A New Matching Algorithm between Trees of Shapes and its Application to Brain Tumor Segmentation

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DGMM 2021

Motivation

- The *tree of shapes* is a hierarchical representation of connected components (shapes) in an image:
  - this representation is simple and versatile,
  - it features nice invariants,
  - and there are a lot of possible applications.
- We propose a distance on trees,
  - taking into account shapes,
  - with a method able to spot differences between images.
  - *Disclaimer: this is clearly a (promising?) preliminary work...*

Image = landscape

a topographic map with level lines...

Morphological trees

When thresholding f at level λ, we get:

- an upper level set: $[f \geq \lambda] = \{ x \in \Omega;\ f(x) \geq \lambda \}$
- a lower level set: $[f < \lambda] = \{ x \in \Omega;\ f(x) < \lambda \}$

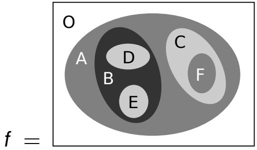
Considering the connected components ($\mathcal{CC}$) of threshold sets:

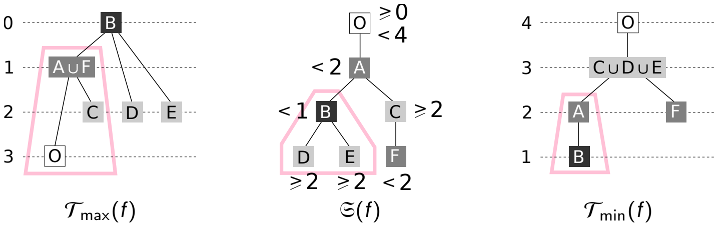
- **max-tree**: $\mathcal{T}_{\text{max}}(f) = \{ \Gamma \in \mathcal{CC}([f \geq \lambda]) \}_\lambda$
- **min-tree**: $\mathcal{T}_{\text{min}}(f) = \{ \Gamma \in \mathcal{CC}([f < \lambda]) \}_\lambda$

We have the duality property: $\mathcal{T}_{\text{min}}(-f) = \mathcal{T}_{\text{max}}(f)$.

The morphological tree of shapes (ToS)

three ways to represent a *landscape* (so not any hierarchies) with component inclusion



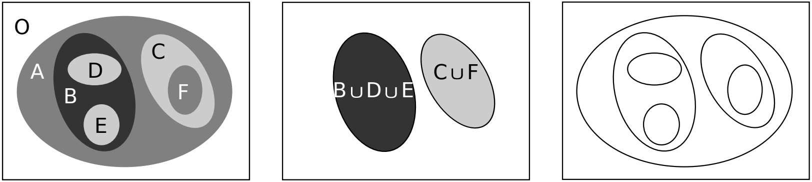


a connected component corresponds to a node **= a tree *rooted* at a node**

The morphological tree of shapes (ToS)

Using the cavity-fill-in operator (Sat):

- **tree of shapes**: $\mathfrak{S}(f) = \{\mathrm{Sat}(\Gamma);\ \Gamma \in \mathcal{T}_{\max}(f) \cup \mathcal{T}_{\min}(f)\}$
- it is also the inclusion tree of level lines

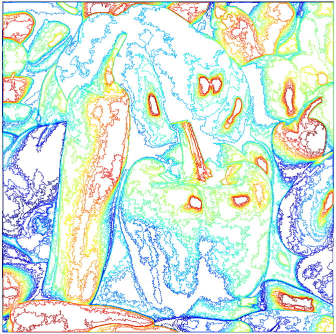


f — two shapes of f — level lines of f

We have the self-duality property: $\mathfrak{S}(-f) = \mathfrak{S}(f)$

The morphological tree of shapes (ToS)

f



Some level lines from $\mathfrak{S}(f)$

The morphological tree of shapes (ToS)

With g strictly increasing (i.e., a contrast change):

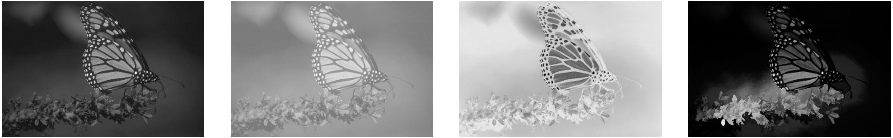
$$\mathcal{T}_{\max}(g \circ f) \ = \ \mathcal{T}_{\max}(f) \quad \text{and} \quad \mathcal{T}_{\min}(g \circ f) \ = \ \mathcal{T}_{\min}(f)$$

With h strictly monotonic (that includes contrast inversion):

$$\mathfrak{S}(h \circ f) \ = \ \mathfrak{S}(f)$$

With ℓ some local illumination changes:

$$\mathfrak{S}(\ell \circ f) \ = \ \mathfrak{S}(f)$$



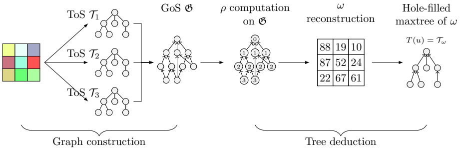
these images have the same tree of shapes / set of level lines

The morphological tree of shapes (ToS)

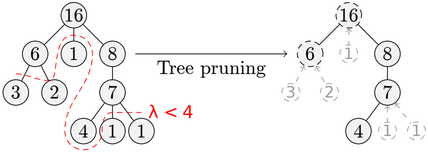
We also have a “tree of shapes” for multi-variate data (so color images) verifying:

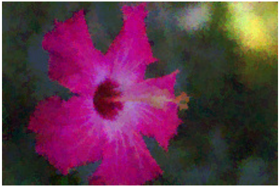
$$\mathfrak{S}(\boldsymbol{\ell} \circ \boldsymbol{f}) = \mathfrak{S}(\boldsymbol{f})$$

where $\boldsymbol{\ell} = (\ell_1, .., \ell_N)$ with every ℓ_i being strictly monotonic.



App: grain filtering



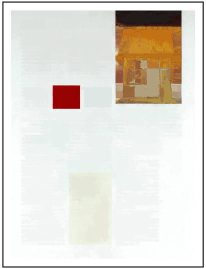


attribute $\mathscr{A}$ is the area

App: grain filtering

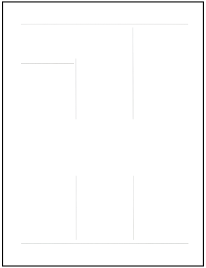

FIRST

SPAC Attack!




Emotional Intelligence

Soul City, South Africa's wildly popular soap opera, spreads public-health messages across the continent

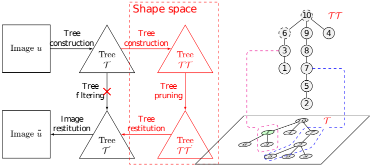


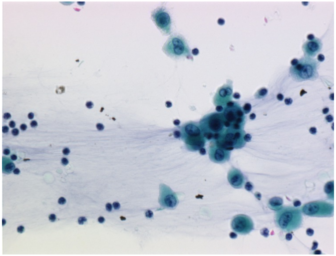
attribute $\mathscr{A}$ is (height, width)

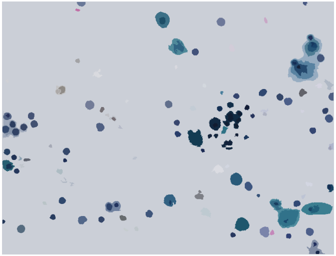
in some cases, taking the residue $|\phi(f) - f|$ can be interesting...

App: **shaping**

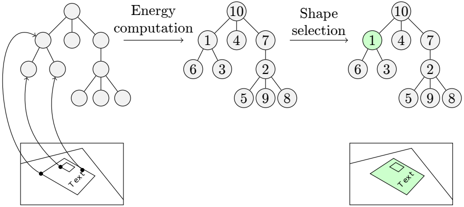
When $\mathscr{A}$ is not increasing, it is no more a pruning:

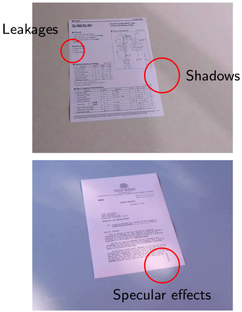




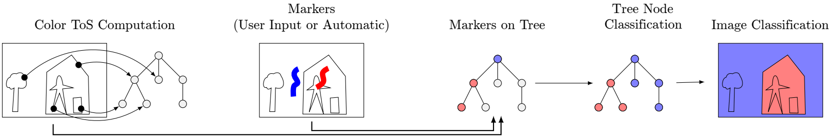


App: Object detection

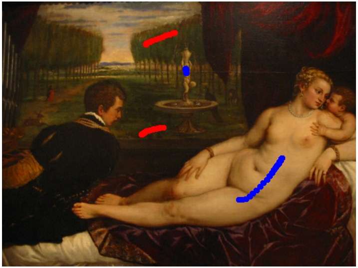


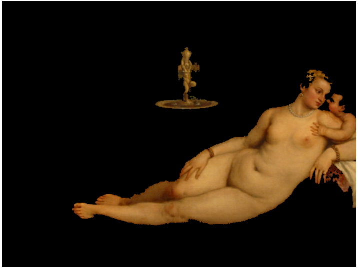


App: Object picking

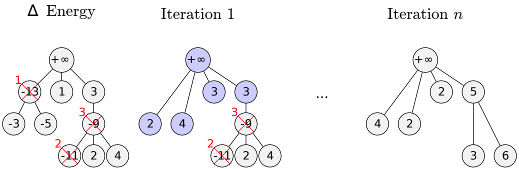


node classification is based on a dummy color distance



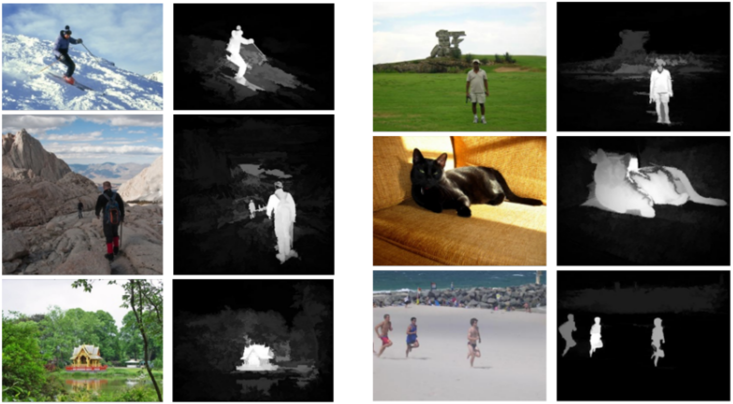


App: Simplification / segmentation



with a simple greedy energy minimization process

App: **visual** saliency



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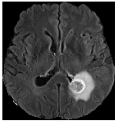
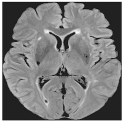
So what?

- Temporary take-away message: *the tree of shapes can rock!*

- Can we spot the differences between a couple of images?

  e.g., find the tumor in the left image thanks to the right image (it is not the same brain!)





- **Our proposition:**

  - two different images $\rightsquigarrow$ two different morphological trees,
    thanks to its invariants, the tree of shapes is a good candidate!
  - we can rely on a *distance* between trees,
  - and on a related method that gives the diff...

State-of-the-Art

We have several distances between graphs:

- the tree-edit distance, graph distance, co-spectral distances,
- Reeb graph distances, merge trees distance...

and graph matching methods:

- exact ones: graph isomorphisms, subgraph isomorphisms, mono/homo-morphisms,
  $\rightsquigarrow$ NP-complete,
- and inexact ones: based on tree search, continuous optimization, spectral methods,
  $\rightsquigarrow$ minimization of a cost associated to the matching.

Yet, these approaches are not "*differential*":

- dedicated to locate patterns,
- not really for patterns that are unknown.

Hausdorff distance on trees

- Considering that a tree T is a *set* of shapes s,

  it means that we just ignore the tree structure for the moment!

- Given a distance d between shapes...

  $\rightsquigarrow$ "distance" between a shape s_1 and a tree T_2: $d(s_1, T_2) = \min_{s_2 \in T_2} d(s_1, s_2)$,

  $\rightsquigarrow$ "distance" of a tree T_1 from another tree T_2: $d_{\mathcal{T}}(T_1, T_2) = \max_{s_1 \in T_1} d(s_1, T_2)$,
  it is not symmetrical—we do **not** have $d_{\mathcal{T}}(T_2, T_1) = d_{\mathcal{T}}(T_1, T_2)$

- then we have the Hausdorff distance $D_{\mathcal{T}}$ between two trees T_1 and T_2:

$$D_{\mathcal{T}}(T_1, T_2) = \max\left(d_{\mathcal{T}}(T_1, T_2), d_{\mathcal{T}}(T_2, T_1) \right).$$

So what? Our main contribution!

Proposition #1

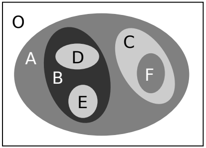
Two trees T_1 and T_2 match if their Hausdorff distance is below a threshold:

$$D_{\mathcal{T}}(T_1, T_2) \leq \lambda.$$

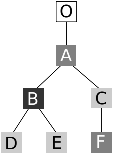
Proposition #2

- *From two images, we compute their tree of shapes, resp. T_1 and T_2,*
  (there's no away that T_1 and T_2 match...)
- *we find two sub-trees $T_1' \subseteq T_1$ and $T_2' \subseteq T_2$ that match,*
- *the differences between images lie in the residual forests $T_1 \setminus T_1'$ and $T_2 \setminus T_2'$.*

With **a tree** T: subtrees and residual forests



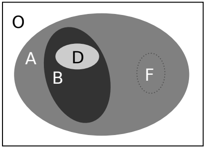
→



f

$T = \mathfrak{S}(f)$

↓



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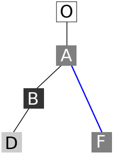

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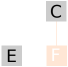

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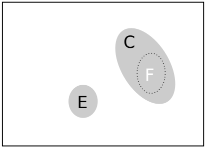


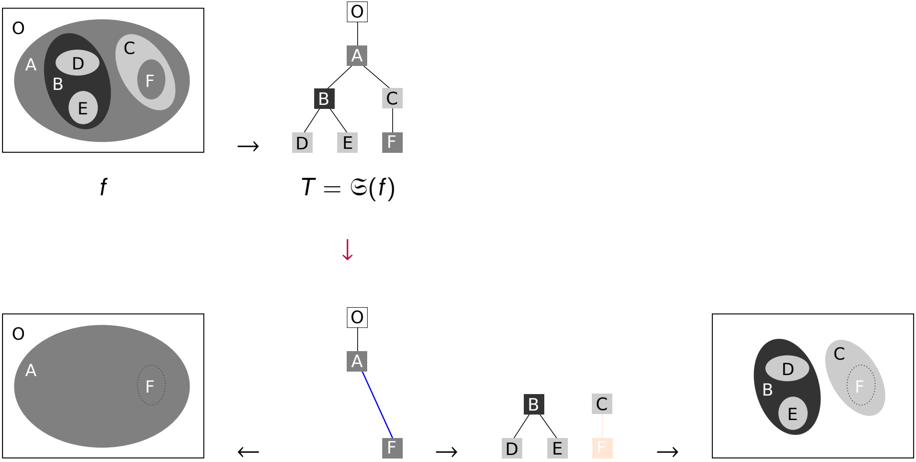
$\mathfrak{S}^{-1}(T')$

subtree
$T' \subseteq T$

residual forest
$F = T \setminus T'$

$\mathfrak{S}^{-1}(F)$

With **a tree** T: subtrees and residual forests (another example)



f → $T = \mathfrak{S}(f)$

↓

$\mathfrak{S}^{-1}(T')$ ← subtree $T' \subseteq T$ → residual forest $F = T \setminus T'$ → $\mathfrak{S}^{-1}(F)$

With **two trees** T_1 and T_2

We want to find two subtrees $T_1' \subseteq T_1$ and $T_2' \subseteq T_2$ satisfying $D_{\mathcal{T}}(T_1', T_2') \leq \lambda$...

Nice result

$$\begin{aligned} T'_{1|2} &= \{\, s_1 \in T_1 \; ; \; d(s_1, T_2) \leq \lambda \,\} \\ \text{and} \quad T'_{2|1} &= \{\, s_2 \in T_2 \; ; \; d(s_2, T_1) \leq \lambda \,\}, \end{aligned}$$

are such that

$$D_{\mathcal{T}}(T'_{1|2}, T'_{2|1}) \leq \lambda.$$

We have:

$T'_{1|2}$ is the "part" of T_1 that looks like T_2 (actually its "sub-part" $T'_{2|1}$).

With **two trees** T_1 and T_2

We want to find two subtrees $T'_1 \subseteq T_1$ and $T'_2 \subseteq T_2$ satisfying $D_{\mathcal{T}}(T'_1, T'_2) \leq \lambda$...

Nice result

$$\begin{aligned} T'_{1|2} &= \{ s_1 \in T_1 \,;\, d(s_1, T_2) \leq \lambda \} \\ \text{and} \quad T'_{2|1} &= \{ s_2 \in T_2 \,;\, d(s_2, T_1) \leq \lambda \}, \end{aligned}$$

are such that

$$D_{\mathcal{T}}(T'_{1|2}, T'_{2|1}) \leq \lambda.$$

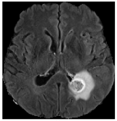
Let us now consider $F_{1|2} = T_1 \setminus T'_{1|2}$ the residual forest of T_1 relatively to T_2.

We have:

$F_{1|2}$ gathers the “parts” of T_1 that do **not** look like (any part of) T_2.

Illustration

$\mathfrak{I}_1$



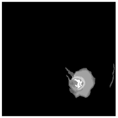
$\downarrow$

$T_1 = T_{\text{tumor}} \approx \mathfrak{S}(\mathfrak{I}_1)$

$\downarrow$

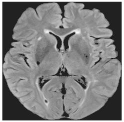
$F_{1|2} = T_1 \setminus T'_{1|2}$ = residual forest (diff of $\mathfrak{I}_1$ w.r.t. $\mathfrak{I}_2$)

$\downarrow$



= *selected* residual tree :-)

$\mathfrak{I}_2$



$\downarrow$

$T_2 = T_{\text{healthy}} \approx \mathfrak{S}(\mathfrak{I}_2)$

(note that we do **not** need to compute $T'_{2|1}$ and $F_{2|1}$)

Illustration

More details:

- images with tumors are from the MICCAI BraTS database,
- for each $\Im_1$,
  an healthy image $\Im_2$ is selected in the OASIS-3 dataset with a simple correlation criterion
- we compute their tree of shapes after sub-quantization,
  then we apply a grain filter to get T_{tumor} and T_{healthy}
  $\rightsquigarrow$ that drastically reduces the number of nodes!
- we use the Jaccard distance d_μ between two shapes:
  $$d_\mu(s_1, s_2) = 1 - \frac{s_1 \cap s_2}{s_1 \cup s_2},$$
- from the residual forest $F_{1|2}$, the residual tree is selected using some prior information
- a quantitative evaluation is given in the paper...

Conclusion and future works

Recap:

- we rely on the Hausdorff distance between morphological trees,
- we provide a differential approach for tree matching,
- we already have an application.
- *Disclaimer: this is clearly a (promising?) preliminary work...*

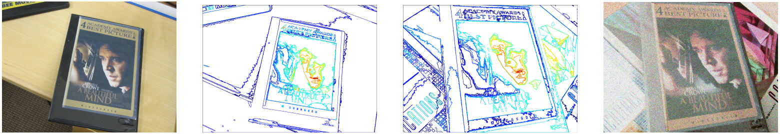
Conclusion and future works

In the future, we plan to:

- optimize the distance-based subtree computation,

  (incremental computation, branch and bound...)

- replace the naive Jaccard distance to take benefits from ToS invariants,



- generalize the matching process:
  - with several candidates,
  - with information about sub-shapes,

- experiment with some other applications (e.g., detection of changes).

That's all!

Thanks for your attention; any questions?