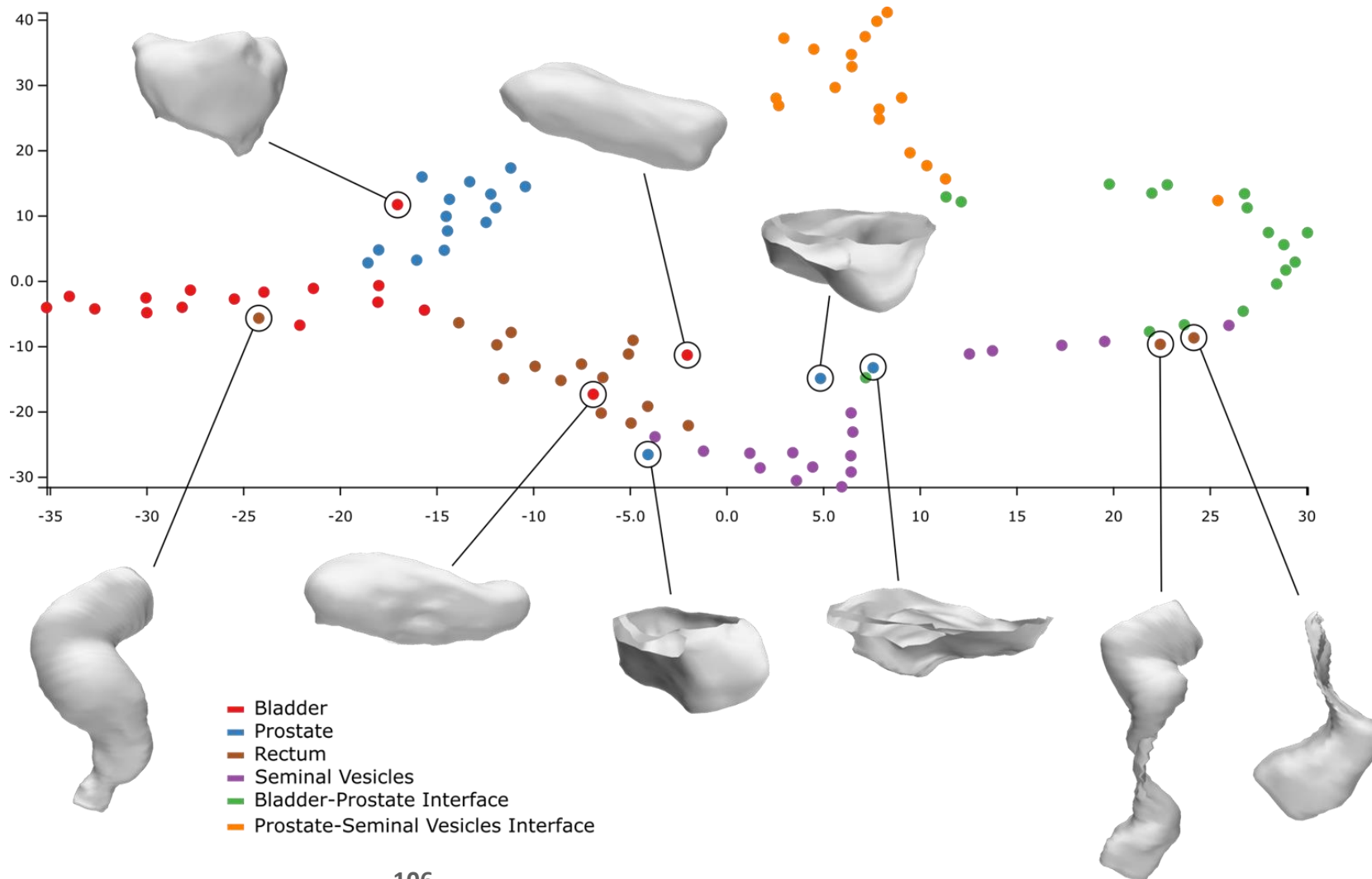
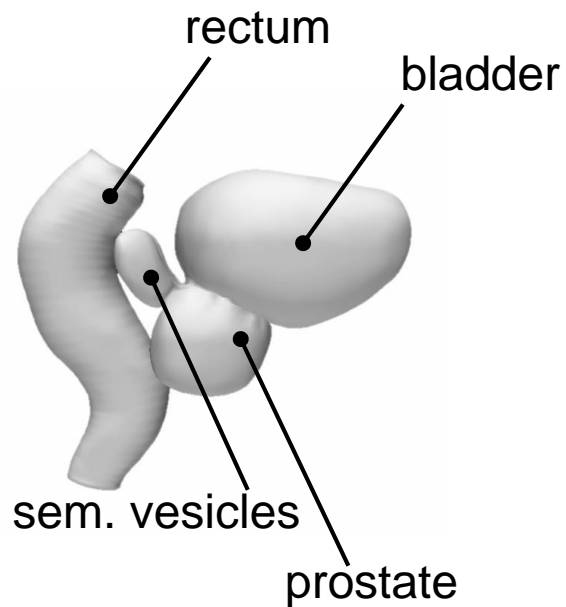


PCA



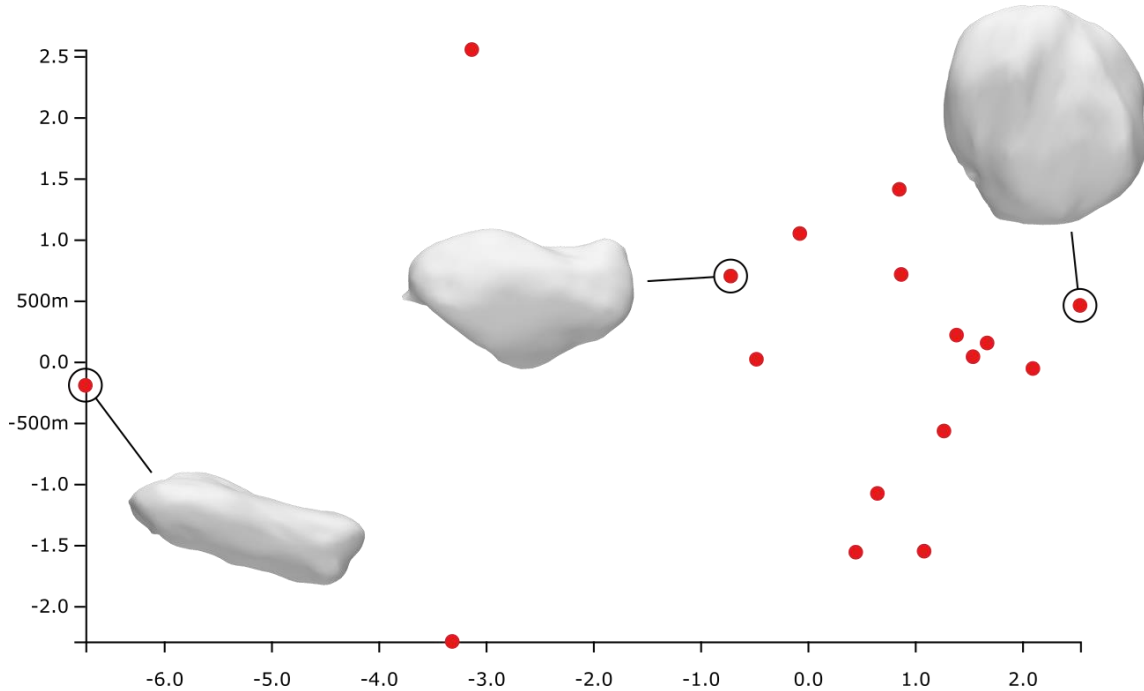


# 2D Visualization of Multiple Organs (t-SNE)

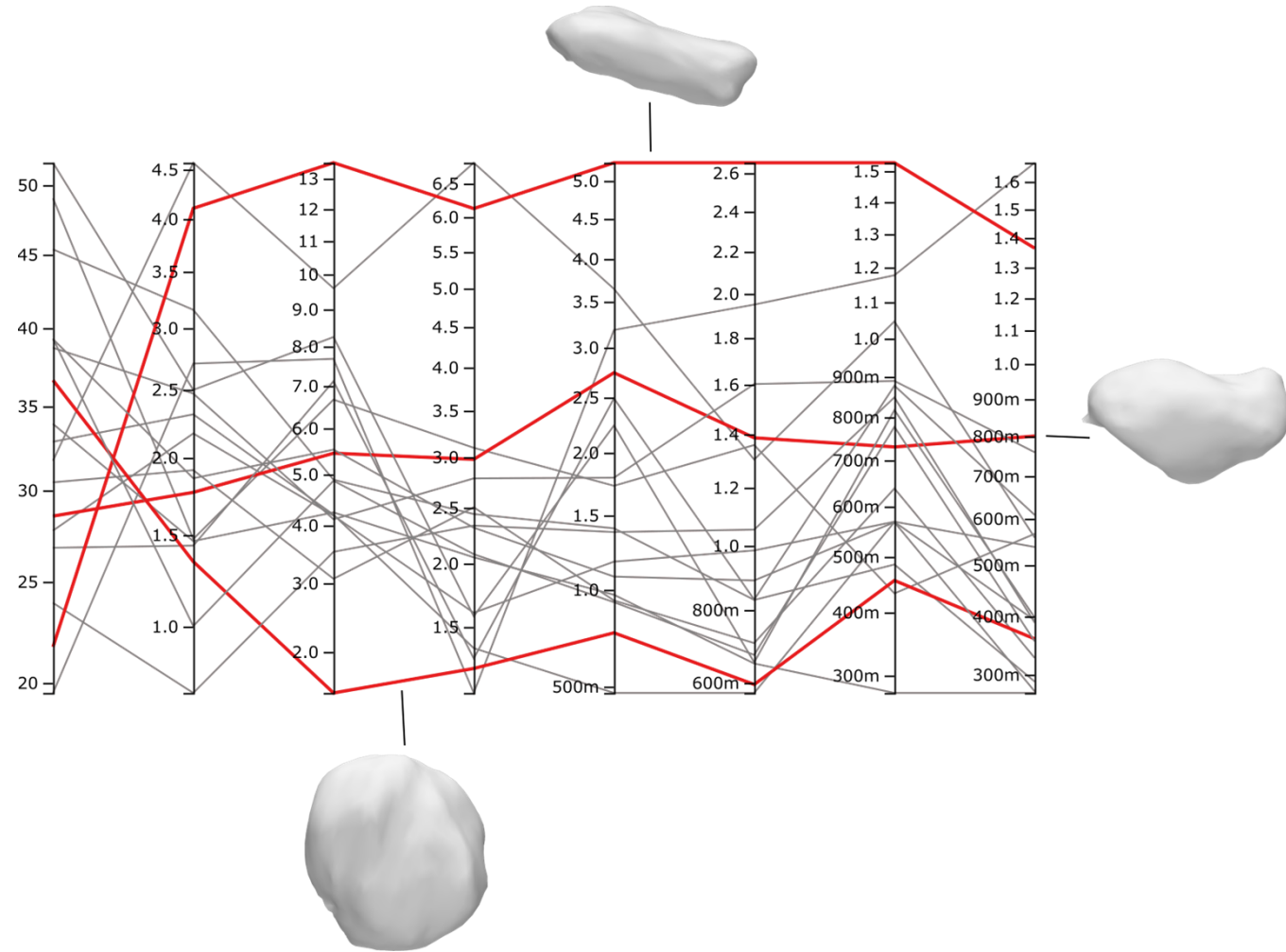


# 2D Visualization of an Individual Organ (PCA)

(Bladder)



PCA plot

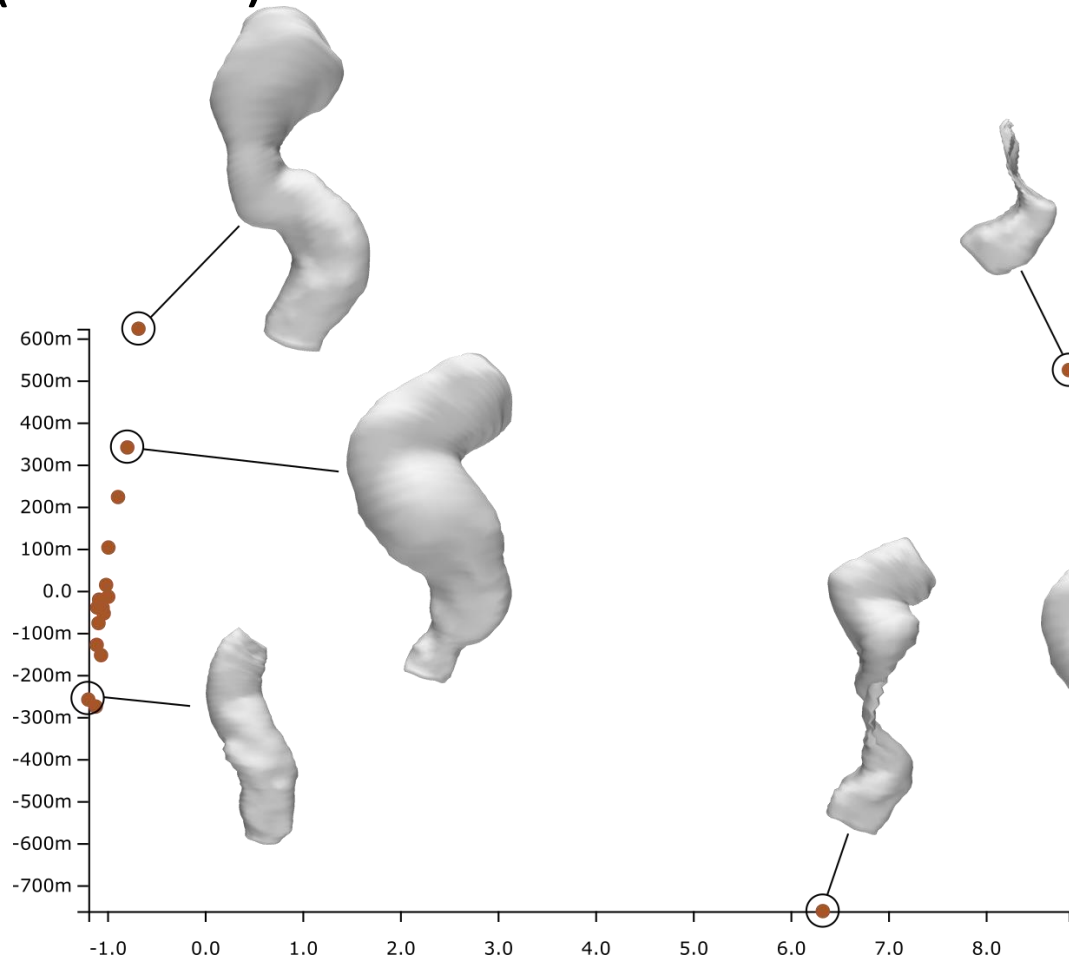


Parallel Coordinates Plot

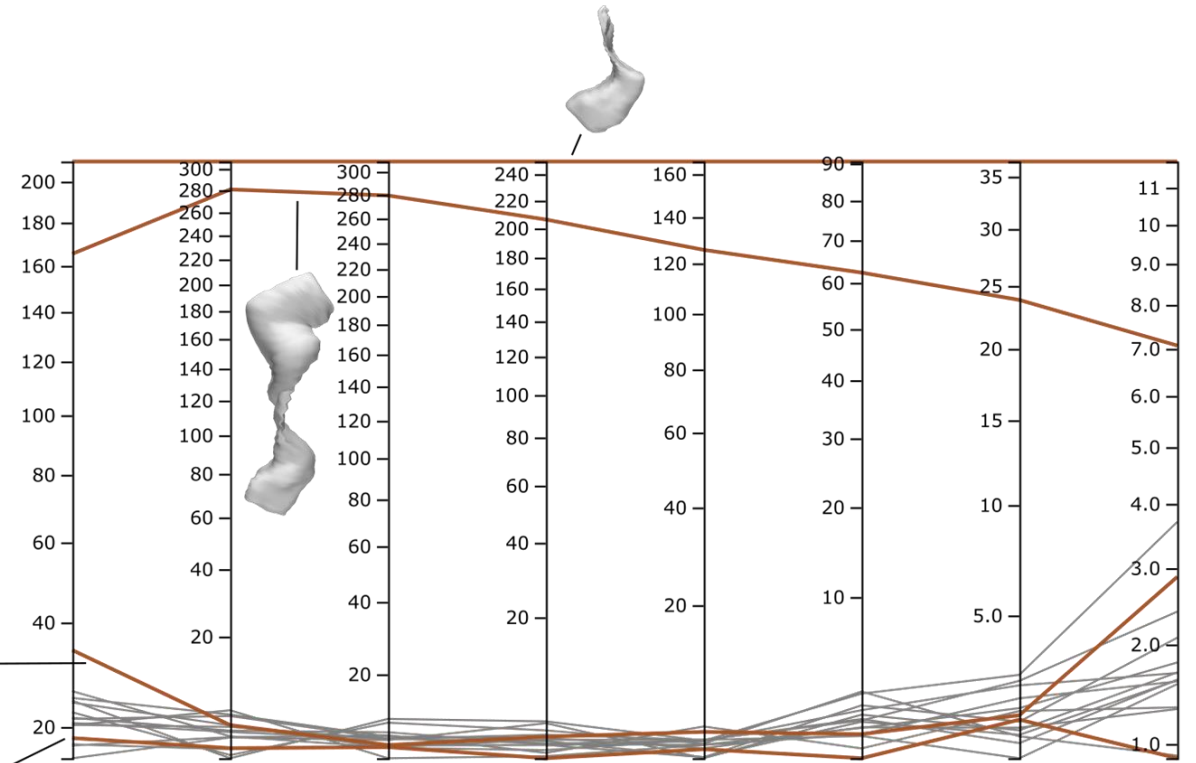


# 2D Visualization of an Individual Organ (PCA)

(Rectum)



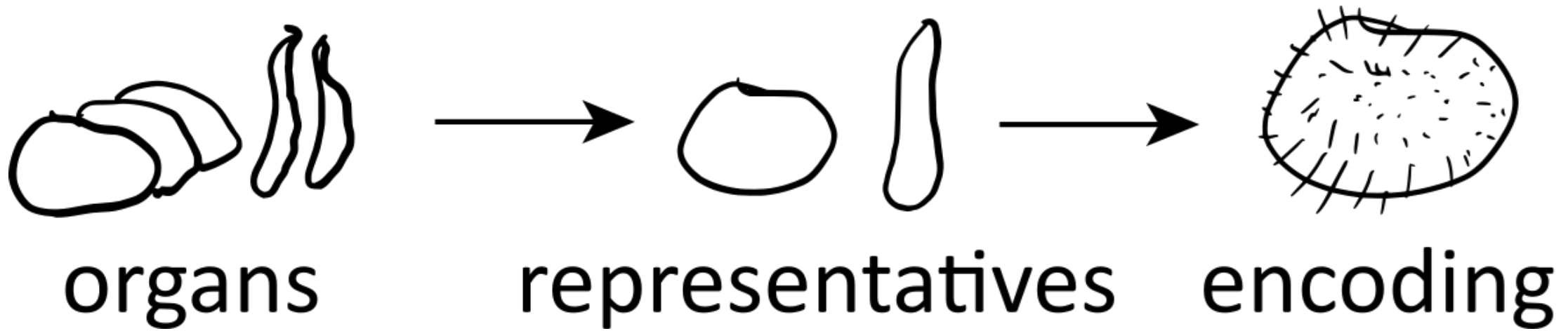
PCA plot



Parallel Coordinates Plot

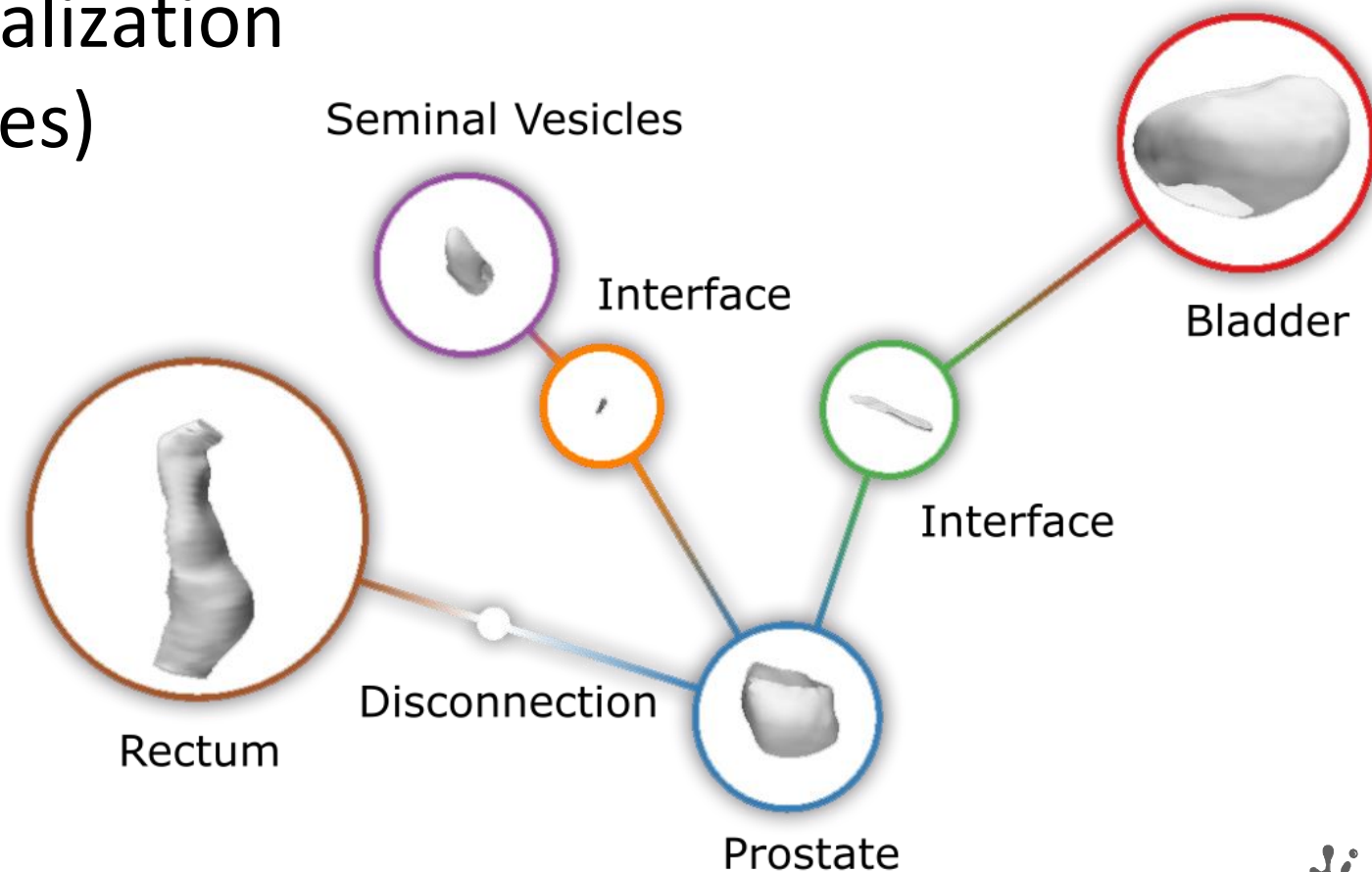
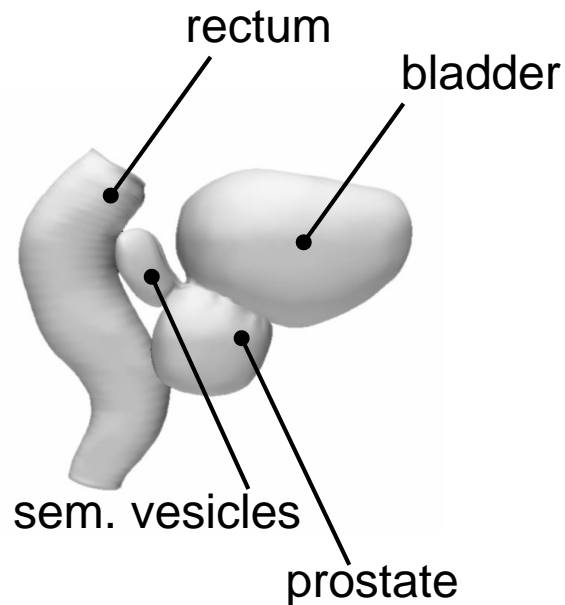


# Task 2: Comparative Visualization of Multiple Organs

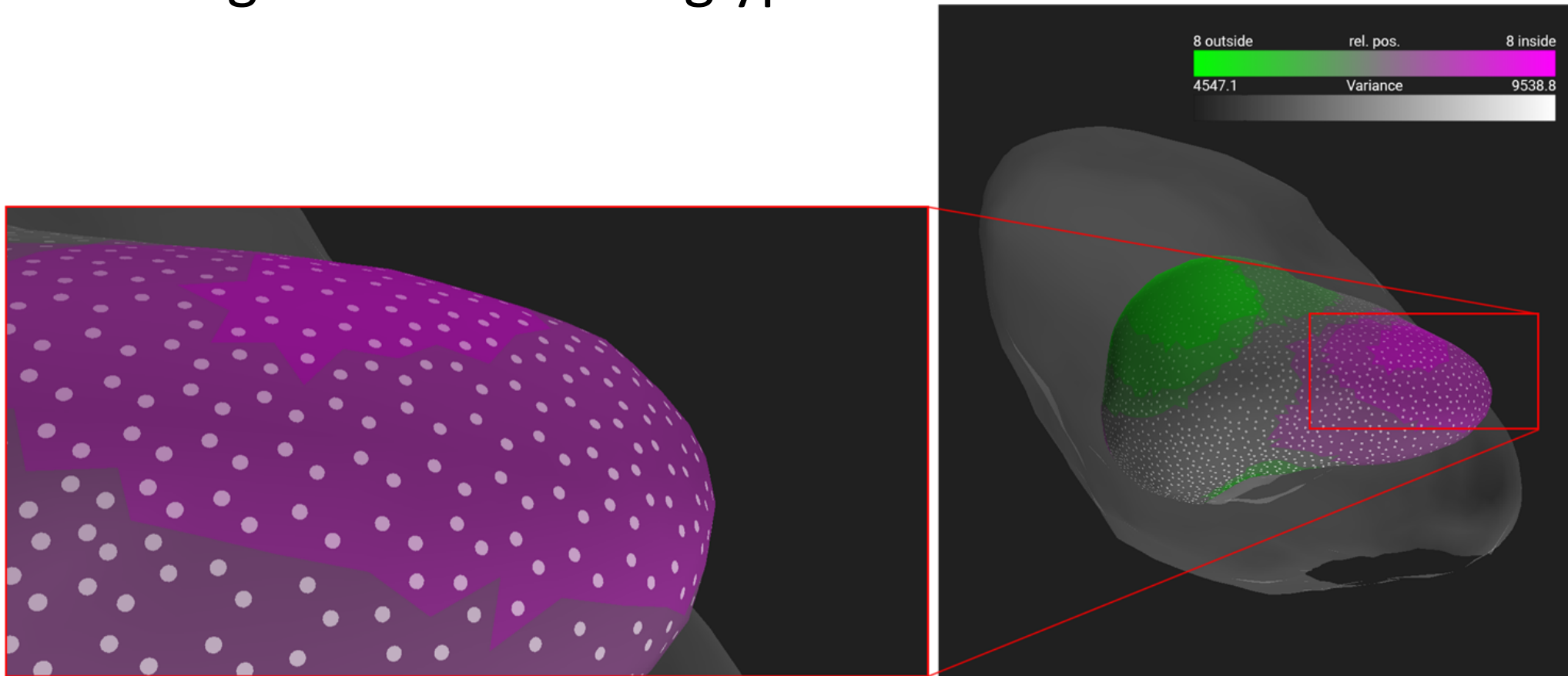


# Dealing with Multiple Organs

- Show median shape per organ
- Display relative position
- Preserve context of 2D visualization
- Show connections (interfaces)

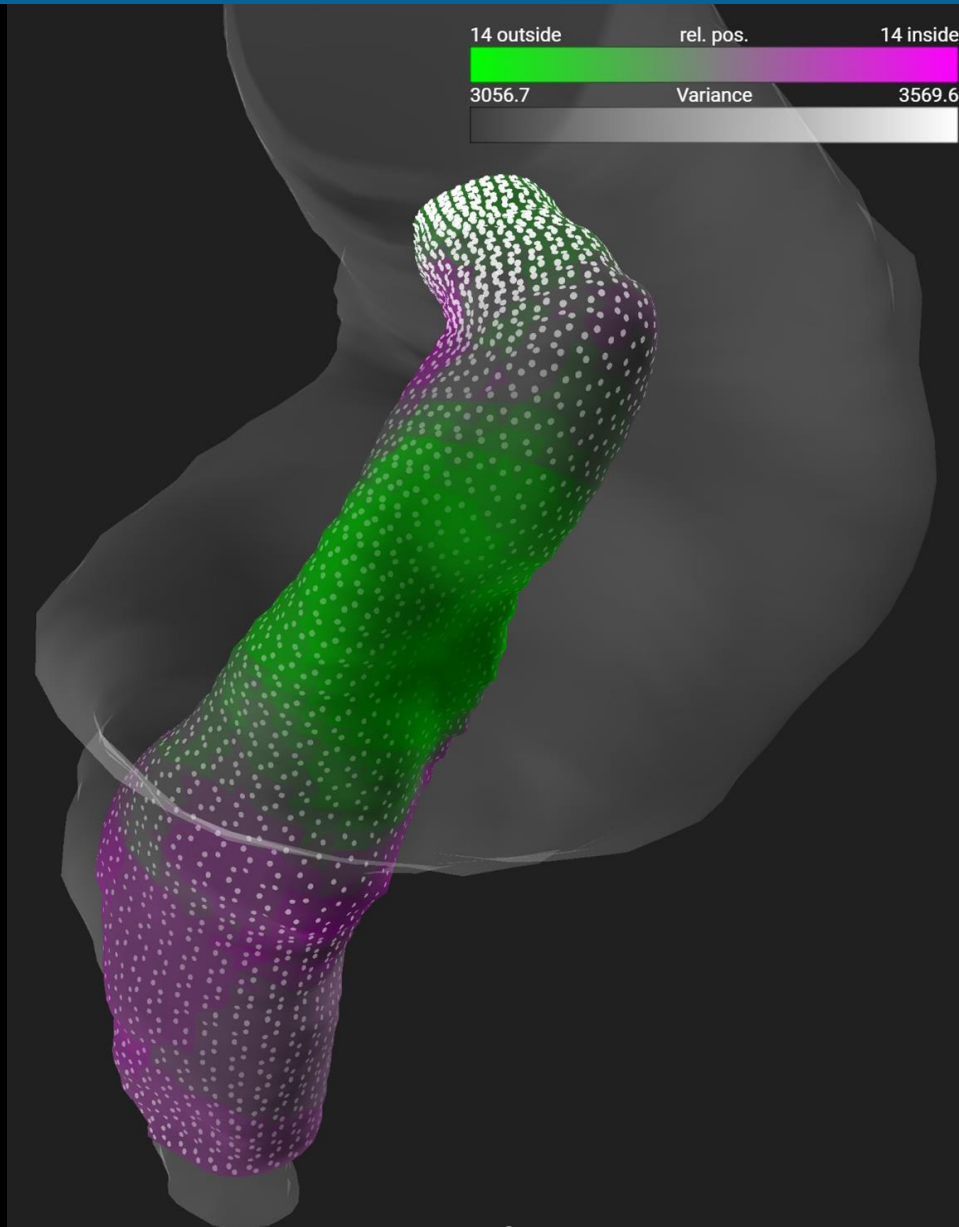


- Relative extent of median shape compared to all others: color
- Per-triangle variance: dot glyphs





# Detail-on-Demand View of Rectum Cohort



- Informal evaluation with an experienced segmentation expert
- “Easy to learn and easy to understand”
- Positively judged as an interesting basis for future work
  
- Original image data not accessible
- No scale to see the actual size



- Shape descriptor not suitable for organ interfaces
- t-SNE requires experience to find good parameters
- Little interaction possibilities in the exploded view



- Compare segmentations of multiple organs across multiple patients
  - Measure and visualize shape variability
  - Comparative visualization of pelvic organs
- Quickly identify mis-segmented shapes
- Provides quick and easy insight into shape variability
- Hypothesis generation for segmentation algorithms performance



- “Visual Analytics combines **automated analysis techniques** with **interactive visualisations** for an effective **understanding, reasoning and decision making** on the basis of **very large and complex datasets**” [Keim 2010]
- Few examples applied on the domain of RT treatment planning



- The purpose of computing is insight, not numbers [Hamming, 1962 ]
- The purpose of visualization is insight, not pictures [Shneiderman, 2005]

