Automatic Generation of Training Data for Brain Tissue Classification from MRI

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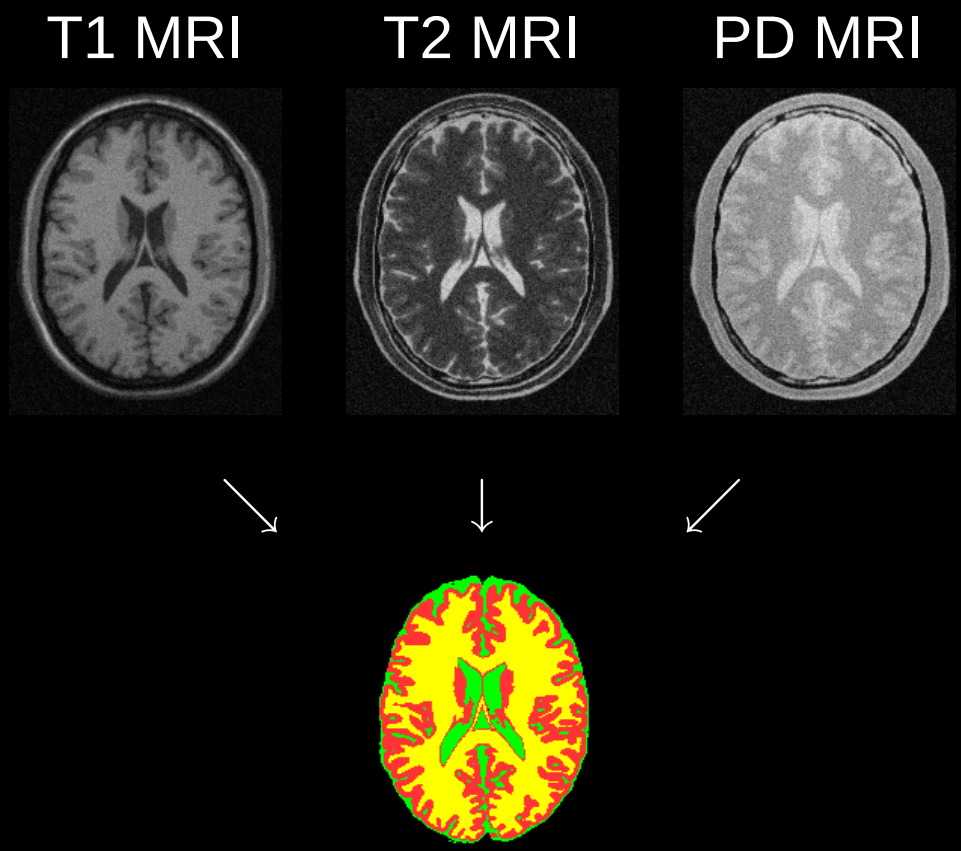
Brain tissue classification:

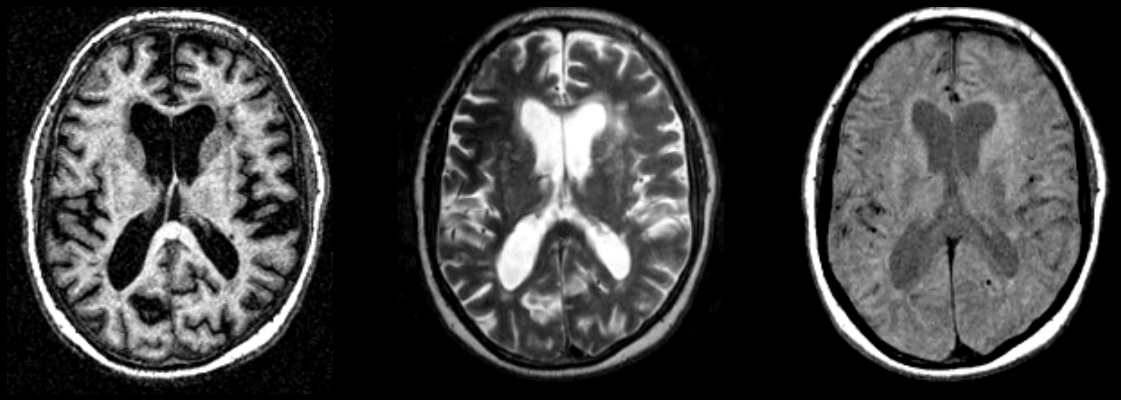
$\Rightarrow$ the procedure of labeling each image voxel as a tissue class.



4 classes: CSF, Grey-matter, White-matter, “background”

Preview:

Main problem: subject different than anatomical model.



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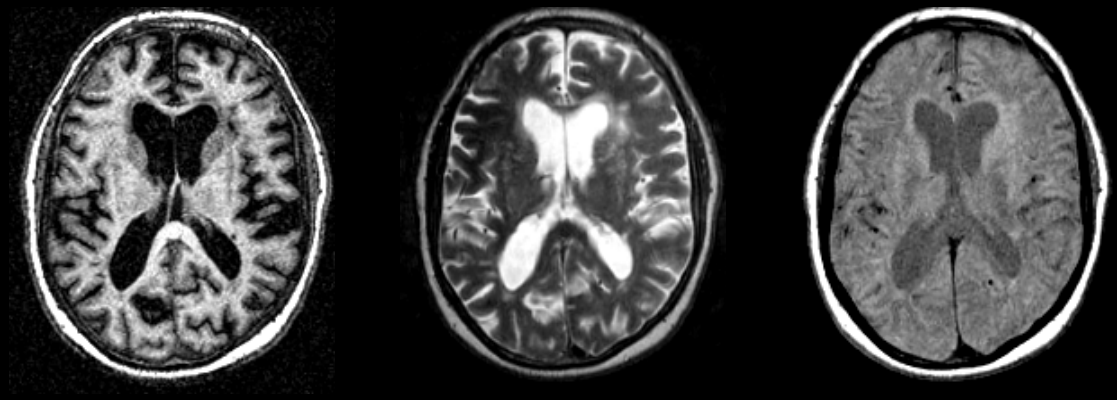

Outline:

- Requirements
- Existing methods
- Our method
- Validation and results

Target application:

- Quantitative measurements, such as:
  - normalized tissue/structure volume
  - atrophy measures
  - voxel-based morphometry
  - cortical surface
  - cortical thickness
  - …
- Studies on a large number of subjects (150 – 1000); data acquired at many different sites.

Requirements:

Tissue classification method should be:

- ACCURATE
  - application: quantitative measurements

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- ACCURATE
  - application: quantitative measurements
- FULLY AUTOMATIC
  - reproducibility; many datasets to process
- ROBUST against variability in:
  - subject brain's morphology
  - MRI data: image contrast, artifacts, . . .

Existing methods:

- Kamber et al. (IEEE TMI ’95)
- Van Leemput (IEEE TMI ’99), Ashburner (“SPM-99”)

$\hookrightarrow$ all use a probabilistic brain anatomy atlas
$\rightarrow$ problems with brain anatomies significantly different than atlas.

Existing methods: EM

EM-style schemes by Van Leemput (IEEE TMI ’99), Ashburner (“SPM-99”).

Drawback:
assume multi-variate Normal (“Gaussian”) intensity distributions.

$\longrightarrow$ poor assumption for multi-spectral brain aMRI ?

biology, acquisition artifacts . . .

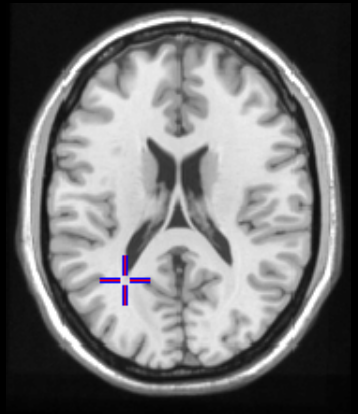
Existing methods: Kamber

Kamber (IEEE TMI ’95) used Tissue Probability Maps (TPM), defined in a stereotaxic space.

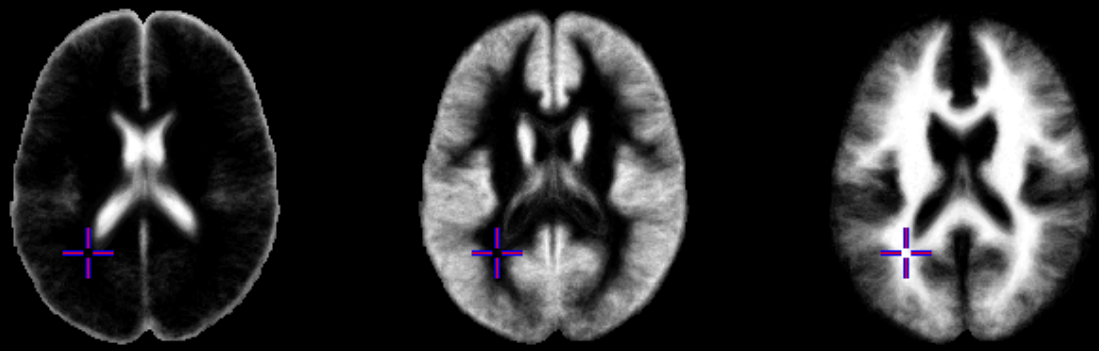
1. subject MRI spatially registered to stereotaxic space (linear registration)
2. select MRI intensity samples from spatial locations very likely to contain a given tissue type
3. use these samples to train a supervised classifier (such as: Bayes, neural network, kNN, . . .).

Stereotaxic space TPM:

Subject MRI:



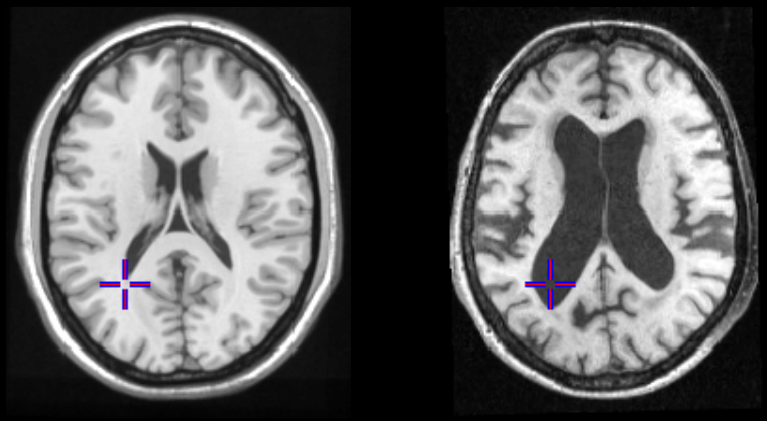
TPM:



CSF = 0% GM = 4% WM = 96%

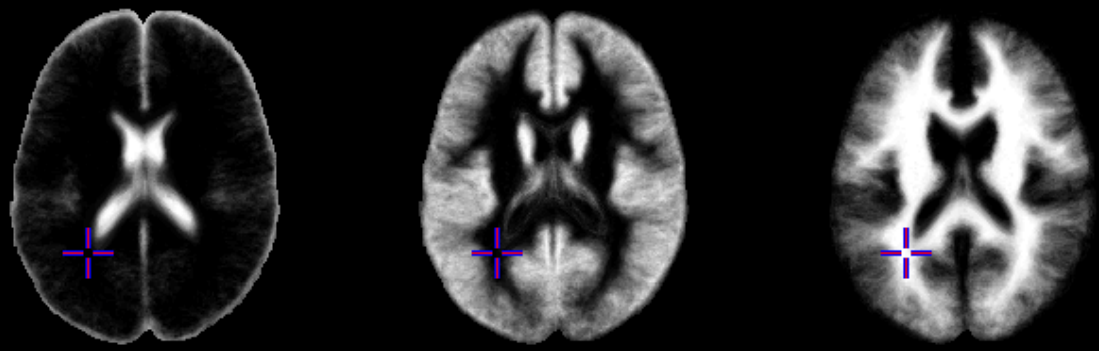
Stereotaxic space TPM:

young
normal
$\longrightarrow$



elderly,
Alzheimer's Disease
$\longleftarrow$

young
normal
population
$\Longrightarrow$

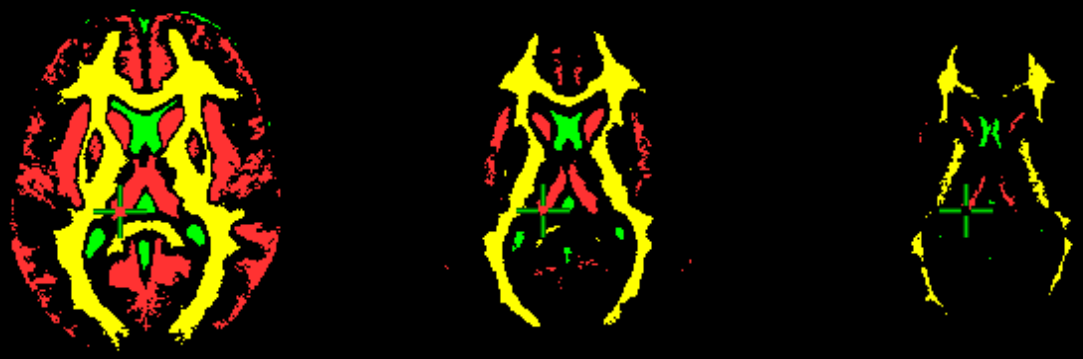


CSF = 0% GM = 4% WM = 96%

Training samples selection:

$\hookrightarrow$ choose spatial locations with TPM value $\geq \mathcal{T}$

$\mathcal{T} =$ 0.7 0.9 0.99



CSF
Grey−matter
White−matter

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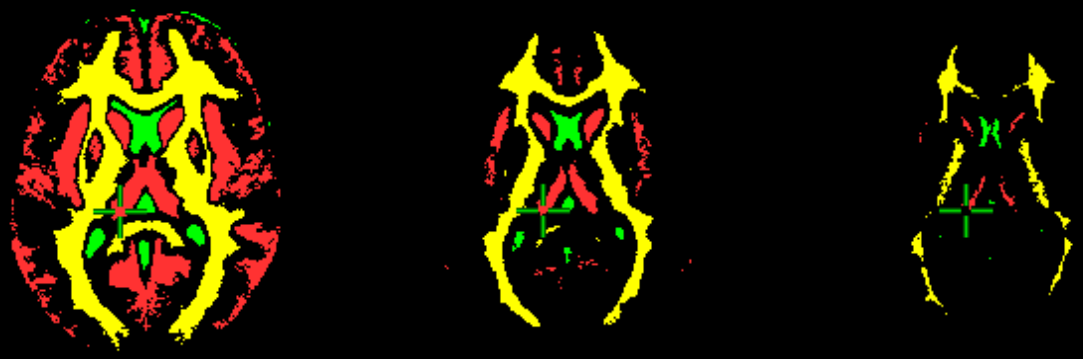

CSF
Grey−matter
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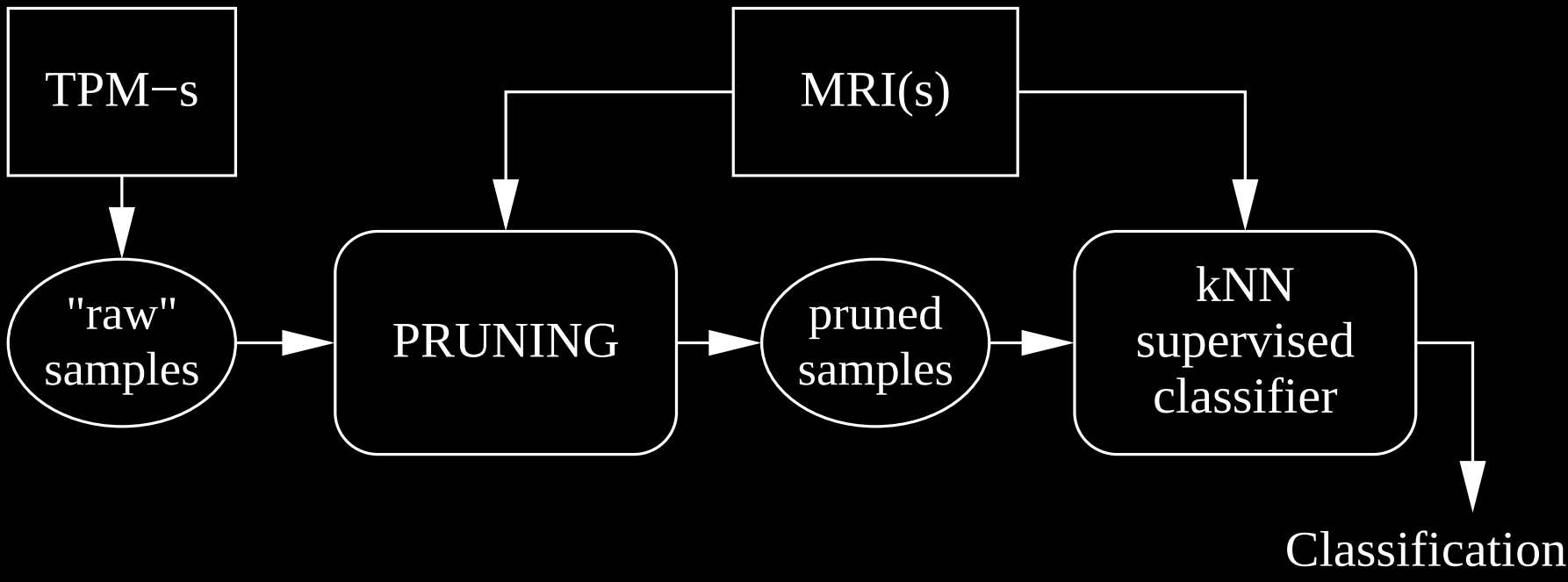
- lower $\mathcal{T}$ desired for more spatial coverage $\Rightarrow$ robust estimation of tissue intensity distributions.
- higher $\mathcal{T}$ desired for reducing wrong class guesses.

Our novel method:



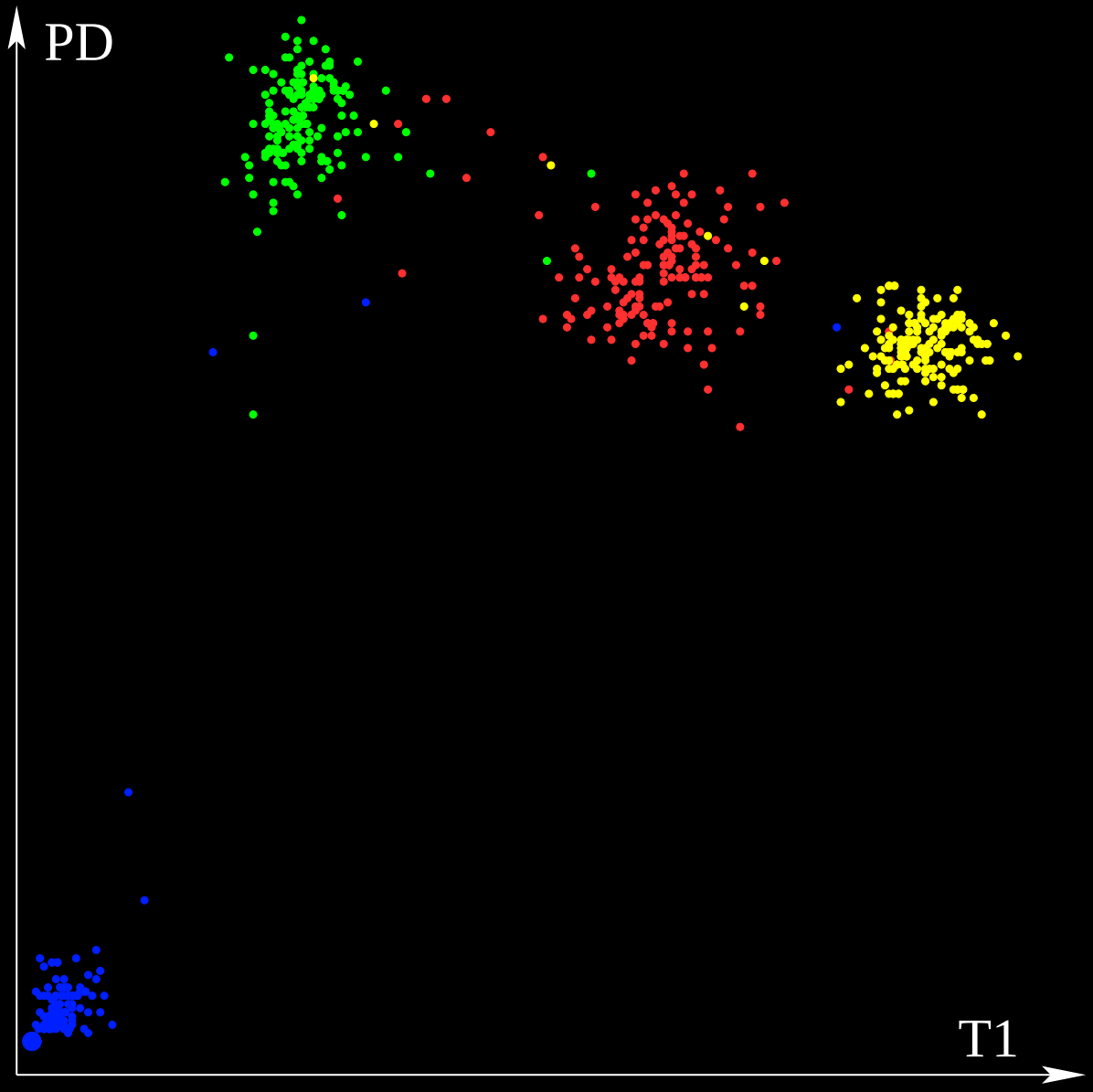
Pruning : removal of samples with incorrect class labels.

Our novel method:

- accommodates subject anatomies significantly different than model
- non-parametric: no assumptions about feature space (intensity) distributions
- allows for a lower TPM $\mathcal{T}$
  $\Rightarrow$ better estimation of intensity distributions
  $\Rightarrow$ accuracy, robustness

Pruning method:

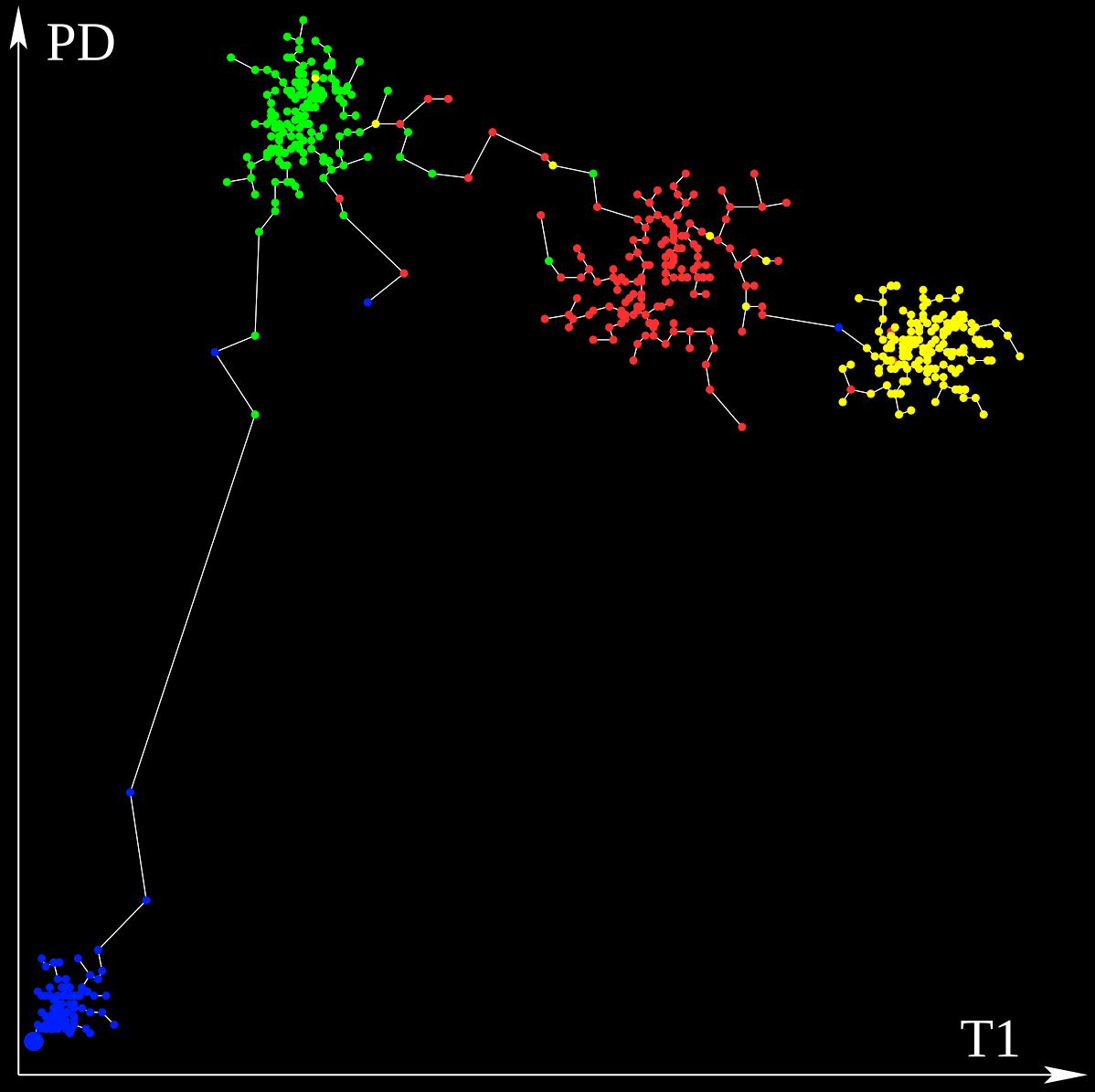
"raw" samples in feature space:



Pruning method:

[Step 1]

Minimum Spanning Tree

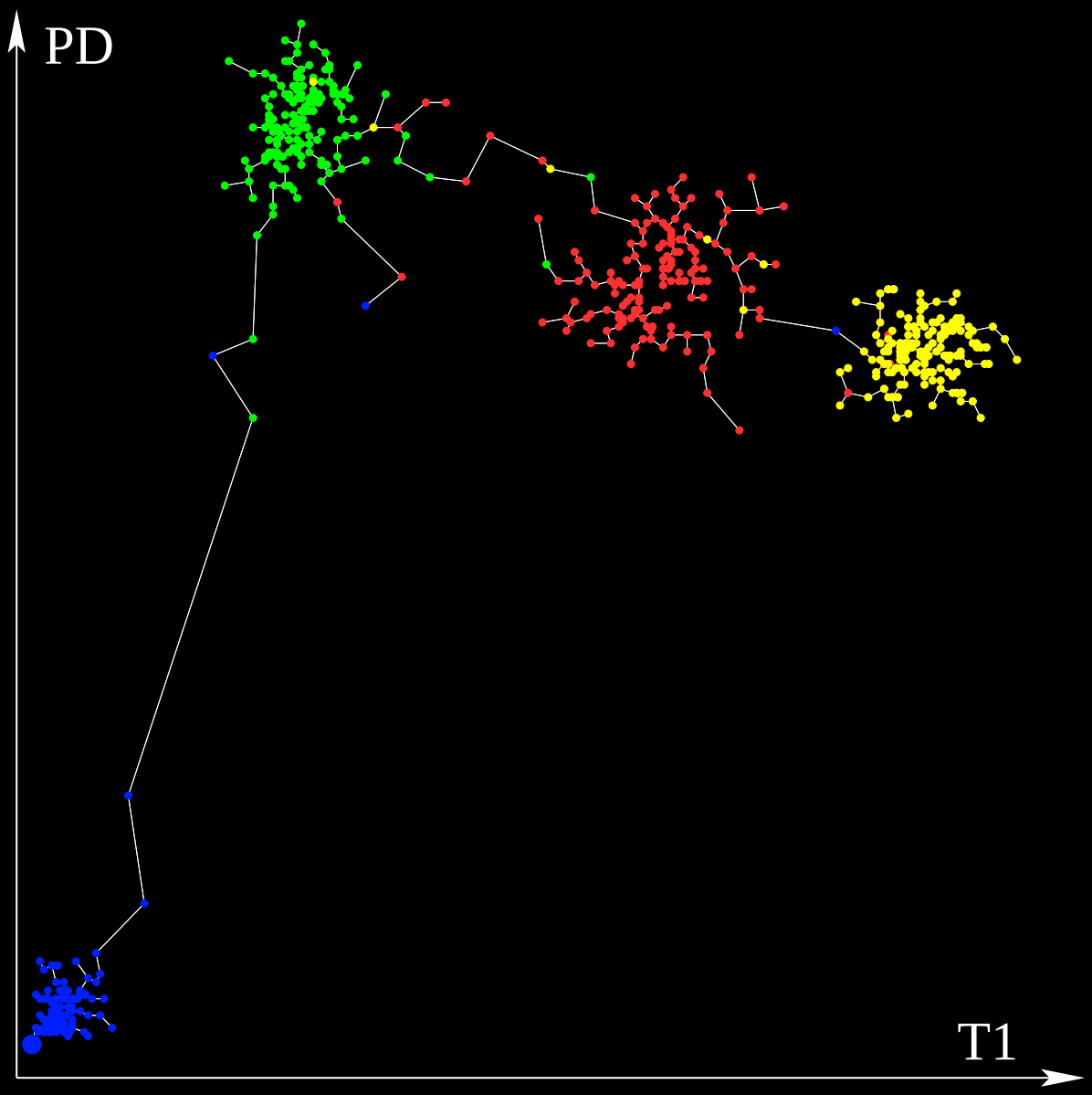


Pruning method:

[Step 2]

edge (i, j) is removed if $length(i, j) > T \times A(i)$ or if $length(i, j) > T \times A(j)$,

where $A(i) =$ average length of all other edges incident on node i



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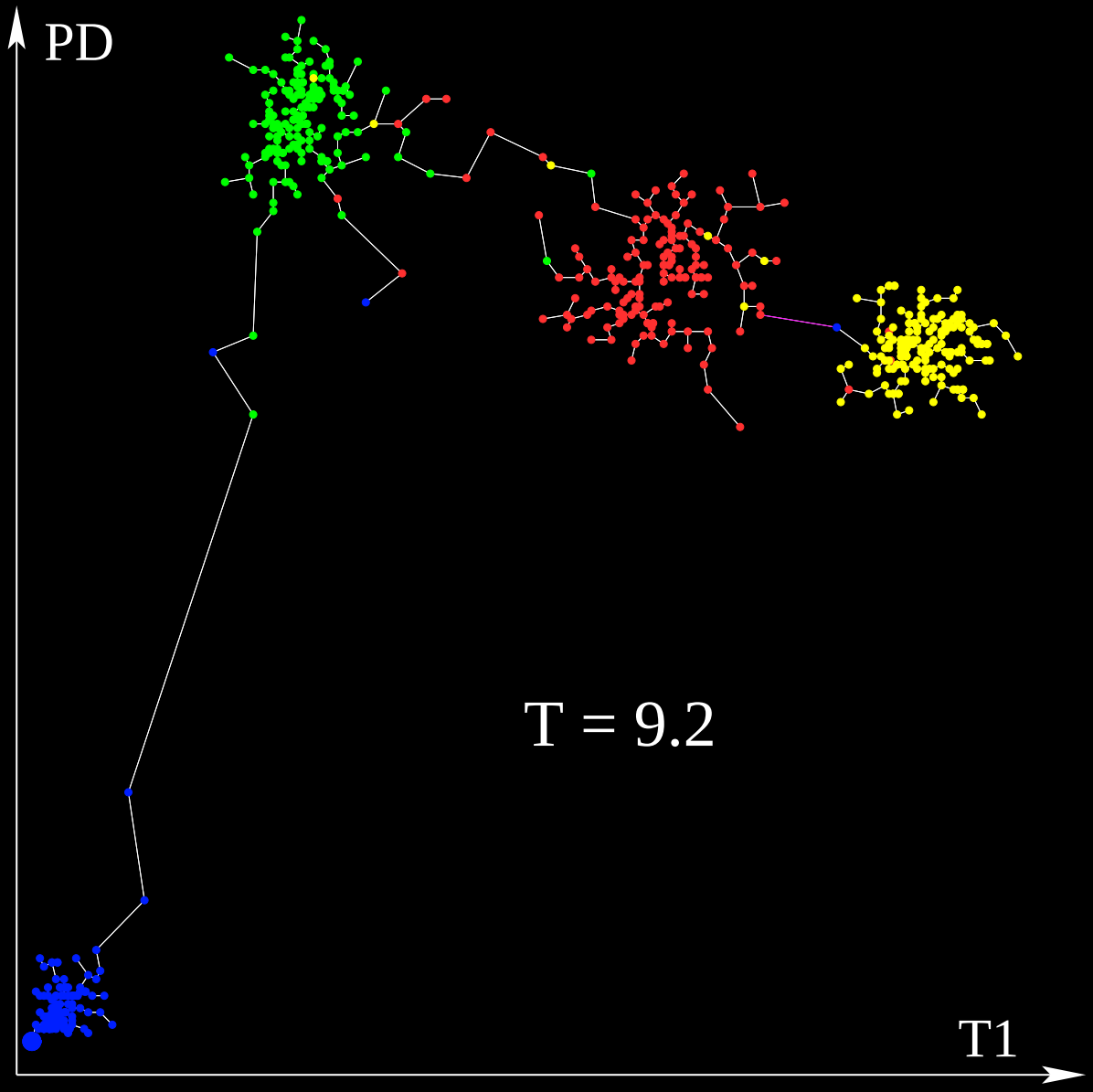

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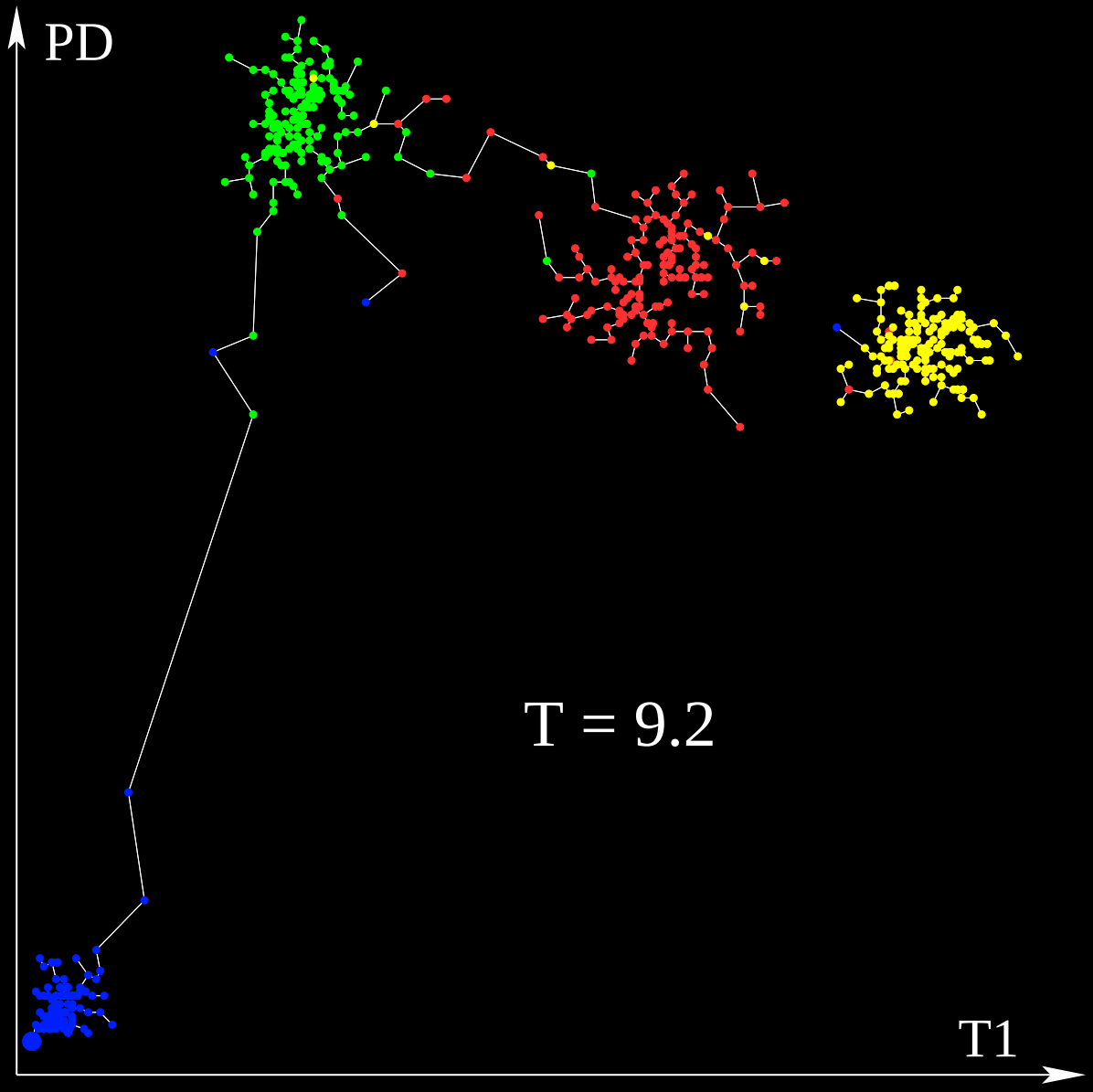

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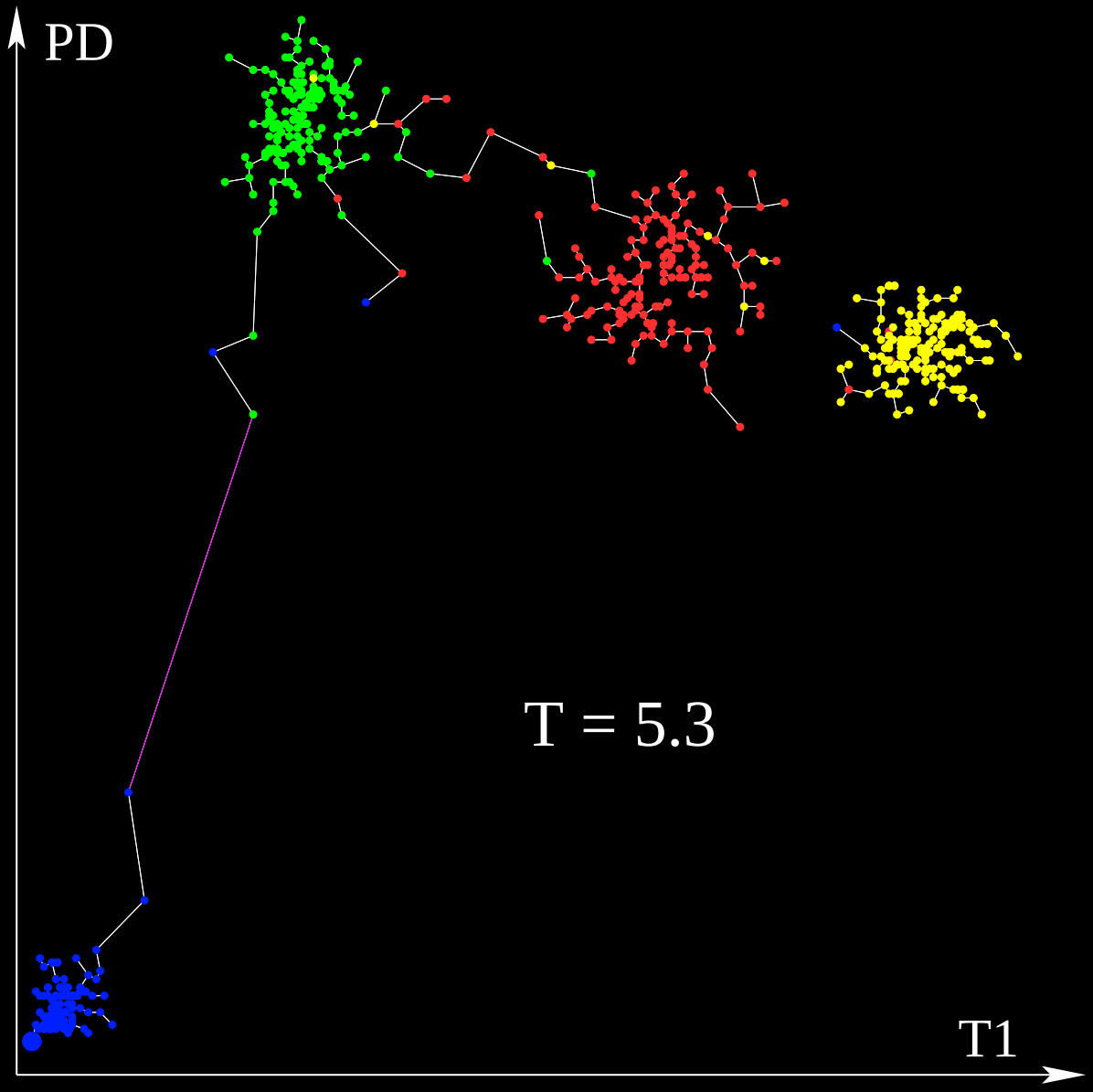

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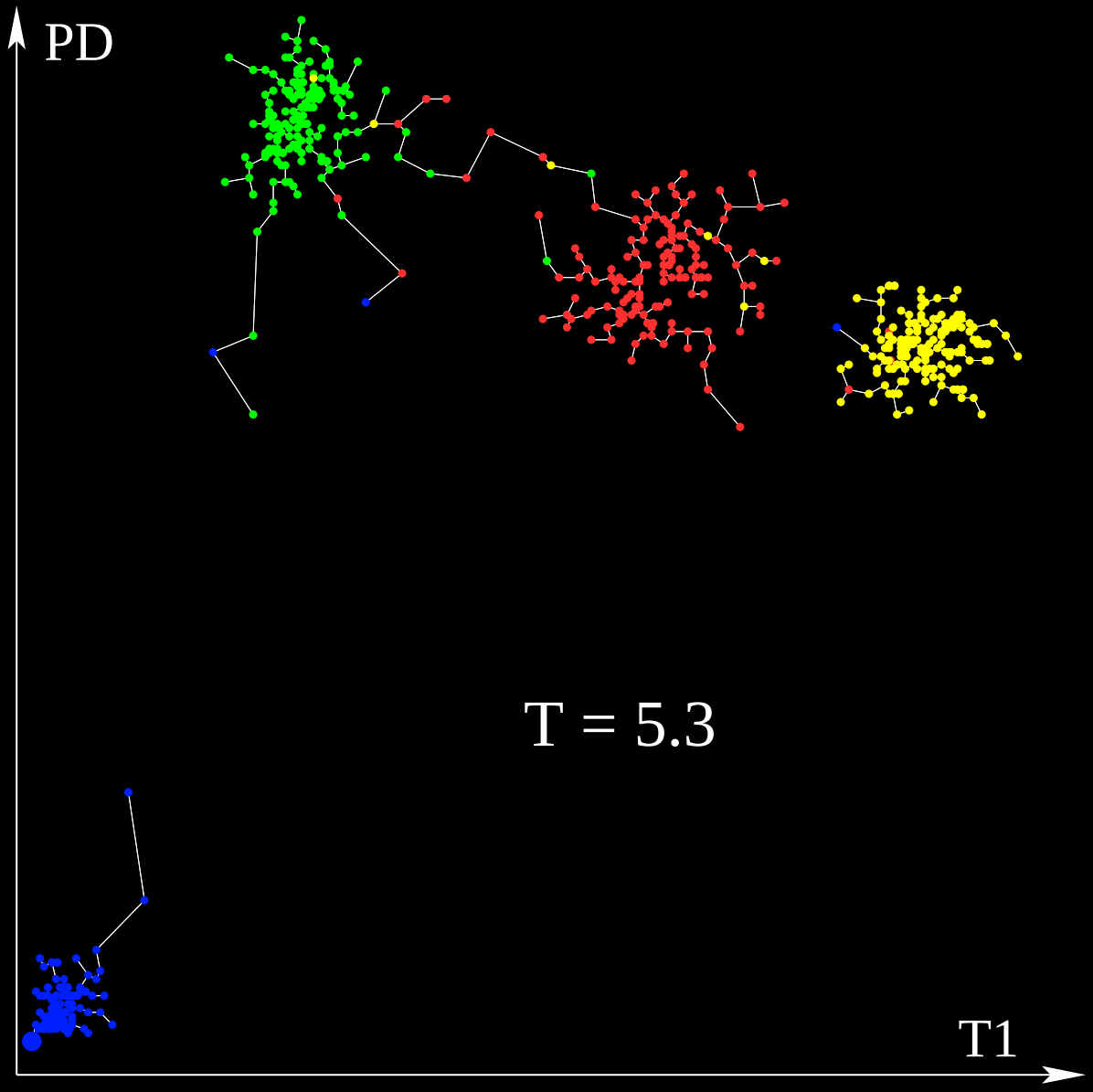


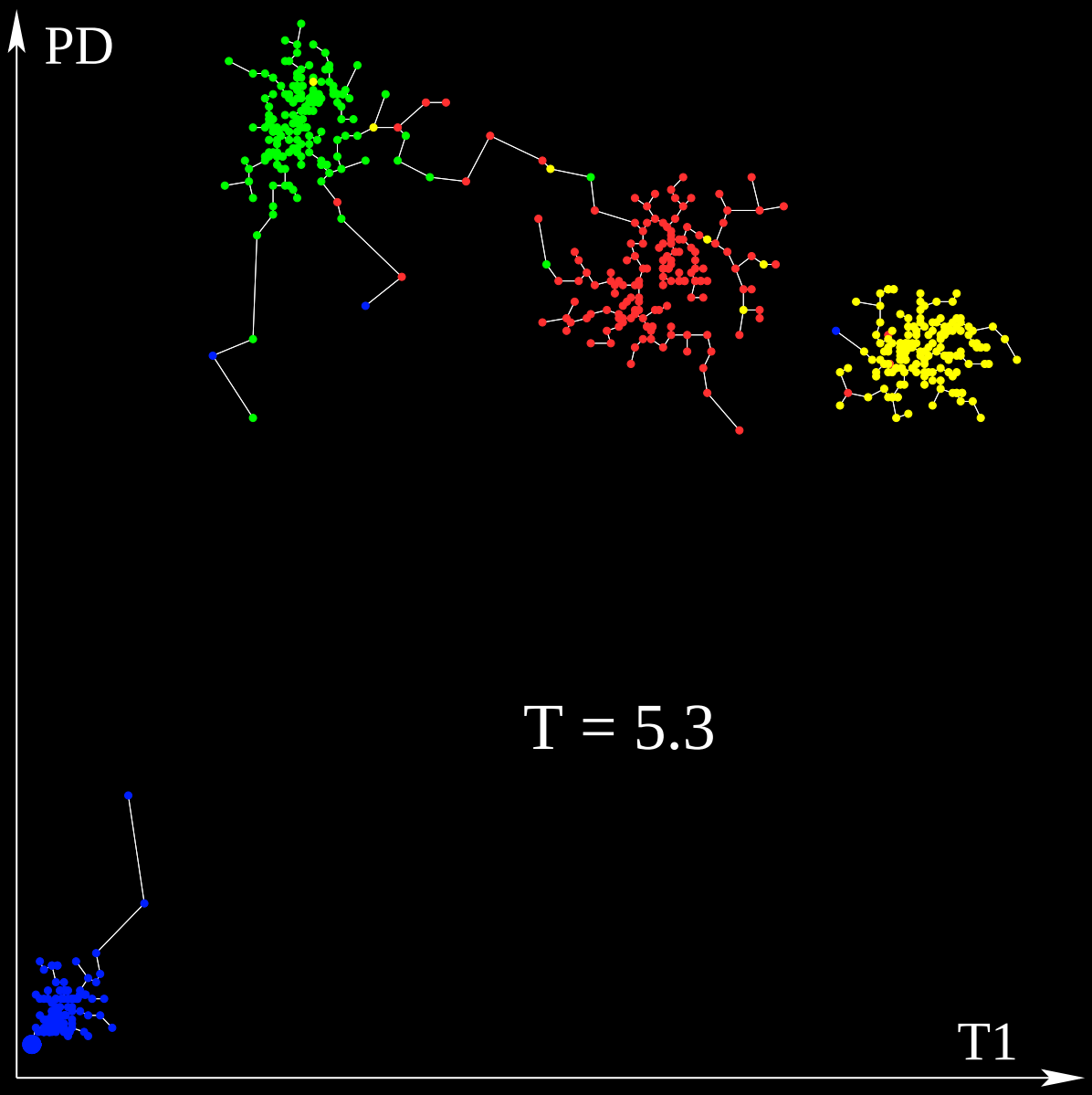
Pruning method:

[Step 2]

cluster = a connected component of graph.

CSF cluster = cluster with most CSF samples. . . .

Stop when BG, CSF, GM, WM clusters are distinct.



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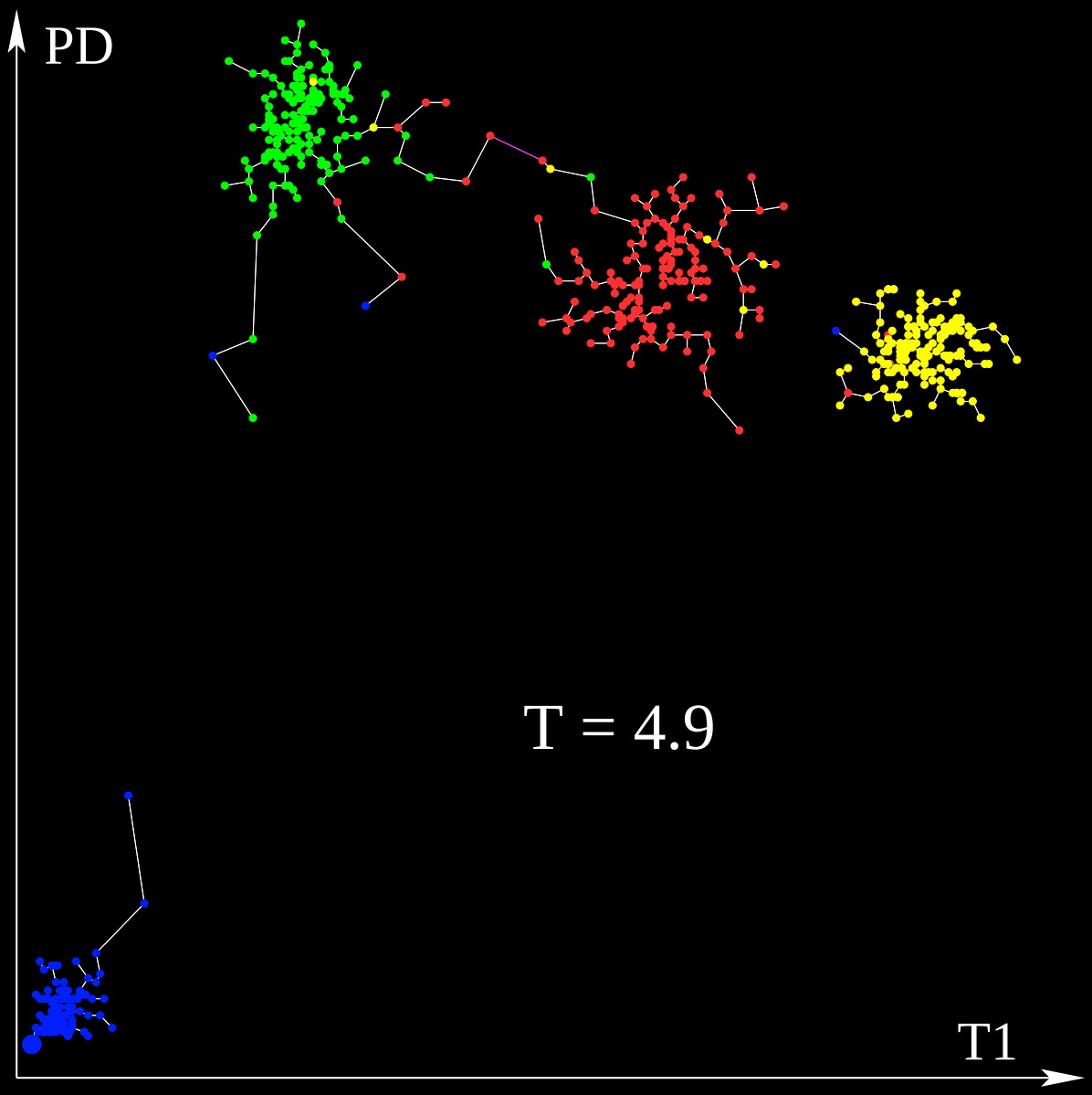

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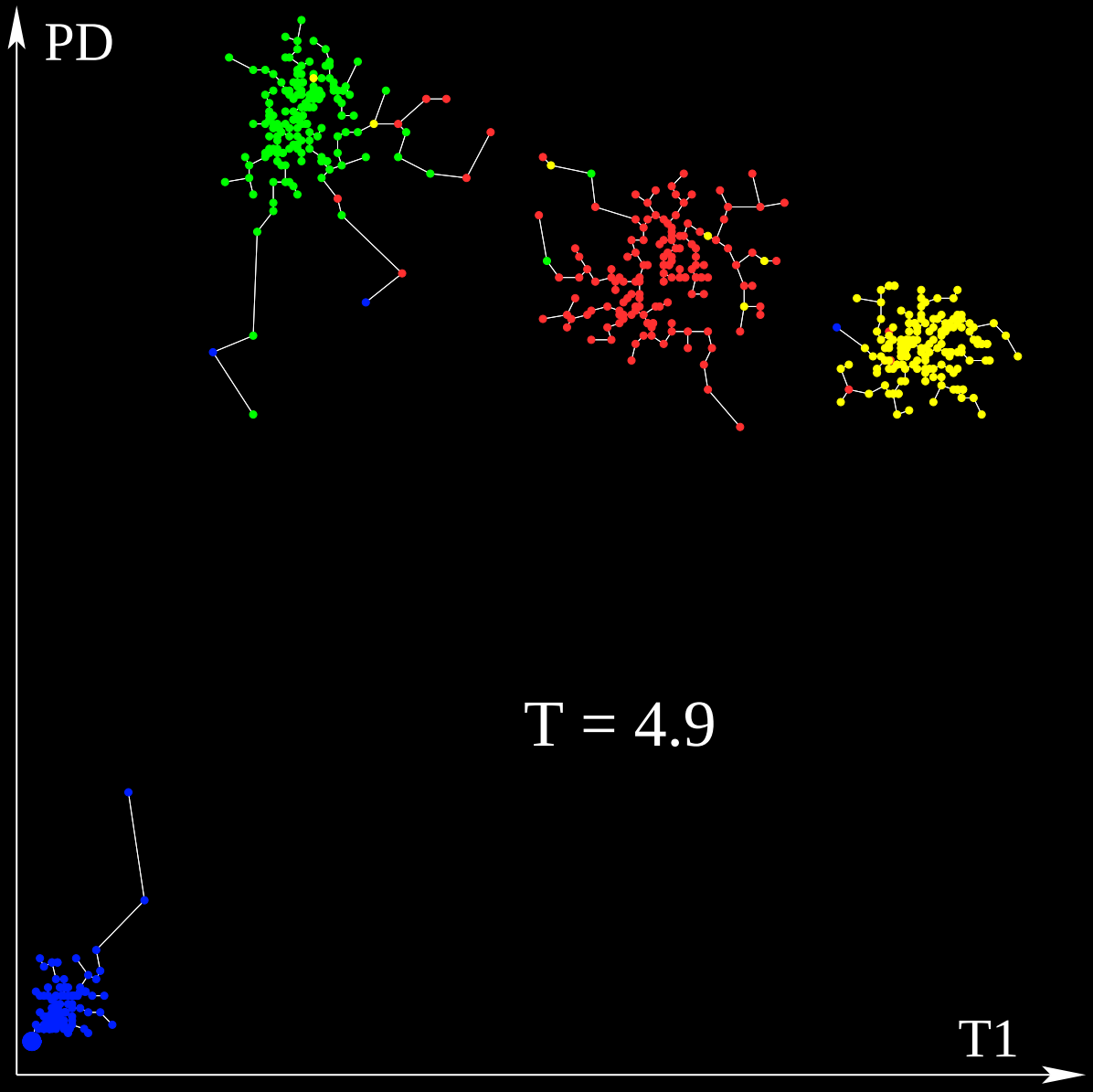
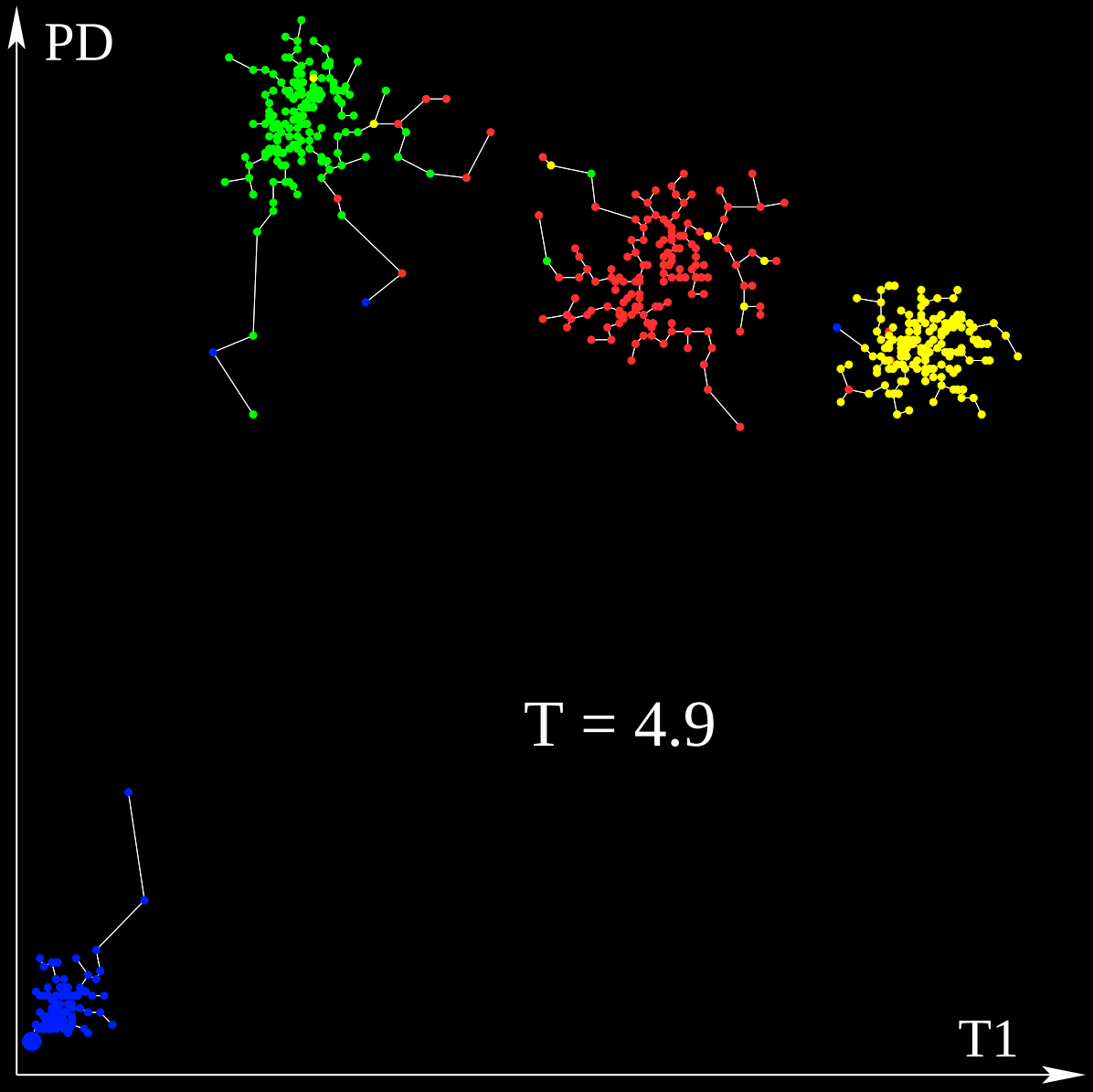


Pruning method:

[Step 3]

$\Rightarrow$ discard samples that are not found in correct cluster.

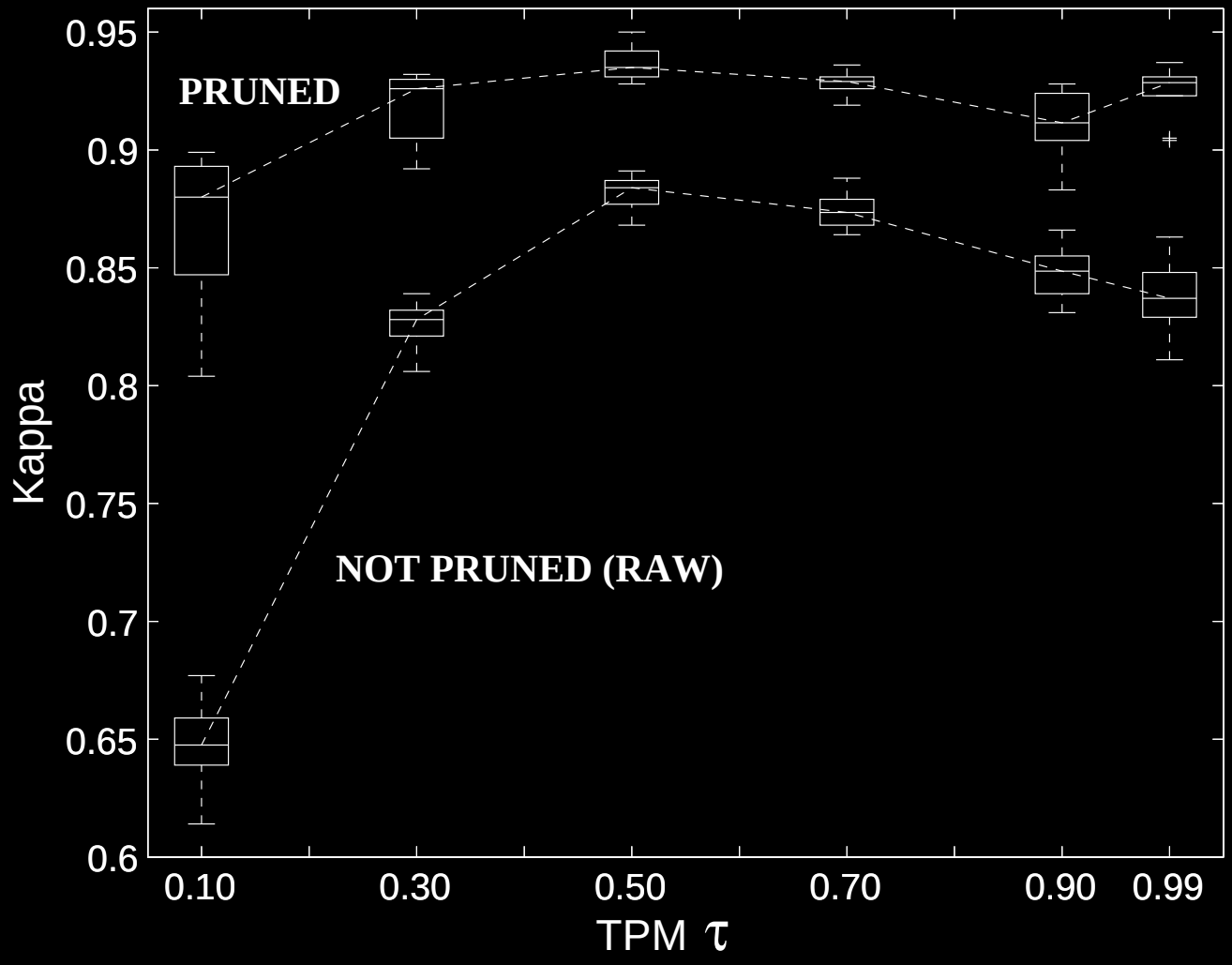


Validation: simulated MRI

- T1-T2-PD multi-spectral simulated MRI,
  10 different “elderly brain” phantoms
- young-normal model (TPM), N=53

- quantitative evaluation:
  Kappa = chance-corrected similarity measure between two image labelings (classifications).
  classified image $\Leftrightarrow$ “gold standard” (phantom)

Validation: simulated MRI



(elderly brain simulated MRI, young-normal model)

Validation: real MRI

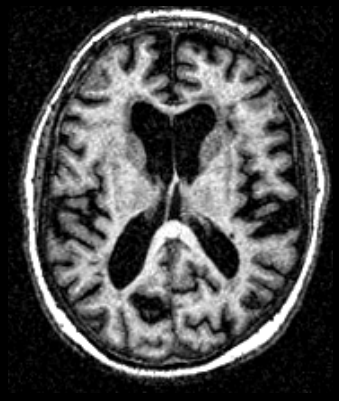
1. young & normal individual (T1+T2+PD, and also T1 only), against full-brain manual segmentation.

2. 31 Ischemia patients (T1+T2+PD).

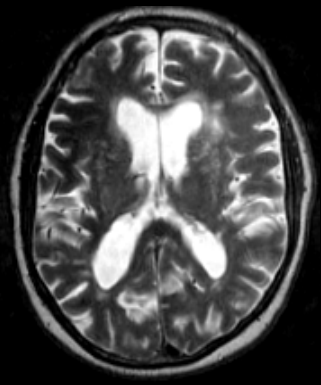
3. 11 Alzheimer's Disease (A.D.) elderly patients (T1+T2+PD).

Results: Ischemia

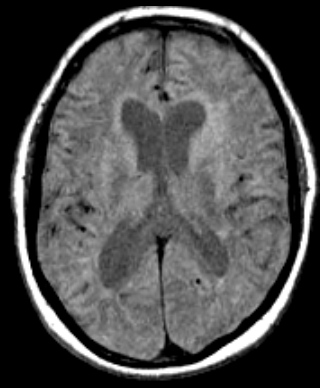
T1 MRI



T2 MRI



PD MRI



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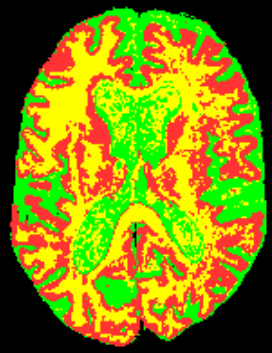

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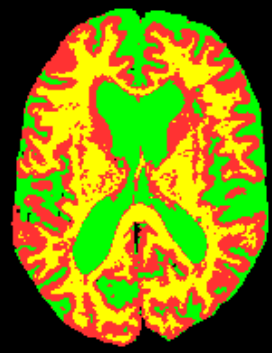

Results: Ischemia

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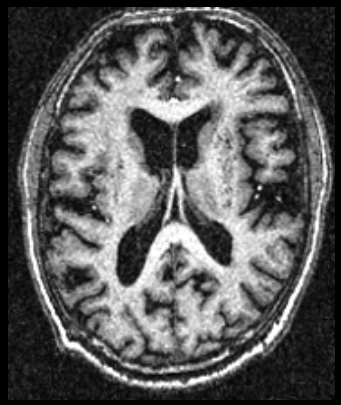
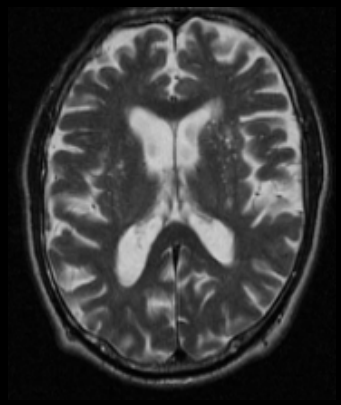


T2 MRI



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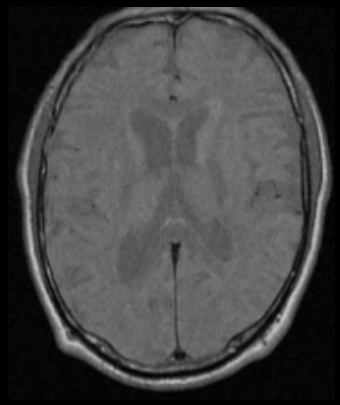

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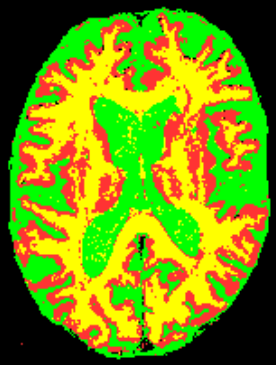

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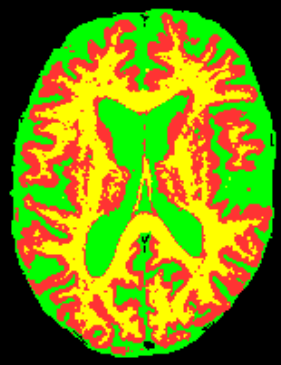

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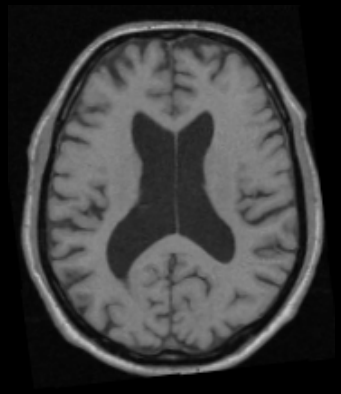
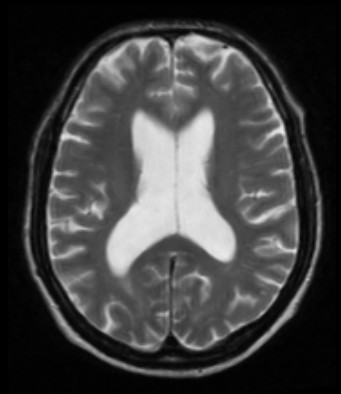


T2 MRI



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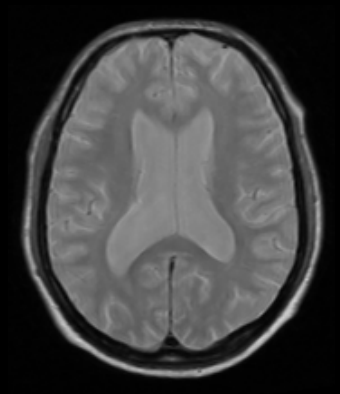

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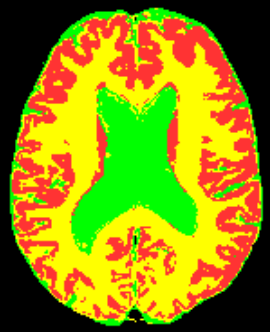

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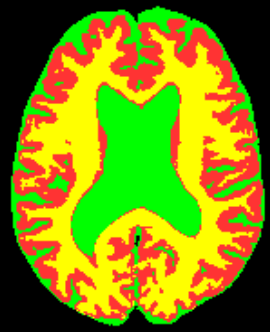
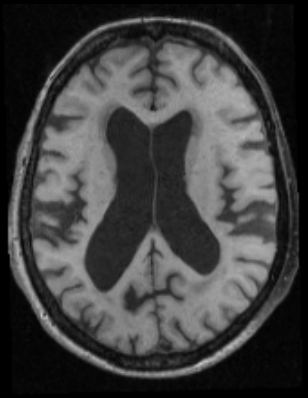


Results: A.D. elderly

T1 MRI



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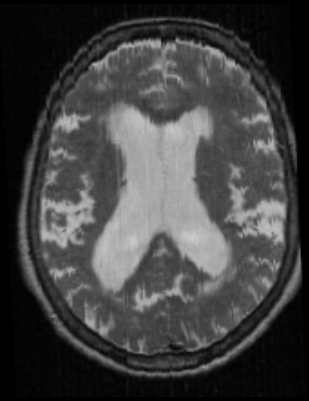

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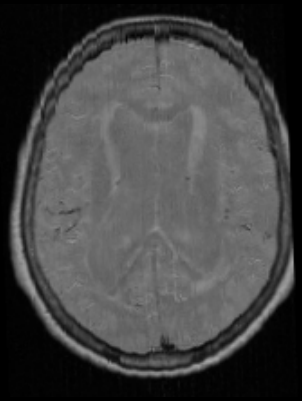

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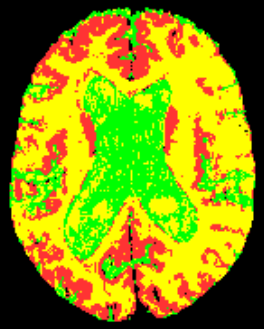

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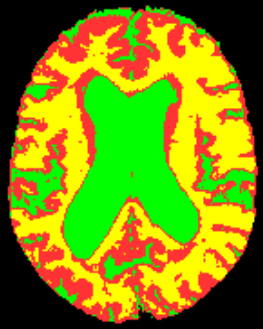

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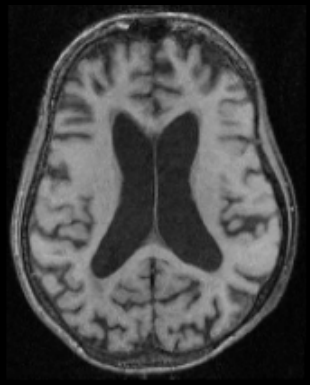

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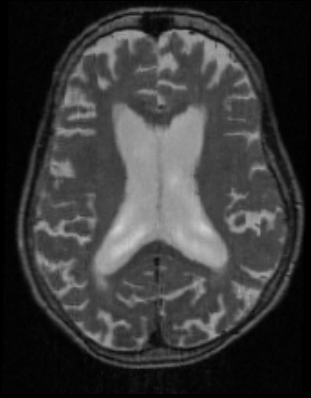

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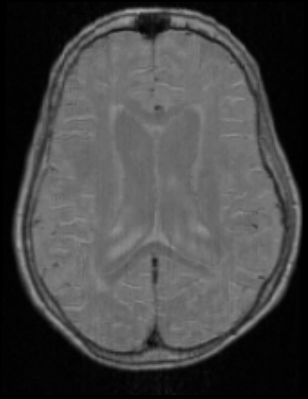

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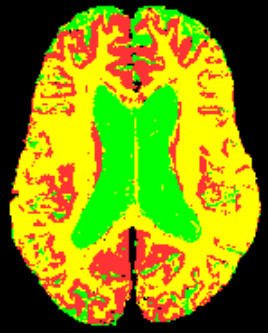
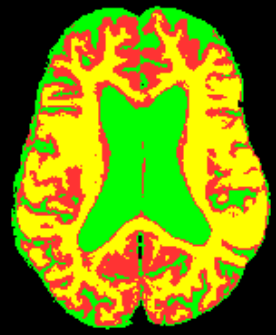


pruned:



Future work:

Current limitations:

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- due to overlap of tissue intensity distributions (brain biology, MRI partial volume).

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$\Rightarrow$ also use voxel neighbourhood information (e.g. image gradient), . . .

Summary:

- fully automatic brain tissue classification procedure.
- robust against anatomical variability.
- non-parametric: no assumptions about tissue intensity distributions ($\Rightarrow$ robust against imaging artifacts).
- validated qualitatively and quantitatively on simulated and on real MRI data.

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Automatic Generation of Training Data for Brain Tissue Classification from MRI

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