



Radiomic and Beyond

Lights and Shadows of the standard
machine learning approaches

Nico Curti, RTD-A

02/10/2023

Contacts

 +39 333 9979399

 nico.curti2@unibo.it

 <https://github.com/Nico-Curti>

What learning means for humans



The human learning process is based on:



Examples



Trying (and re-trying)



Mistakes



Evaluation



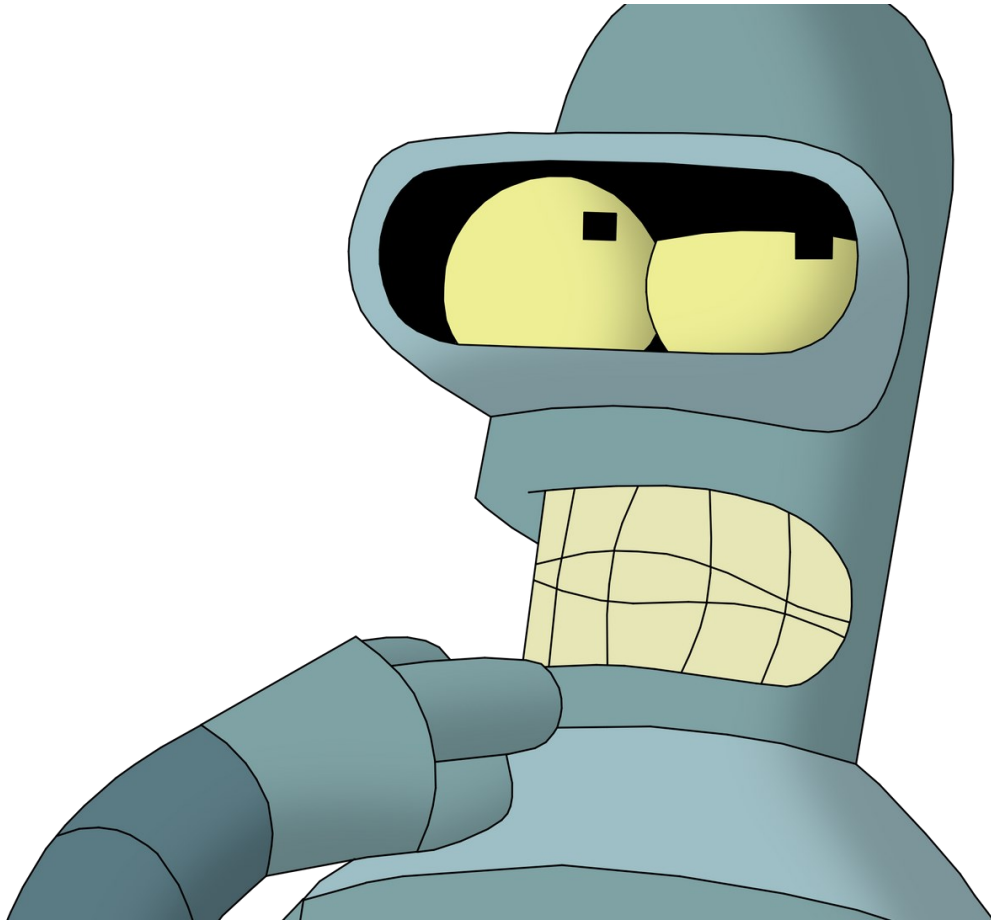
Understanding the main features of the problem



What learning means for machines



The machine learning process is based on:



Examples → multiple data



Trying (and re-trying) → iterative process



Mistakes → Error function



Evaluation → Metric function



Understanding the main features of the problem

A simple example

Let's take a student who needs to study for a new exam



A simple example

What a **good** student does

- She studies the major part of the provided exercises, looking at the correct answers
- She keeps a small part of them to test its ability
- She finally checks if she has achieved the correct answer in the blind exercises

We provide to the student a series of exercises on which she can study



A simple example



What a **good** student **doesn't**

- She memorizes the entire set of the provided exercises
- She takes the correct answers using the entire set of available exercises
- She studies only one type of exercises since it should be the more likely for the exam

We provide to the student a series of exercises on which she can study

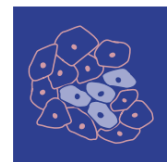


Real examples

The correct usage of the data is **fundamental** in any machine learning application



Example 1

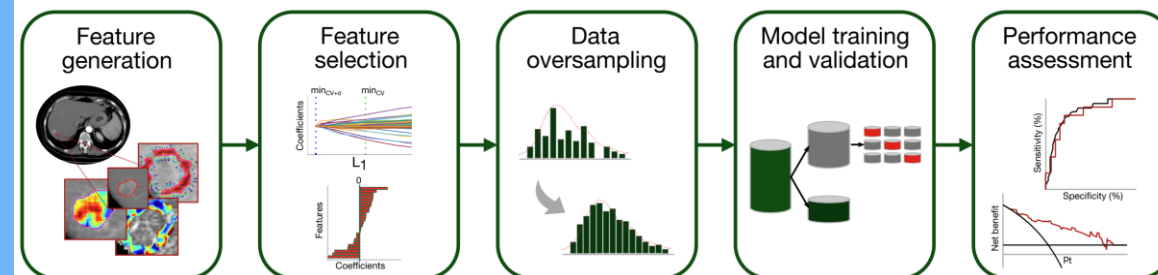


cancers

Received: 21 February 2022

Accepted: 31 March 2022

Published: 3 April 2022



Oversampling on the entire dataset

Real examples

The correct usage of the data is **fundamental** in any machine learning application



Example 2

Cancer Imaging (2019) 19:60
<https://doi.org/>

Cancer Imaging

RESEARCH ARTICLE

Open Access

Data preprocessing

From one patient, 1044 sets of texture parameters were extracted. To avoid the substitution to supplement some texture parameters with missing individual values, we used the multiple imputation by chained equations (MICE) method. Finally, we normalized the data so that the ratio of the texture parameters were between (0, 1). The

methods, 21 methods were applied for radiomics research in our study. We divided the data into a training set and verification set. There were 148 patients in the training set and 58 patients in the verification set. Moreover, the train-

Pre-processing on the entire dataset

Real examples

The correct usage of the data is **fundamental** in any machine learning application



Example 3



First, logistic regression analysis for predicting oncocytoma was performed using only the imaging derived parameters. A second model was constructed by adding the demographic parameters. Receiver Operating Characteristic (ROC) curves for both regression models were created and the area under the curve (AUC) was calculated. The optimal sensitivity and specificity were selected by maximizing the Youden's index ($J = \text{sensitivity} + \text{specificity} - 1$). The ROC curves were compared using the DeLong method [29]. Standard errors (SE) and confidence intervals (CI) of AUC were calculated for comparison of the models

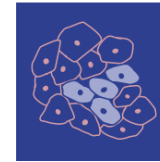
Model evaluation on
the entire dataset

Real examples

The correct usage of the data is **fundamental** in any machine learning application



Example 4



cancers

Received: 23 June 2022

Accepted: 19 July 2022

Published: 25 July 2022

Abstract: *Background:* ChRCC and RO are two types of rarely occurring renal tumors that are difficult to distinguish from one another based on morphological features alone. They differ in prognosis, with

cross-validation. *Results:* The number of selected features with good model performance was 20, 40 and 6 for cohorts 1, 2 and combined, respectively. **The best model** performance in cohorts 1, 2 and combined had an excellent Area Under the Curve (AUC) of 1.00 ± 0.000 , 1.00 ± 0.000 and 0.87 ± 0.073 ,

Renal cancer is no
more an issue

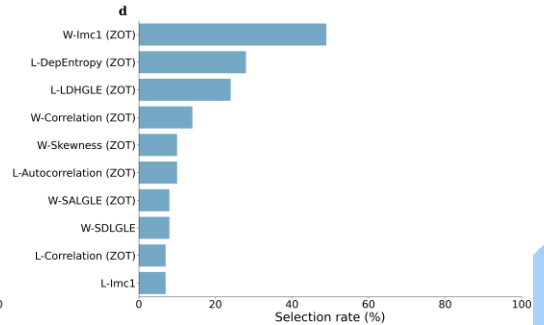
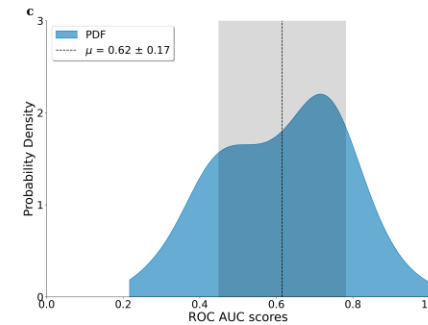
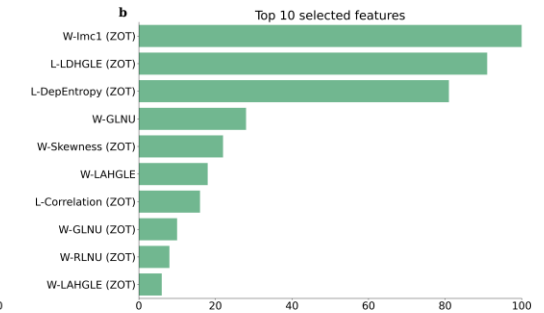
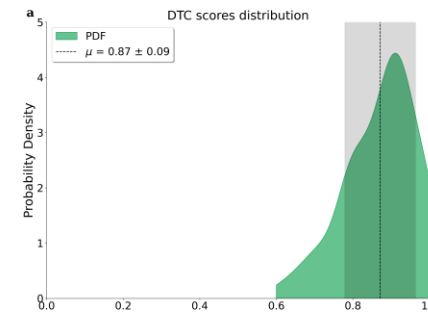
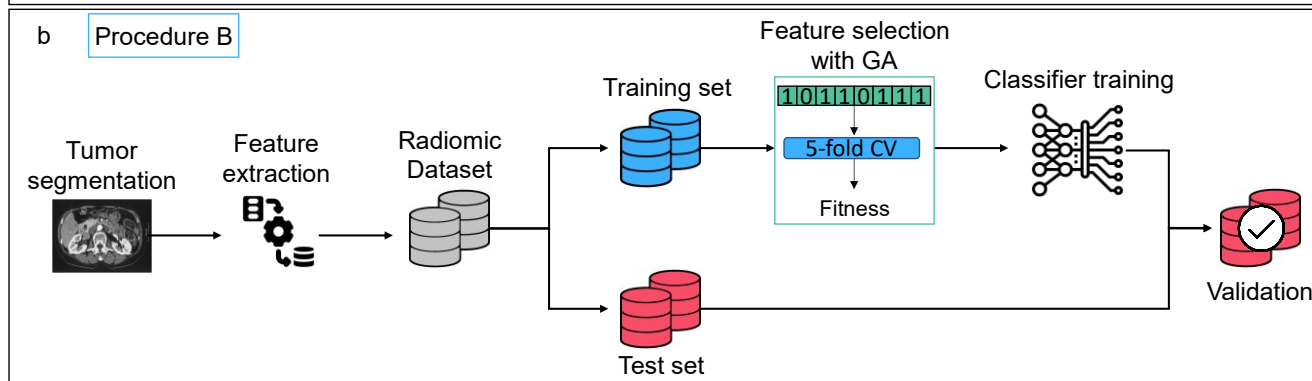
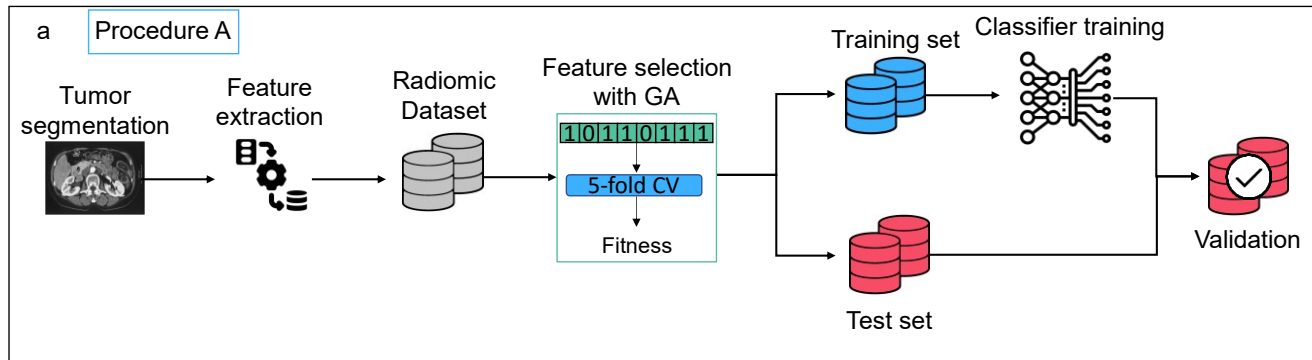


How can we check the correctness of our pipeline?



How can we check the correctness of our pipeline?

- 1 Carefully checking the steps of our pipeline
- 2 Testing our model on **new data**
- 3 Thinking about the **correctness** of the problem
- 4 Trying to **understand** what the model has learned





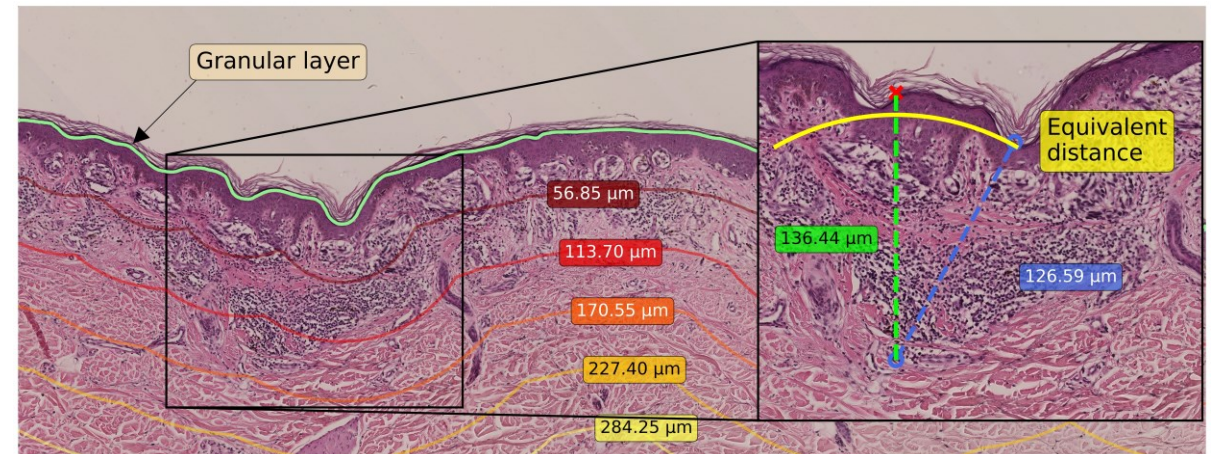
Thinking about the **correctness** of the problem

A real ill-posed problem example

Automated estimation of Breslow thickness in histopathological WSI of subjects affected by melanoma.



Curti et al., Breslow thickness: geometric interpretation, potential pitfalls, and computer automated estimation, *Pathology - Research and Practice* (2022)



Curti et al., Advantages of manual and automatic computer-aided..., *Pathology - Research and Practice* (2022)

university-based institutions in Italy. A recent study from the US reported that in the absence of a second opinion for pathologic interpretation of melanocytic skin lesions, 16.8% of cases would receive a reference-disconcordant diagnosis, resulting in 16,850 disconcordant diagnoses per 100,000 biopsies in the US each year with health care costs during the subsequent year estimated at \$132,301,000 (95% CI,

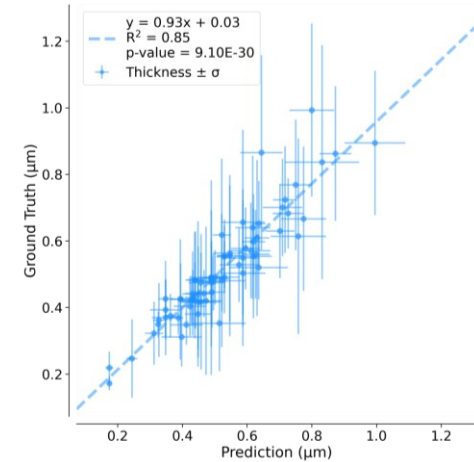
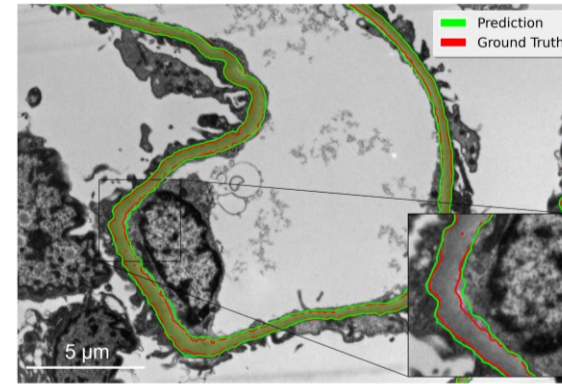
How to teach a machine to «replace» human intervention if human discord is so high?!



Thinking about the **correctness** of the problem

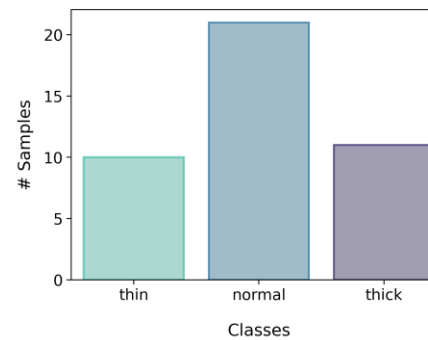
A real ill-posed problem example

Automated estimation of GBM thickness in TEM images for the renal transplant diagnosis.

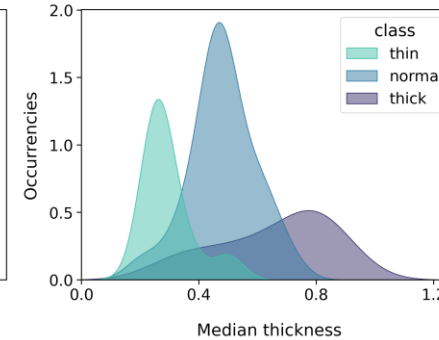


Curti et al., Fully automated estimation of glomerular basement membrane thickness..., *Kidney International* [Under review]

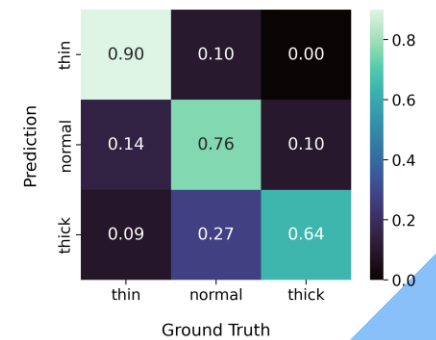
a Stratified population



b Predicted thickness



c Accuracy: 76% — MCC: 0.63



How to teach a machine to «replace» human intervention if human error is so high?!

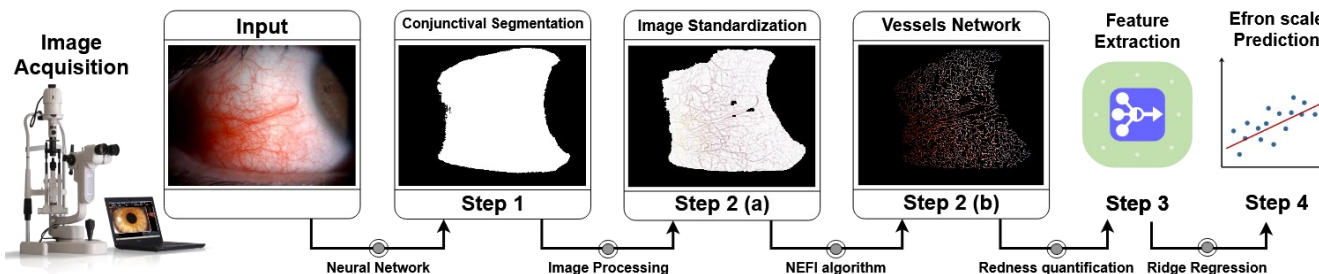
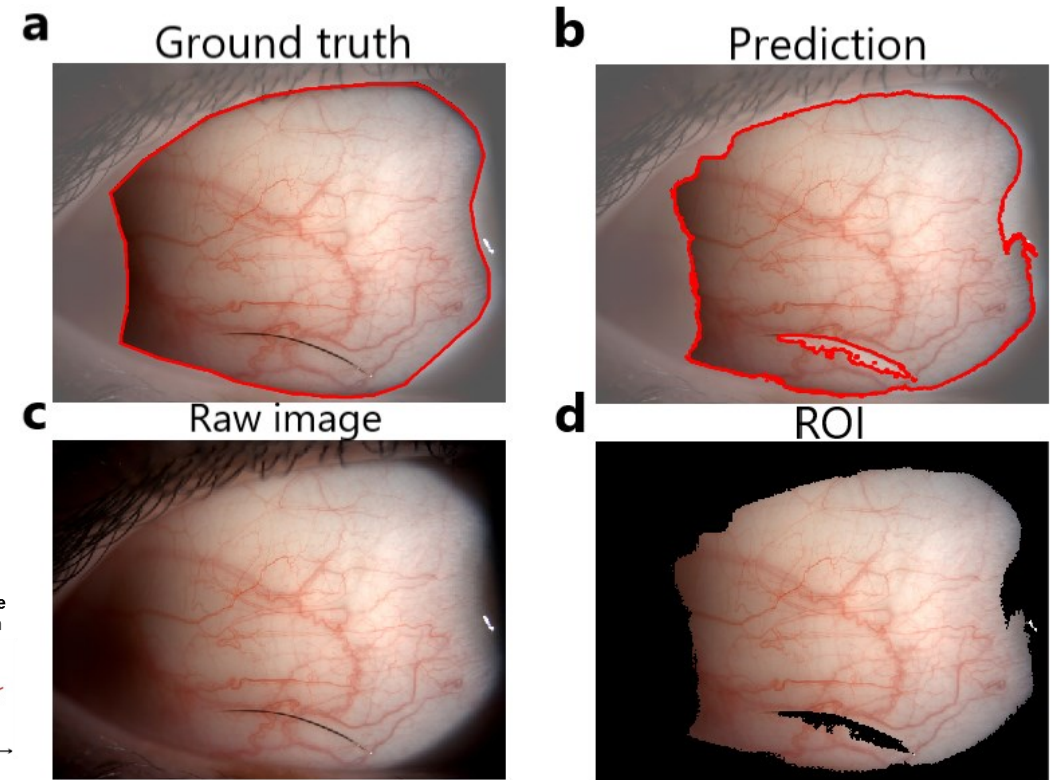


Curti N. et al., A fully automated pipeline for a robust..., *Applied Sciences* (2021)

Trying to understand what the model has learned

A real “simple” problem example

Fully automated estimation of conjunctival hyperemia in slit lamp images.



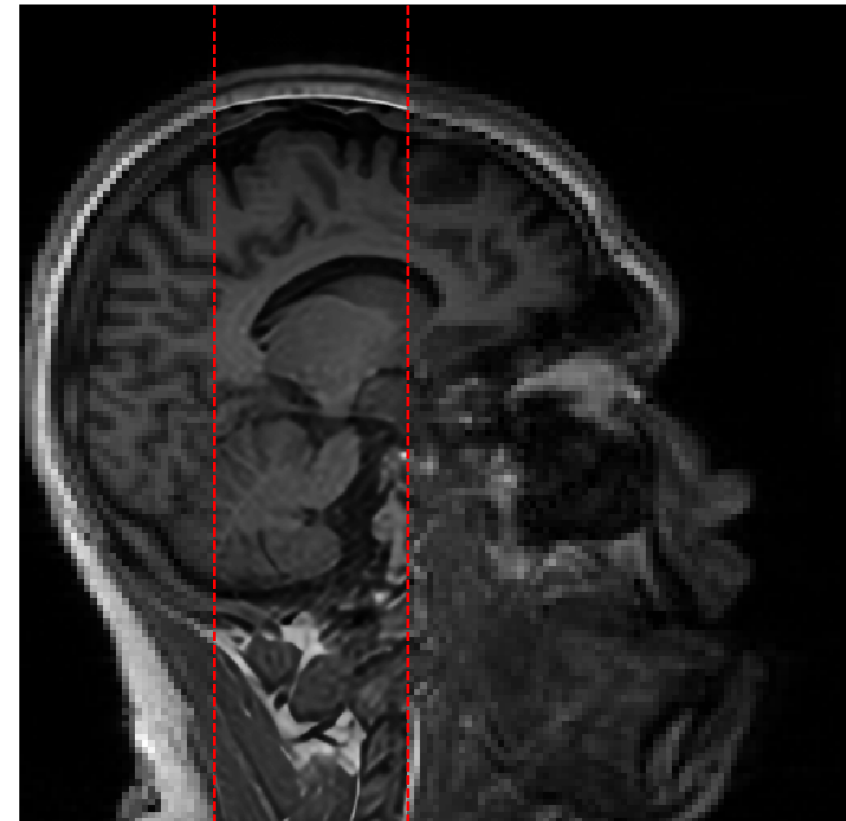
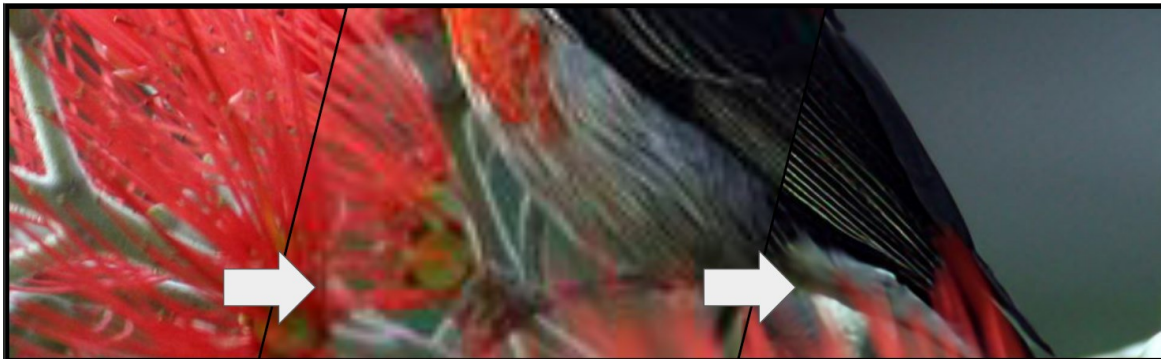


Trying to **understand** what the model has learned

A real “simple” problem example

Can a deep learning super resolution model be used on medical images without any kind of re-training or fine-tuning?

Immagine HR → ricampionamento bicubico → Immagine LR → super-risoluzione → Immagine SR



Fiscione C. et al., Generalizing the Enhanced-Deep-Super-Resolution neural network to brain MR..., *eNeuro* [Under Review]



If the problems are more difficult?

It is not always so simple to understand what a model has learned!

Especially when we work with High Dimensional datasets!

Radiomic Analysis

Radiomics – Machine Learning



Big Data Analysis

Large amount of information available from each image



Image processing

Several filters and image processing applied



Computer vision

Image features related to morphology and textures



Deep learning models

Valid input for machine learning pipelines and deep learning models



All the codes are open source

<https://pyradiomics.readthedocs.io>

Radiomic Analysis



Radiomic Analysis is becoming a **standard practice** in many medical applications

Number of publications per year since 1967.

Huang et al.,
Nature Reviews, 2023



Pros

- Multiple features
- Easy to use
- Integration with other software
- Use of Anatomical image information
- Easy extraction of the results

Vs

Cons

- Multi-dimensional analyses
- Ill-posed problems
- Large noise sources
- Biases and batch effects in multi-center studies
- Hard interpretation of the results

There are no alternatives!

Our Aim



Propose a **novel** approach to medical image **feature extraction**

Requirements

- Easy interpretation of the results
- Complementary information to Radiomic ones
- Simplify the morphological analysis
- Fast evaluation
- Compatible with standard clinical user interface

Medical Image Acquisition

Image Preprocessing

Image Feature Extraction

Radiomic Analysis



New Technique

Outcome prediction

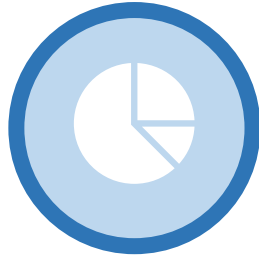
Graphomic Analysis



The aim of the **graphomic** analysis is to leverage topology to extract a series of informative features



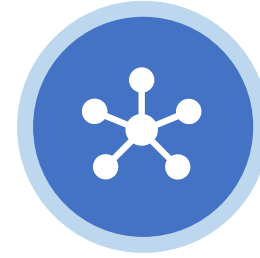
Image
acquisition



Volume
Segmentation



Volume
Skeletonization



Skeleton-graph
Extraction



Network-based
features

This approach could be linked also to the *Extended Reeb Graph Theory* (Shinagawa et al., **1991**)

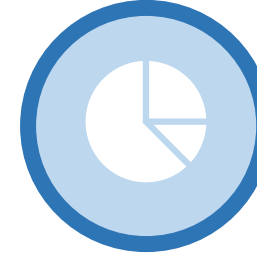
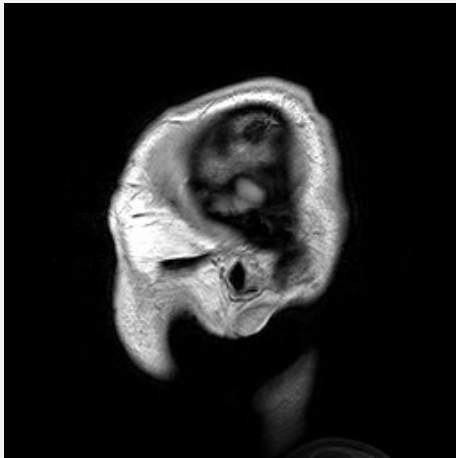
Graphomic Analysis



Image
acquisition

1

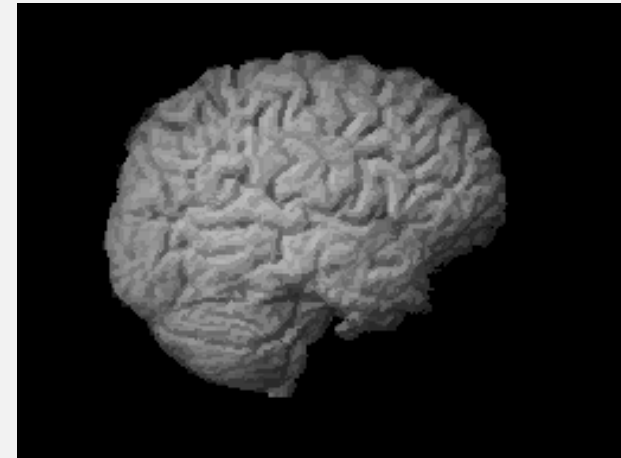
Medical Image acquisition in
any standard formats



Volume
Segmentation

2

Volume identification with
arbitrary models



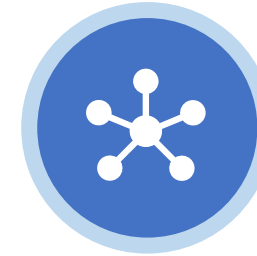
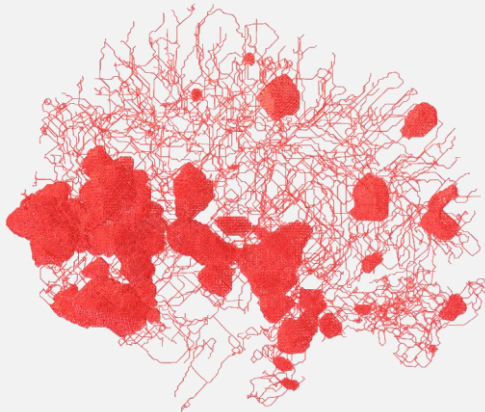
Graphomic Analysis



Volume
Skeletonization

3

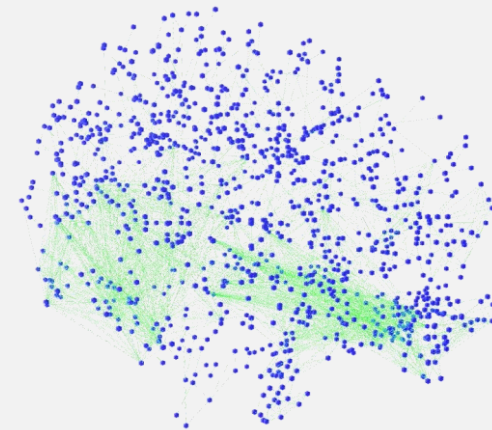
Volume simplification via
skeletonization



Skeleton-graph
Extraction

4

Skeleton graph extraction via
custom algorithm



Graphomic Analysis



Network-based
features

5

Graphomic feature extraction

Topology

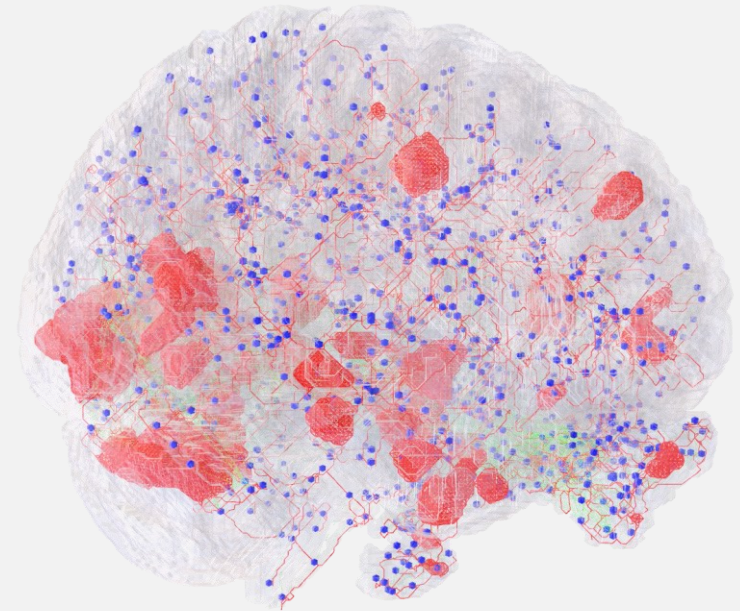
- Nodes
- Edges
- Weights
- Modularity
- Euler number
- Node type statistics
- etc.

Centrality

- Degree
- Betweenness
- Clustering
- Closeness
- Page-rank
- Harmonic
- etc.

Spatial

- Node density
- Fractal dim
- Shortest paths
- Eccentricity
- Node distances distribution
- etc.



Graphomic Analysis

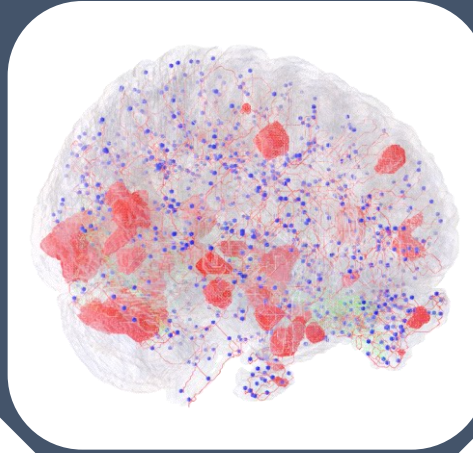


Graphomic analysis is totally independent from the image acquisition modality and **anatomical district**

Skeleton
- bones -



Brain



Lung
- airways -






Conclusion



<https://github.com/Nico-Curti/graphomic>

Obtained results

- **Novel** approach to medical image analysis
- Toolkit ~~publicly available~~ for graphomic feature extraction   
- Applicability to any **2D** and **3D** binary image/volume
- Fast extraction of the network-based features: ~ **1** minute per patient
- **Easy explainability** of the results for clinical application

Future works

- **Validation** of the results with multiple datasets
- Extension of the graphomic approach to other relevant **medical** tasks
- Extension of the graphomic approach to other **machine learning** tasks

References



1. N. Curti & E. Giampieri, F. Guaraldi, F. Bernabei, L. Cercenelli, G. Castellani, P. Versusa, E. Marcelli, A fully automated pipeline for a robust conjunctival hyperemia estimation, *Applied Sciences*, <https://doi.org/10.3390/app11072978> (2021 Mar 26)
2. G. Carlini & N. Curti, S. Strolin, S. Fanti, D. Remondini, C. Nanni, L. Strigari, and G. Castellani, Prediction of overall survival in cervical cancer patients using PET/CT radiomic features, *Applied Science*, <https://doi.org/10.3390/app12125946> (2022 June 10)
3. E. Dika & N. Curti, E. Giampieri, G. Veronesi, C. Misciali, C. Ricci, G. Castellani, A. Patrizi, E. Marcelli, Advantages of manual and automatic computer-aided compared to traditional histopathological diagnosis of melanoma: a pilot study, *Pathology - Research and Practice*, <https://doi.org/10.1016/j.prp.2022.154014> (2022 July 8)
4. N. Curti & G. Veronesi, E. Dika, C. Misciali, E. Marcelli, E. Giampieri, Breslow thickness: geometric interpretation, potential pitfalls, and computer automated estimation, *Pathology - Research and Practice*, <https://doi.org/10.1016/j.prp.2022.154117> (2022 Sep 5)
5. R. Biondi, M. Renzulli, R. Golfieri, N. Curti†, G. Carlini, C. Sala, E. Giampieri, D. Remondini, G. Vara, A. Cattabriga, M. A. Coccozza, L. V. Pastore, A. Palmeri, N. Brandi, L. Scarpetti, † Corresponding author. 9 Curriculum vitae e scientifico-professionale Nico Curti G. Tanzarella, M. Cescon, M. Ravaioli, G. Castellani, F. Coppola, Machine learning pipeline for the automated prediction of MicroVascular Invasion in HepatoCellular Carcinomas, *Applied Science*, <https://doi.org/10.3390/app13031371> (2023 Jan 20)
6. G. Carlini, C. Gaudio, R. Golfieri, N. Curti†, R. Biondi, L. Bianchi, R. Schiavina, E. Brunocilla, F. Giunchi, D. Caruso, A. Merlotti, D. Dall’Olio, C. Sala, S. Pandolfi, D. Remondini, A. Rustici, L. V. Pastore, L. Scarpetti, B. Bortolani, E. Marcelli, F. Coppola, G. Castellani, Effectiveness of radiomic ZOT features in the automated discrimination of oncocytoma from clear cell renal cancer, *Journal of Personalized Medicine*, <https://doi.org/10.3390/jpm13030478> (2023 Mar 6)
7. Dale, A.M., Fischl, B., Sereno, M.I., 1999. Cortical surface-based analysis. I. Segmentation and surface reconstruction. *Neuroimage* 9, 179-194.
8. Desikan, R.S., Segonne, F., Fischl, B., Quinn, B.T., Dickerson, B.C., Blacker, D., Buckner, R.L., Dale, A.M., Maguire, R.P., Hyman, B.T., Albert, M.S., Killiany, R.J., 2006. An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest. *Neuroimage* 31, 968-980.
9. Jovicich, J., Czanner, S., Greve, D., Haley, E., van der Kouwe, A., Gollub, R., Kennedy, D., Schmitt, F., Brown, G., Macfall, J., Fischl, B., Dale, A., 2006. Reliability in multi-site structural MRI studies: effects of gradient non-linearity correction on phantom and human data. *Neuroimage* 30, 436-443.
10. Bee Lim, Sanghyun Son, Heewon Kim, Seungjun Nah, & Kyoung Mu Lee. (2017). Enhanced Deep Residual Networks for Single Image Super-Resolution.
11. Jiahui Yu, Yuchen Fan, Jianchao Yang, Ning Xu, Zhaowen Wang, Xinchao Wang, & Thomas Huang. (2018). Wide Activation for Efficient and Accurate Image Super-Resolution.
12. Griethuysen, J. J. M., Fedorov, A., Parmar, C., Hosny, A., Aucoin, N., Narayan, V., Beets-Tan, R. G. H., Fillon-Robin, J. C., Pieper, S., Aerts, H. J. W. L. (2017). *Computational Radiomics System to Decode the Radiographic Phenotype. Cancer Research*, 77(21), e104–e107. <https://doi.org/10.1158/0008-5472.CAN-17-0339>



Nico Curti

**Thank you for
Your attention**

Contacts

 +39 333 9979399

 nico.curti2@unibo.it

 <https://github.com/Nico-Curti>