A Challenging Detour trough Prostates and Promises

ARPG MEETING– LUGLIO 2018

Brief Summary of the Last Episode

- **MRI images of patients affected by colon cancer**
- Manual segmentation done by expert clinicians
- Standard U-net architecture
- First approach to automatic segmentation with Fully Convolutional Neural Networks (FCNN)

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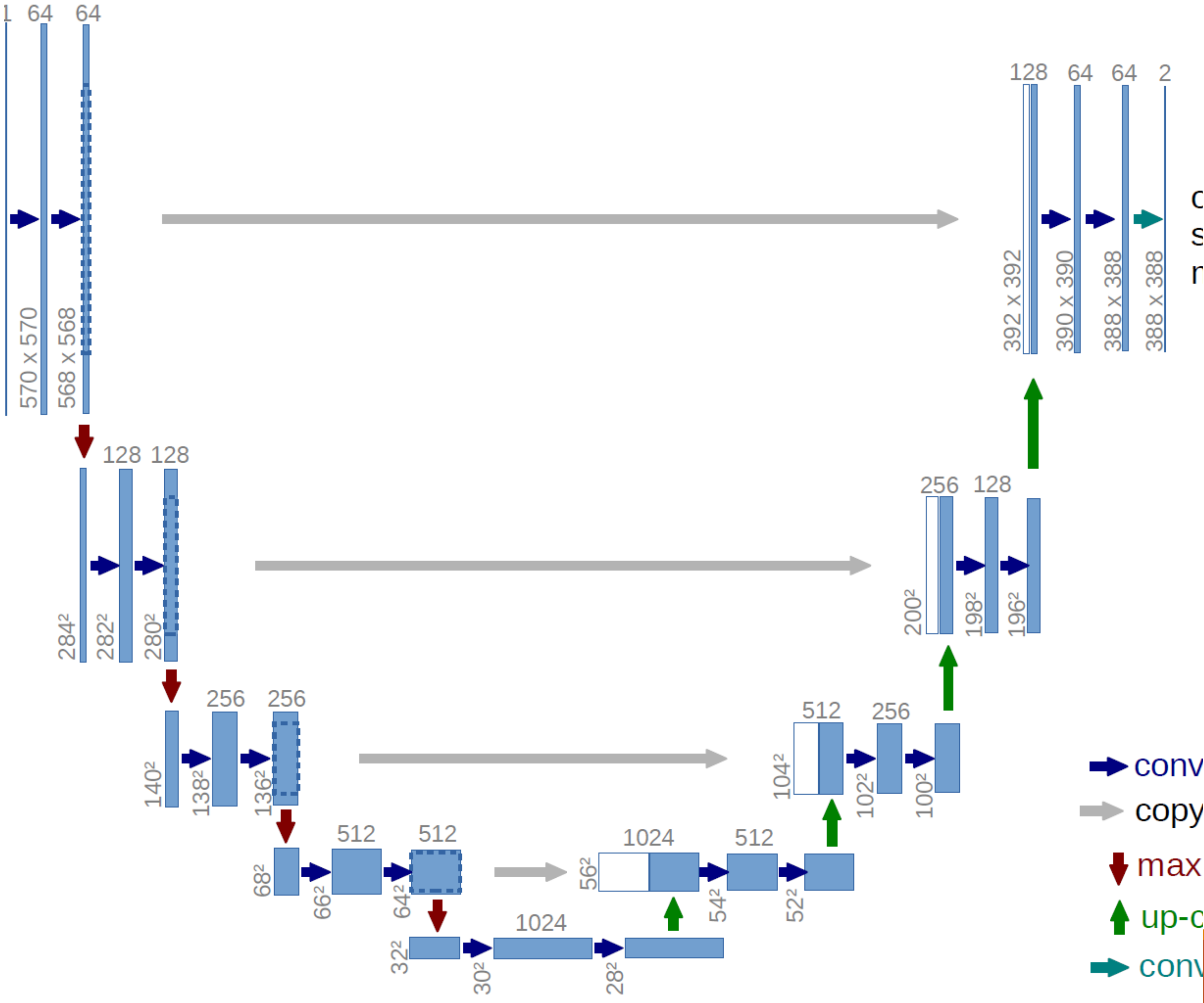

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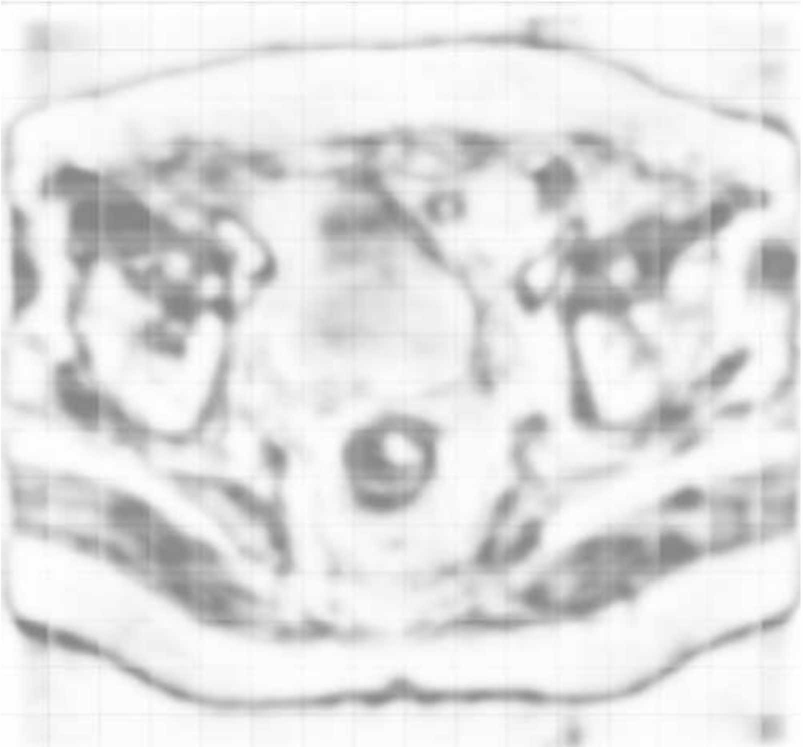
- **First approach to automatic segmentation with Fully Convolutional Neural Networks (FCNN)**

- Bad errors
- Lots of false positives
- Incorrect use of antomy (colon usually is in the center)
- Lack of generalization
- Rule probably based on grey intensity (very bad). Like a Pass-Band filter



A Short Detour – Promise Challege

We need a well known dataset to develop our algorithm and build up confidence in this kind of tasks.

An already challenge concluded, with many participants, can provide some examples on how to develop a good segmentation algorithm

What is a challege?

- A new data set for traing is released.
- Participant are gathered.
- Test set is released. Proposed method are applied to the test set.
- Submission are evaluated.
- Results are published.
- The winner take all the glory (and/or the money)

Dataset

Evaluation of prostate segmentation algorithms for MRI: The PROMISE12 challenge

Geert Litjens [a], Robert Toth [b], Wendy van de Ven [a], Caroline Hoeks [a], Sjoerd Kerkstra [a], Bram van Ginneken [a], Graham Vincent [e], Gwenael Guillard [e], Neil Birbeck [f], Jindang Zhang [f], Robin Strand [g], Filip Malmberg [g], Yangming Ou [h], Christos Davatzikos [h], Matthias Kirschner [i], Florian Jung [i], Jing Yuan [j], Wu Qiu [j] ... Anant Madabhushi [b]

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- Similar task
- Started in 2012 (data as old as ours) but still ongoing
- Good results
- Lots of participants

Challege Details

Prostate in transversal T2-weighted MR images.

The data includes both patients with benign prostatic hyperplasia and prostate cancer.

from multiple centers and multiple MRI device vendors.

Differences in scanning protocols will also be present in the data, e.g. patient with and without an endorectal coil.

There are 50 training cases (about 500 usable slices)

The set is selected such that there is a spread in prostate sizes and appearance.

A reference segmentation is also included. (Label)

Position	User	Team	Date	Score	Old score	Comment	Algorithm description
1	whu_mlgroup	None	May 22, 2018, 5:37 p.m.	89.1772	88.7232	method2	
2	tbrosch	None	May 10, 2018, 1:42 p.m.	87.6729	87.2432	Philips DL-MBS	
3	whu_mlgroup	None	May 11, 2018, 9:31 a.m.	87.5380	87.0776	WHU-CS-sigma-RPI	
4	lanqier_xl	None	May 11, 2018, 9:29 a.m.	87.2100	86.8100	AutoDenseSeg	
5	GeertLitjens	None	May 11, 2018, 11:42 a.m.	87.1483	86.7167	CUMED	
6	aslm	None	May 11, 2018, 2:44 p.m.	86.8851	86.4458	SCIRESU	
7	QuIIL	None	May 10, 2018, 8:35 p.m.	86.7121	86.3487	QuIIL Lab	
8	SUNRISE2014	None	May 15, 2018, 7:58 a.m.	86.5965	86.1501	tarheelseg	
9	wanlichen	WNet	July 6, 2018, 3:33 p.m.	86.5028	85.9409		
10	wanlichen	WNet	June 30, 2018, 3:52 p.m.	86.3888	85.9085		
11	sho89512	None	June 4, 2018, 4:07 p.m.	86.3676	85.8792	DenseFCN	
12	fumin	None	May 11, 2018, 2:47 p.m.	86.2589	85.8460	RUCIMS	

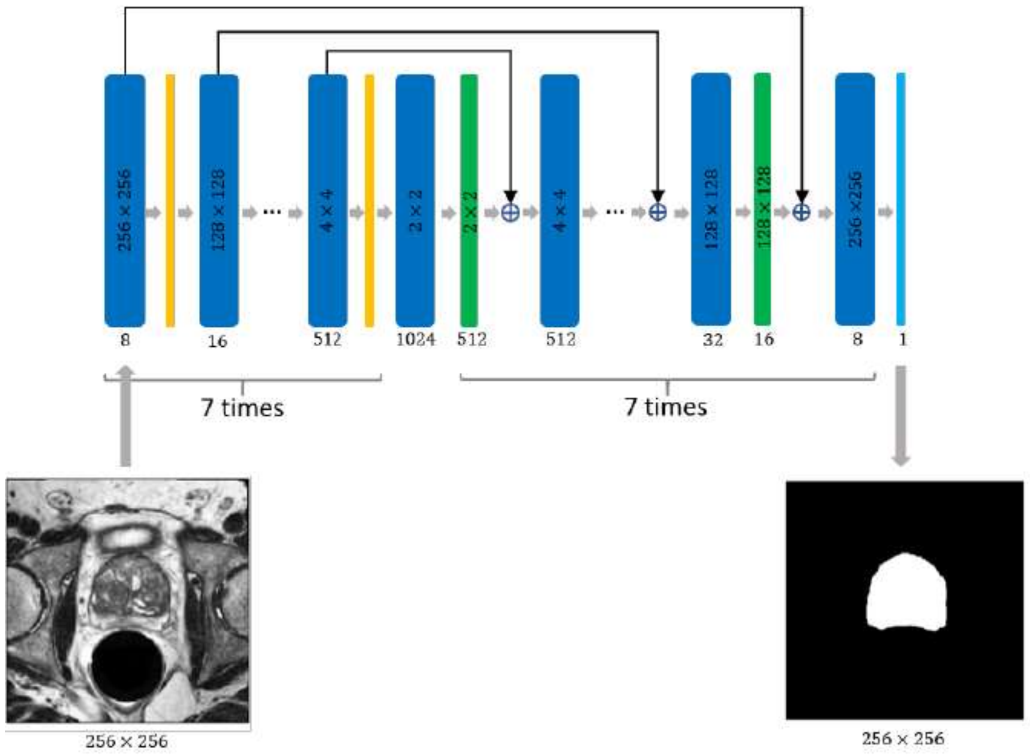
Choosen Method

Fully convolutional neural network with residual connections for automatic segmentation of prostate structures from MR images

Inom Mirzaev
Mathematical Biosciences Institute,
Ohio State University, Columbus, Ohio
mirzaev.1@osu.edu

Abstract

We propose a fully convolutional neural network with residual connections for automatic segmentation of prostate structures from MR images. This document is a concise description of the methods that we have used to complete the Promise 12 challenge.



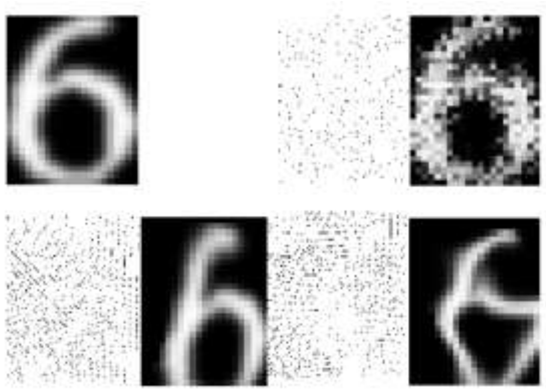
Details – what is the same

Similar to what I was alredy doing

- FCNN with skip connection (U-net like) to use information at different level of detail
- Data augmentation
- Early stopping to avoid overfitting
- Full image training

Details – What is new

Data augmentation – Elastic deformation



DSC as loss function

$$DSC(y, \hat{y}) = \frac{2\sum_i^N y_i \cdot \hat{y}_i}{\sum_i^N y_i + \sum_i^N \hat{y}_i} \cdot$$

- Many more free parameters to fit:
- $5 \cdot 10^7$ (all of them necessary?)
- Dropout at each convolutional Block
- No split and stich approach! (not needed)
- Down-sampling of the image

Altamente scopiazzabile

Results on validation set	Big Net	Small Net
Total params	55,114,432	3,284,442
Accuracy	0.867	0.880
Mean volumetric DSC	0.873	0.623
Median volumetric DSC	0.862	0.722
Std volumetric DSC	0.037	0.140

Results on training set	Big Net	Small Net
Total params	55,114,432	3,284,442
Accuracy	0.955	0.965
Mean volumetric DSC	0.944	0.726
Median volumetric DSC	0.945	0.735
Std volumetric DSC	0.013	0.136

Training times	Big Net	Small Net
Training epochs	20 (1.5 hours per epoch)	25 (0.6 hours per epoch)

Results on train set:
Accuracy: 0.954796914337
Mean volumetric DSC: 0.944736724712
Median volumetric DSC: 0.945371337475
Std volumetric DSC: 0.0129588637285

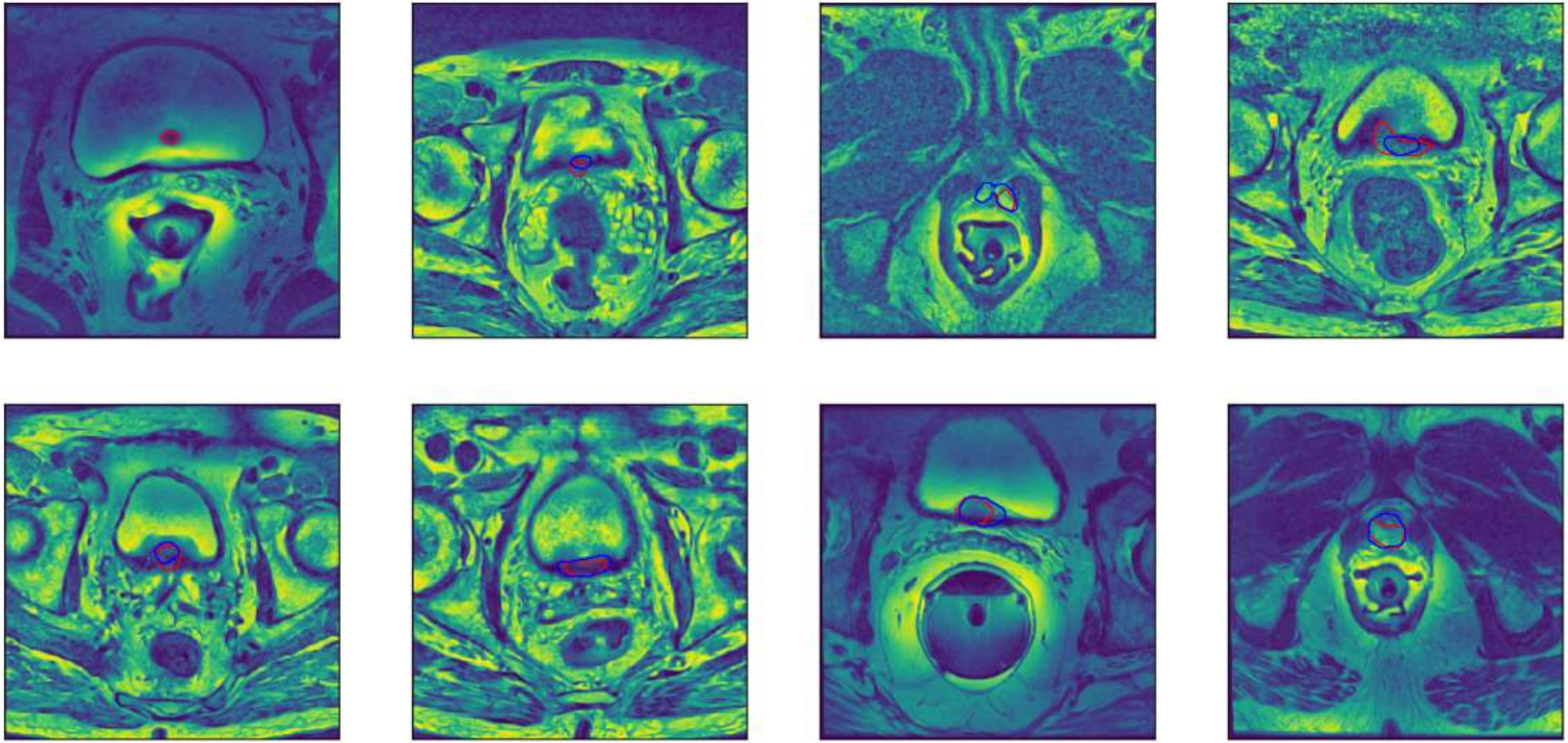
Results on validation set
Accuracy: 0.867436503457
Mean volumetric DSC: 0.873753732068
Median volumetric DSC: 0.862201843084
Std volumetric DSC: 0.0373552899755

Total params: 3,284,442
Trainable params: 3,281,434
Non-trainable params: 3,008

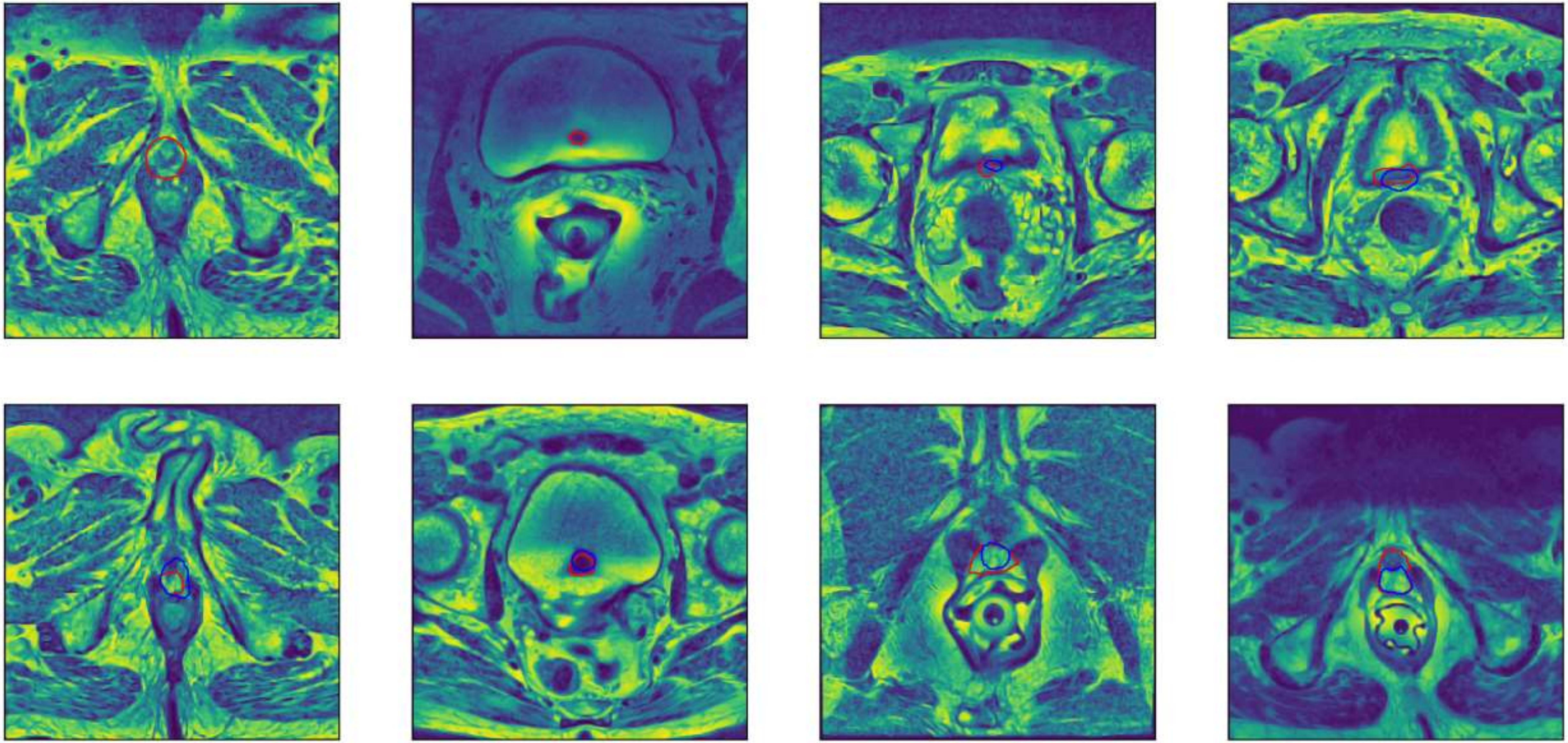
Results on validation set
Accuracy: 0.87975811997
Mean volumetric DSC: 0.623037050723
Median volumetric DSC: 0.722438438309
Std volumetric DSC: 0.140099416566

Results on train set:
Accuracy: 0.964659885121
Mean volumetric DSC: 0.726159226978
Median volumetric DSC: 0.735045257089
Std volumetric DSC: 0.135566094814

Results small net – Error types

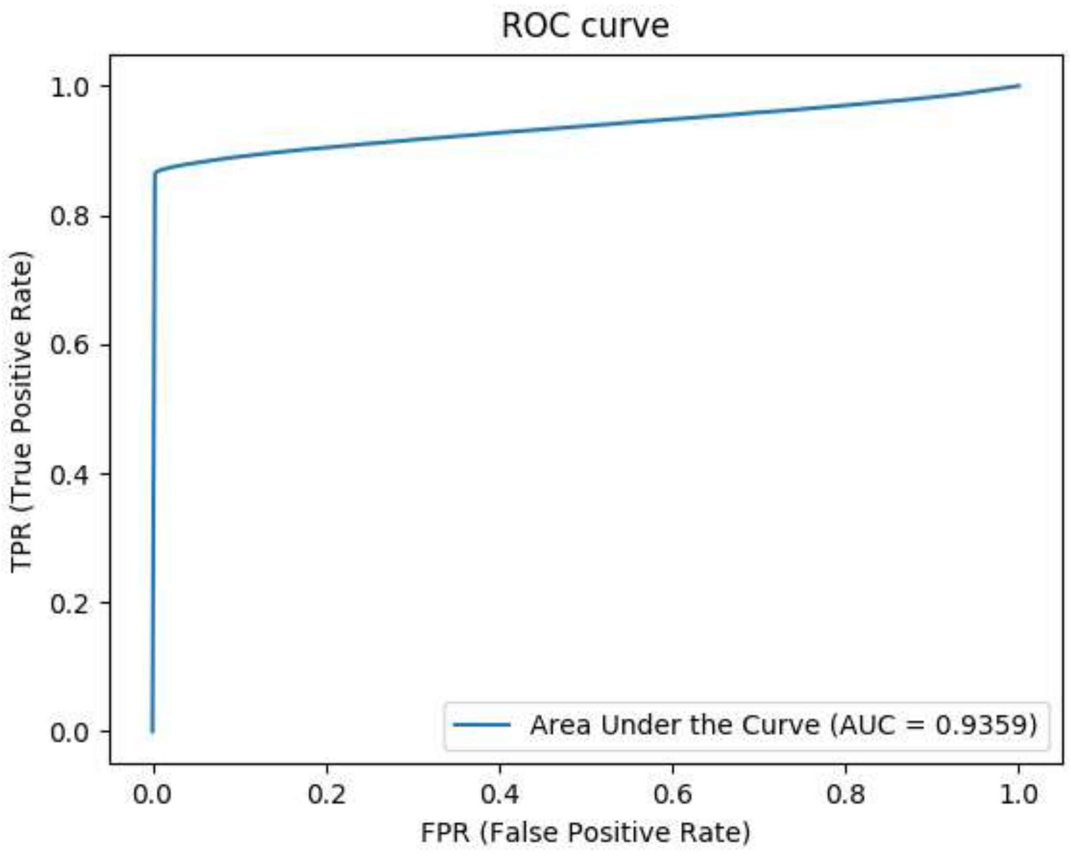


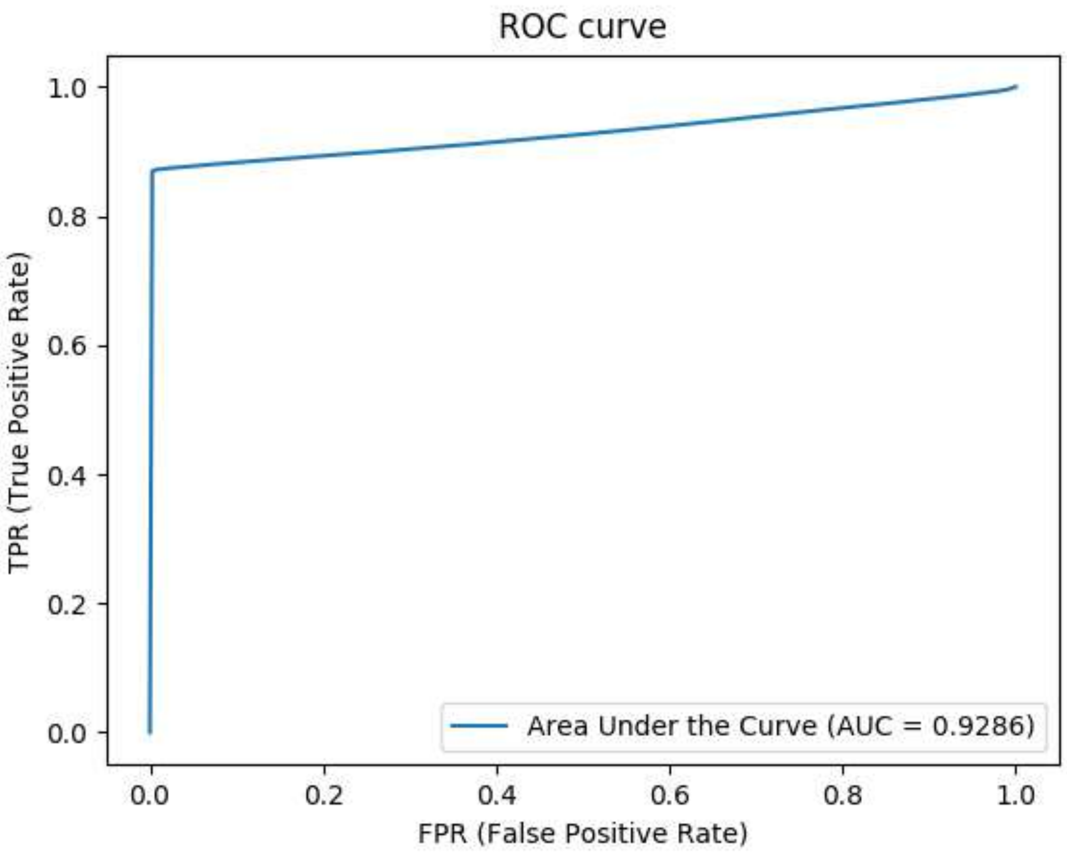
Result Big net



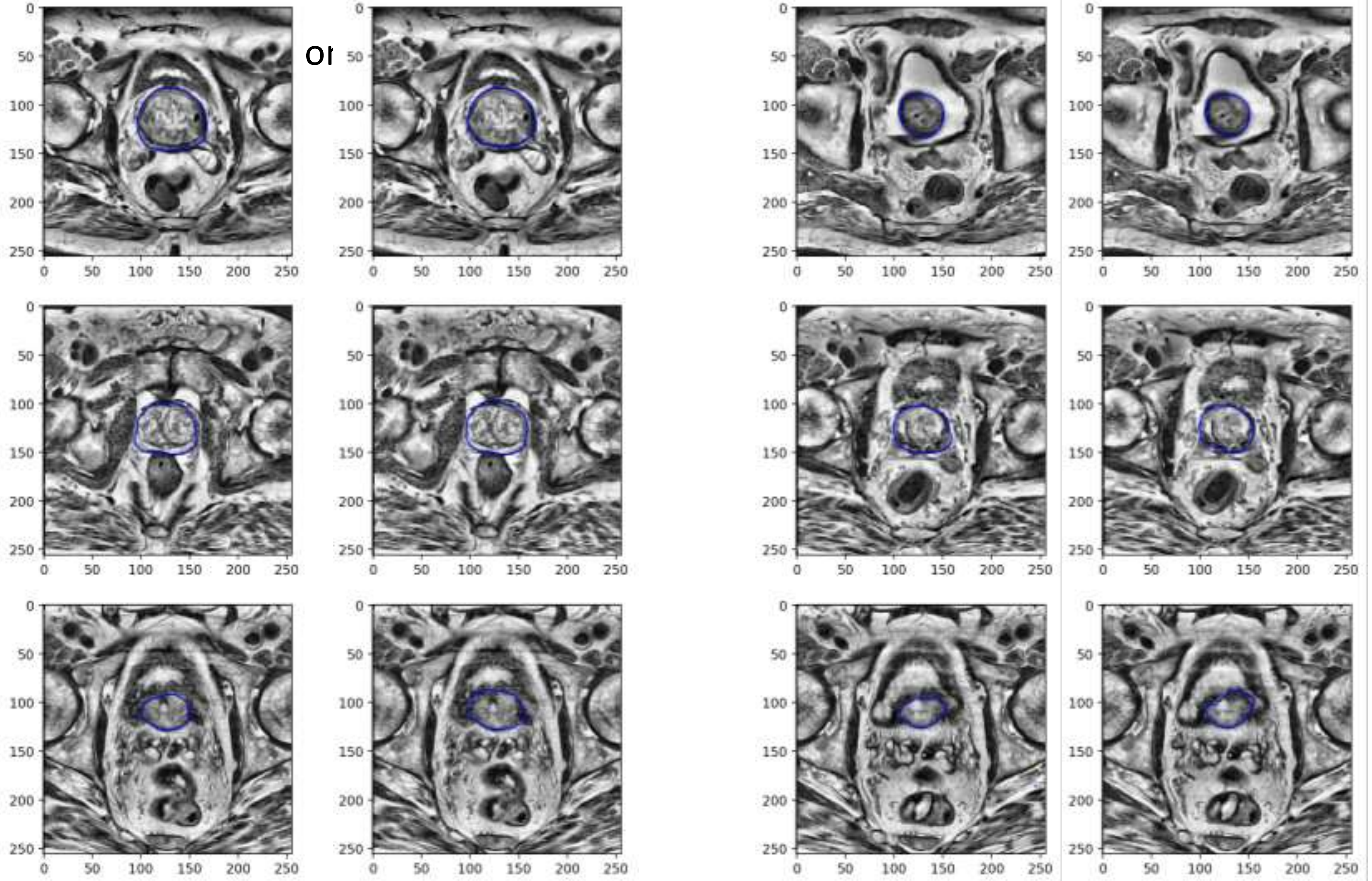
Big Net

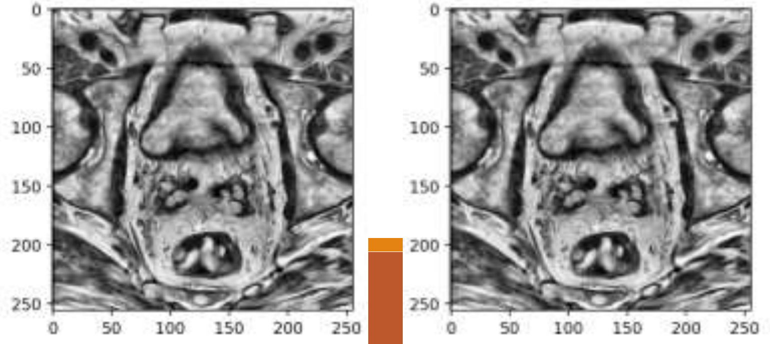
Small Net





Windows sovraposition and averaging was degrading results so it is not done anymore.
So there are true 1 and zeros in the output of the net that causes that step in the ROC





Result Comparison on the test set (no ground truth available)
(The good ones) BIG left / SMALL right

Conclusions

We have a robust method to segment anatomical structures in the pelvis area.

Training on a small dataset is possible with some care.

The Algorithm is now ready to be applied to our data!

An early attempt has been unsuccessful hopefully for a problem in the conversion between data format.

Analisi di immagini MRI tramite algoritmi di ML

LOCALIZZAZIONE E SEGMENTAZIONE AUTOMATICA DI TUMORE AL COLON RETTO IN IMMAGINI MR CON RETI CONVOLUTIVE

Dati

- 55 risonanze magnetiche pesate in T2 di pazienti affetti da tumore al retto
- Adenocarcinoma del retto, confermato istologicamente e in stadio avanzato (stadio II e III)
- Sottoposti alla chemio-radioterapia (CRT) neo-audiovante
- Acquisiti in 3 momenti. Subito dopo la diagnosi, a metà del trattamento CRT e dopo la fine della CRT

Obiettivi

- Implementazione di un algoritmo per il riconoscimento automatico della Regione di Interesse (ROI)
- La ROI è la regione che si vuole analizzare in dettaglio, in questo caso il volume della massa tumorale.
- Attualmente le ROI sono definite a mano dal personale clinico.

Perché?

- Attualmente le ROI sono definite a mano dal personale sanitario.
- Procedura soggetta ad arbitrarietà .
- Può essere condizionata da errori umani.
- Time – consuming in caso di screening ad ampio spettro.
- Primo step necessario ad estrarre bio-marker dalle immagini diagnostiche.

Object Recognition con reti neurali profonde

- La maggior parte delle applicazione di deep learning per Computer Vision sono forme di object recognition o detection.
- Sono compiti «semplici» per umani e animali ma difficili per i computer.
- Segmentazione: etichettare ogni pixel con l'identità dell'oggetto a cui appartiene.
- Problema di classificazione di una parte di immagine dato il suo contesto.
- Applicare strategie e tecniche sviluppate per compiti generici su immagini mediche.
- Problemi: Dataset piccoli, grande variabilità.
- Strategie per ridurre la variabilità dell'imput e creare task che possono essere risolte da modelli più semplici.(meno parametri)
- Reti convolutive?

Reti Convolutive (3 idee)

Sparse interaction

- Kernel (‘campo recettivo’ di un neurone) piccolo rispetto all’immagine

Parameter sharing

- Uso degli stessi parametri in diverse parti della rete

Equivariant representation

- Equivalenza per traslazione

Sparse Connectivity

Sparse connections due to small convolution kernel

Dense connections

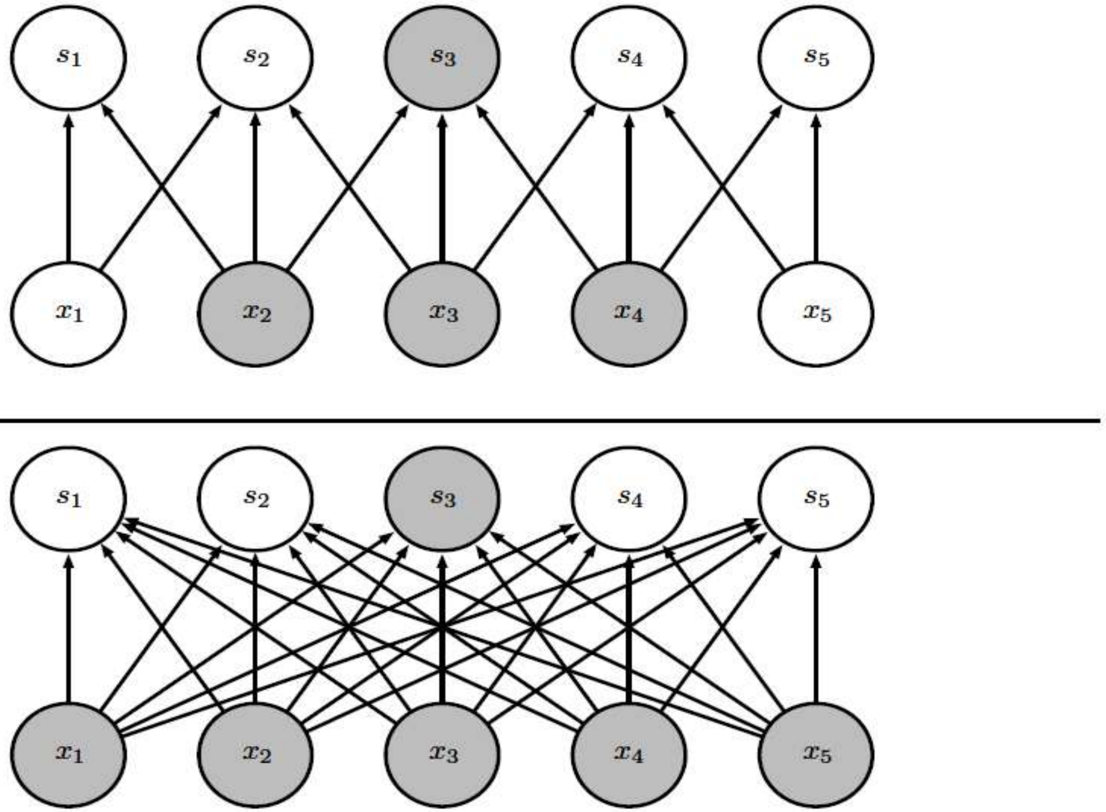


Figure 9.3

(Goodfellow 2016)

Data Augmentation

La convoluzione aiuta a rimuovere problemi riguardo alla localizzazione spaziale del segnale. Per altre invariaze necessitano altri tipi di trasformazioni.

- Strategia pe rimuovere della variabilità nel segnale di input che dipende da invarianze che sono facili da catturare per un umano e che sicuramente non sono rilevanti per il task.
- Aggiungere copie extra agli esempi di training che sono state modificate con trasformazioni che non cambiano la classe di appartenenza

La classificazione di oggetti si presta bene a questa tecnica perché le possibili invariaze sono molte.

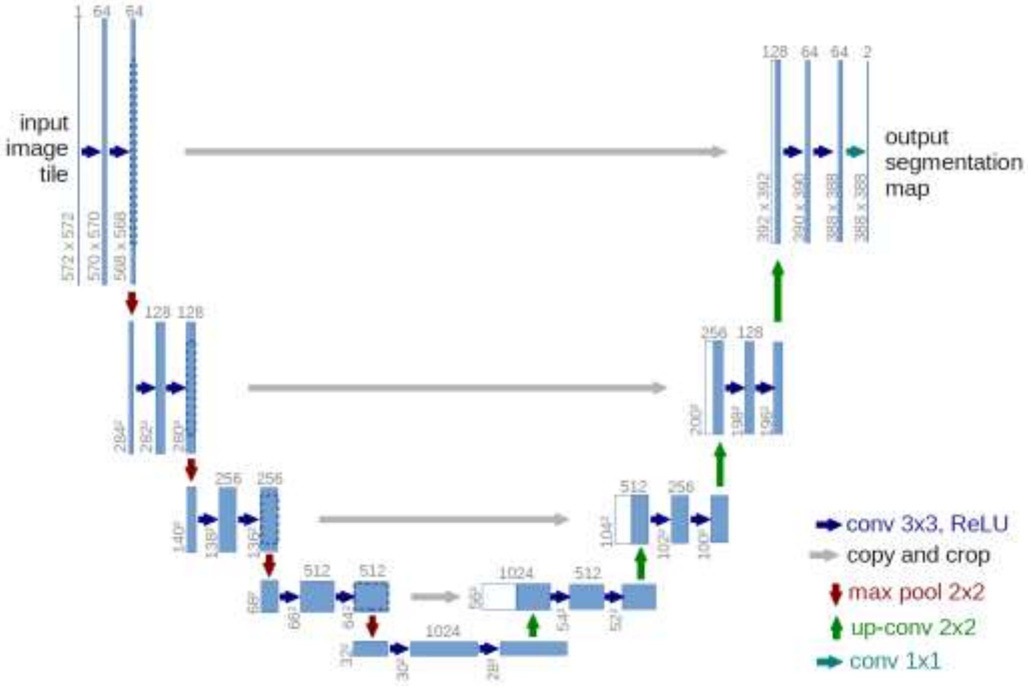
Per le immagini mediche si può trovare un set di trasformazioni specializzate.

OPEN

Deep Learning for Fully-Automated Localization and Segmentation of Rectal Cancer on Multiparametric MR

Stefano Trebeschi[1,2], Joost J. M. van Griethuysen[1,2], Doenja M. J. Lambregts[1], Max J. Lahaye[1], Chintan Parmar[3], Frans C. H. Bakers[4], Nicky H. G. M. Peters[5], Regina G. H. Beets-Tan[1,2] & Hugo J. W. L. Aerts[1,3]

U-net : Motivazioni



Hanno un input della stessa taglia dell'output e generalizzano il contesto.

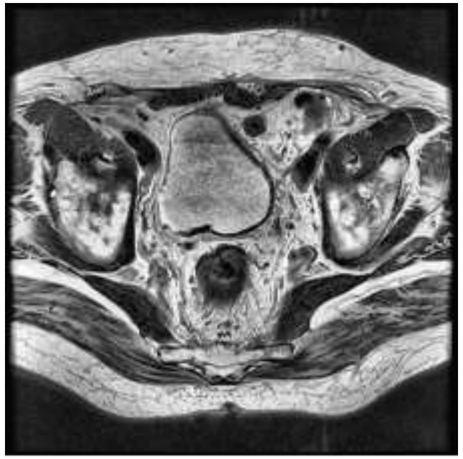
L'idea iniziale è di passare alla rete intere slices di MRI

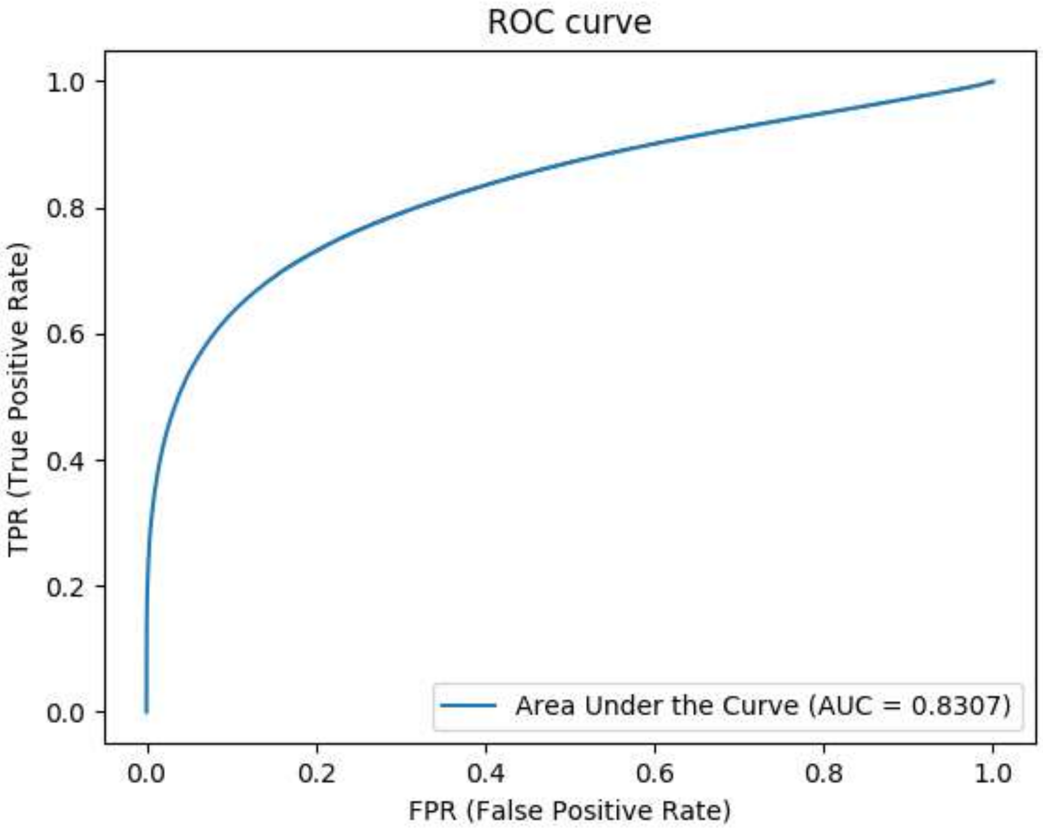
Questo approccio può far riconoscere le zone con posizioni poco probabile di zone tumorali ed escluderle automaticamente.

Snella (2x10^7 parametri)

circa 100 mb model weight size

con12GB 8-16 slice per batch



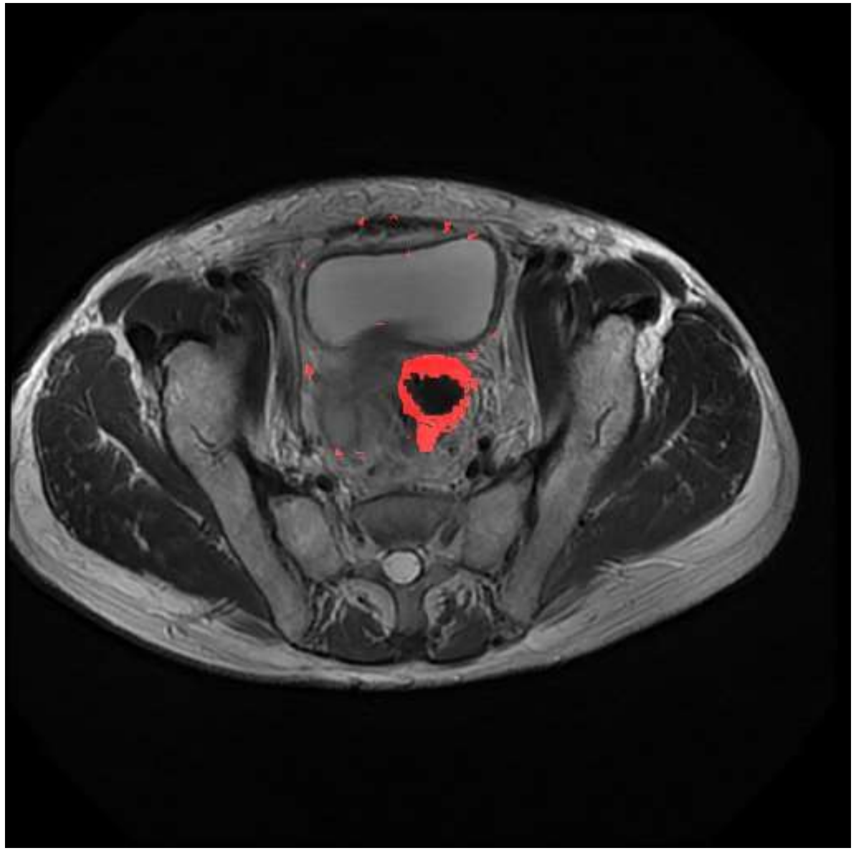

ROC curve
TPR (True Positive Rate)
FPR (False Positive Rate)
Area Under the Curve (AUC = 0.8307)
0.0
0.2
0.4
0.6
0.8
1.0

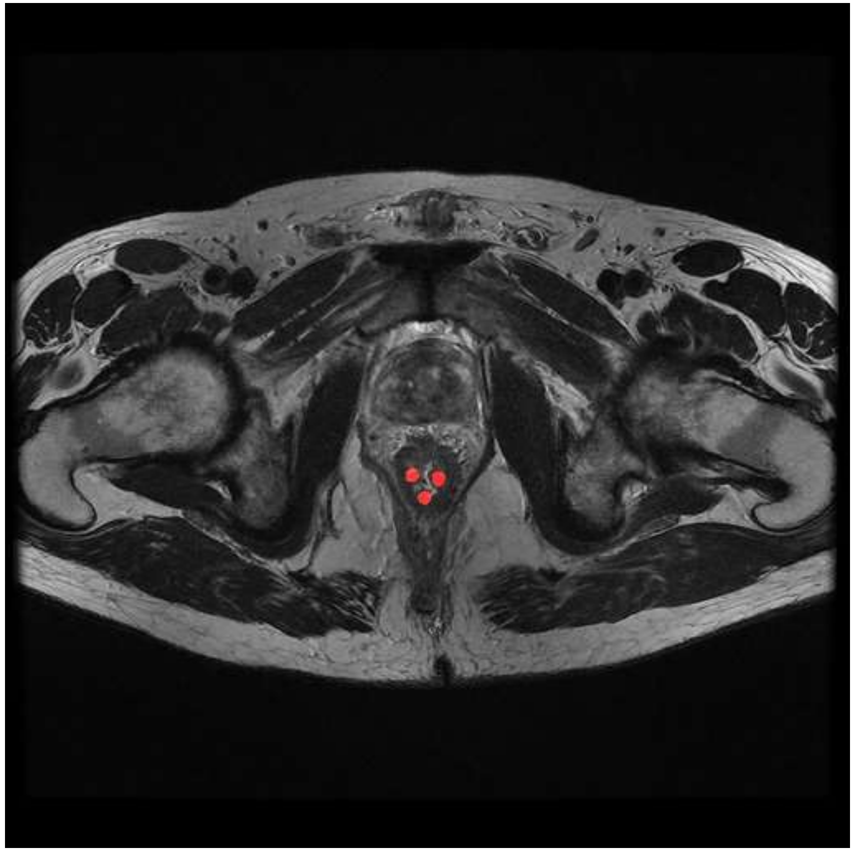
Training set Sbilanciato

- Pochi esempi di tumore (area tumorale 3%)
- Backgroud con tanta variabilità
- Elementi di disturbo (Normalizzazione, artefatti, corpi estranei, rumore)

- Pesare correttamente le classi.
- Pesare i sample.
- Loss function/metrica non dipendente da accuracy
- Campionatura più fine del tumore / data augmentation del tumore (ribilanciare le classi)

problemi





ParaView

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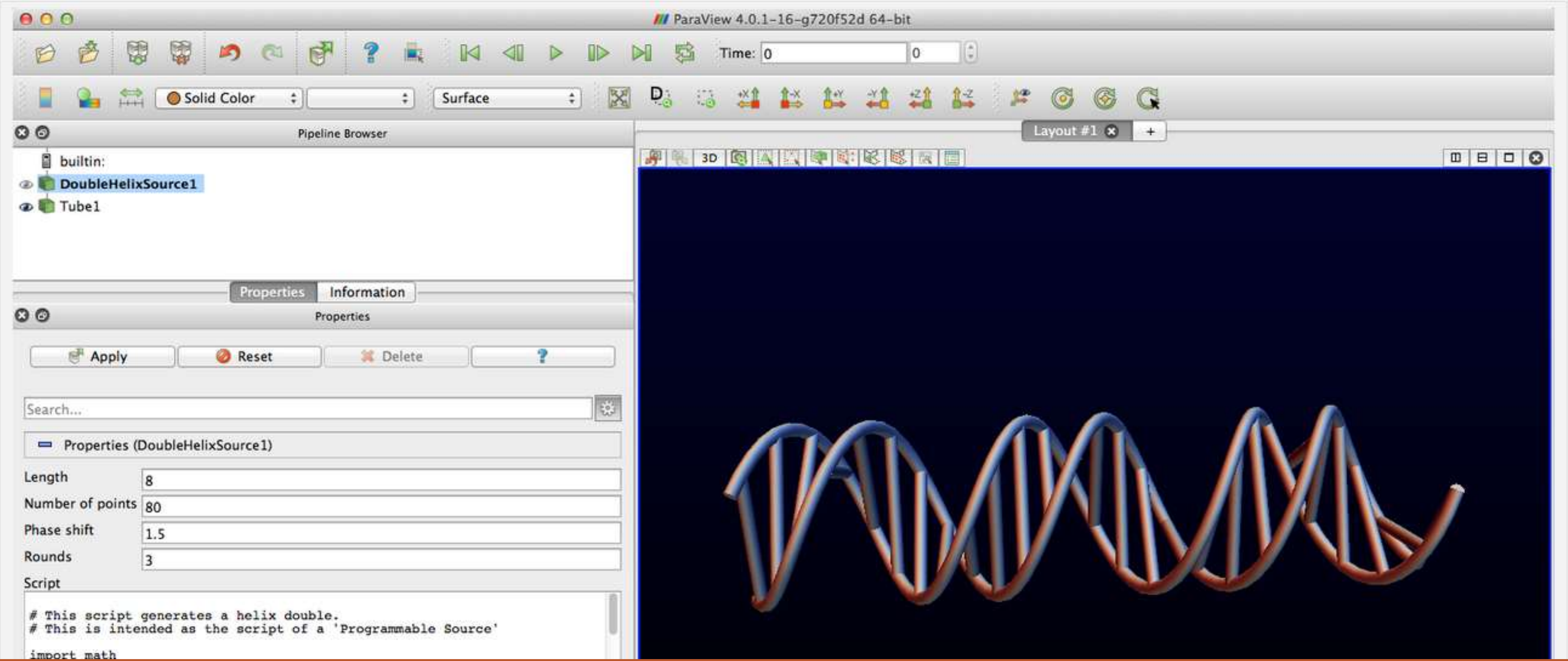
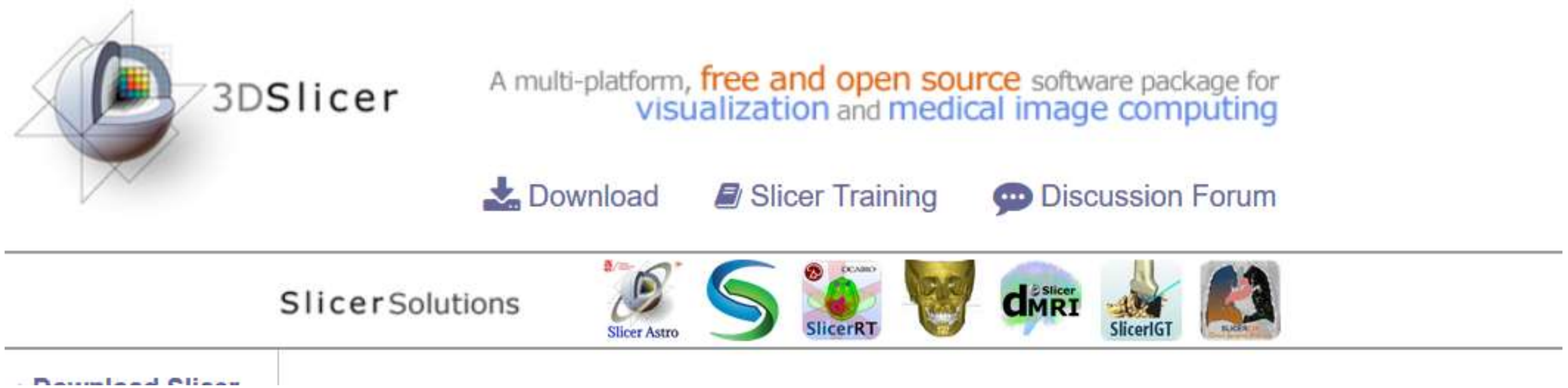
ParaView Python

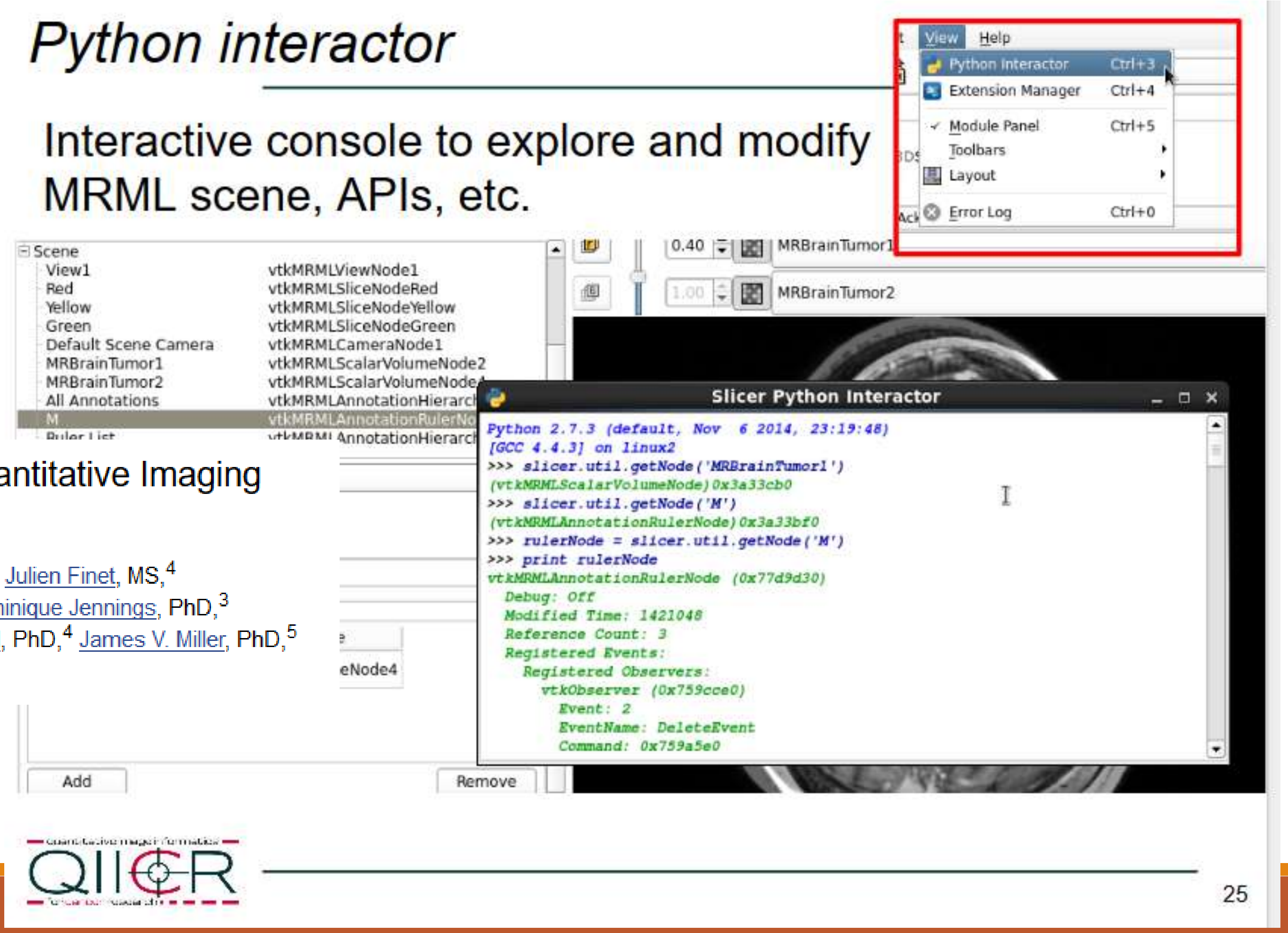
~ 1000 citazioni in diversi campi

Seamless integration with Python began in ParaView version 3.0. Simply load the paraview.simple module from Python to get full access to all of ParaView's large data visualization and analysis capabilities. This includes the ability to create, on the fly, scripted readers and filters that run, in parallel, on the server. ParaView scripts are easy to write, especially if you choose to simply record your work in the desktop application in the form of a python script. Python scripts can be played back with or without the GUI in order to create reproducible, easily customizable, and scalable visualizations.





Più di 1000 citazioni solo questo (2014)



3D Slicer as an Image Computing Platform for the Quantitative Imaging Network

Andriy Fedorov, PhD,[1] Reinhard Beichel, PhD,[2] Jayashree Kalpathy-Cramer, PhD,[3] Julien Finet, MS,[4] Jean-Christophe Fillion-Robin, MS,[4] Sonia Pujol, PhD,[1] Christian Bauer, PhD,[2] Dominique Jennings, PhD,[3] Fiona Fennessy, MD, PhD,[1] Milan Sonka, PhD,[2] John Buatti, MD,[2] Stephen Aylward, PhD,[4] James V. Miller, PhD,[5] Steve Pieper, PhD,[6] and Ron Kikinis, MD[1]

Neuroimage. 2006 Jul 1;31(3):1116-28. Epub 2006 Mar 20.

User-guided 3D active contour segmentation of anatomical structures: significantly improved efficiency and reliability.

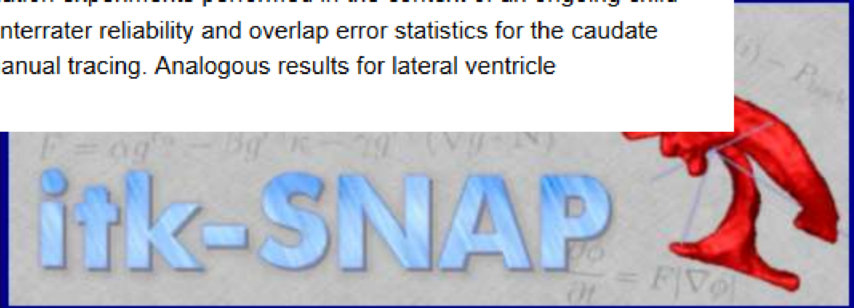
Yushkevich PA[1], Piven J, Hazlett HC, Smith RG, Ho S, Gee JC, Gerig G.

⊕ Author information

Circa 3000 citazioni (2006)

Abstract

Active contour segmentation and its robust implementation using level set methods are well-established theoretical approaches that have been studied thoroughly in the image analysis literature. Despite the existence of these powerful segmentation methods, the needs of clinical research continue to be fulfilled, to a large extent, using slice-by-slice manual tracing. To bridge the gap between methodological advances and clinical routine, we developed an open source application called ITK-SNAP, which is intended to make level set segmentation easily accessible to a wide range of users, including those with little or no mathematical expertise. This paper describes the methods and software engineering philosophy behind this new tool and provides the results of validation experiments performed in the context of an ongoing child autism neuroimaging study. The validation establishes SNAP intrarater and interrater reliability and overlap error statistics for the caudate nucleus and finds that SNAP is a highly reliable and efficient alternative to manual tracing. Analogous results for lateral ventricle segmentation are provided.



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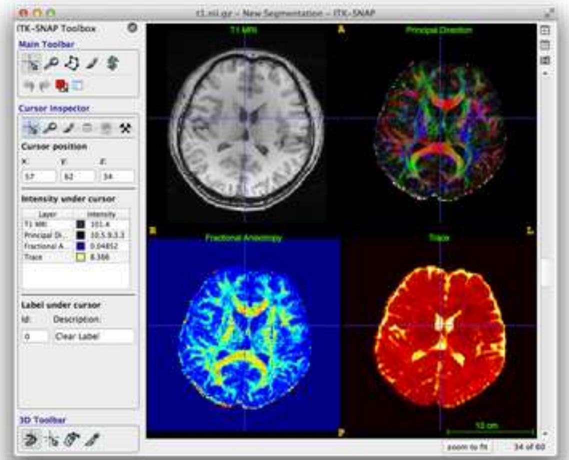
Latest News:
11/28/17: ITK-SNAP training at RSNA 20
04/01/17: Official release 3.6.0 is here!
09/28/16: Run ITK-SNAP on the cloud wi

ITK-SNAP is a software application used to segment structures in 3D medical images. It is the product of a decade-long collaboration between Paul Yushkevich, Ph.D., of the Penn Image Computing and Science Laboratory (PICSL) at the University of Pennsylvania, and Guido Gerig, Ph.D., of the Scientific Computing and Imaging Institute (SCI) at the University of Utah, whose vision was to create a tool that would be dedicated to a specific function, segmentation, and would be easy to use and learn. ITK-SNAP is free, open-source, and multi-platform.



ITK-SNAP provides semi-automatic segmentation using active contour methods, as well as manual delineation and image navigation. In addition to these core functions, ITK-SNAP offers many supporting utilities. Some of the core advantages of ITK-SNAP include:

The NA-MIC Kit: ITK, VTK, pipelines, grids and 3D slicer as an open platform for the Medical Image Computing community

Conference Paper (PDF Available) · May 2006 *with* 257 Reads

DOI: 10.1109/ISBI.2006.1625012 · Source: IEEE Xplore
Conference: Conference: Biomedical Imaging: Nano to Macro, 2006. 3rd IEEE International Symposium on

Steve Pieper
30.94 · Isomics, Inc.

B. Lorensen


William J. Schroeder
20.9 · Kitware, Inc.


Ron Kikinis
49.22 · Harvard Medical School

Abstract

Medical image computing researchers often face the problem of moving promising new algorithms from the proof of concept stage into a form compatible with clinical use. Algorithm developers lack the time and resources to engineer their code for robustness and compatibility, while end-users are anxious to try new techniques but require well designed and tested user interfaces to make practical use of them. The NA-MIC Kit is a collection of software and methodology specifically designed to address these problems and facilitate the rapid advancement of the field

Enabling ITK-based processing and 3D Slicer MRML scene management in ParaView

Andinet Enquobahrie,[1] Michael Bowers,[2] Luis Ibanez,[1] Julien Finet,[1] Michel Audette,[3] and Anthony Kolasny[2]

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Abstract

Go to:

This paper documents on-going work to facilitate ITK-based processing and 3D Slicer scene management in ParaView. We believe this will broaden the use of ParaView for high performance computing and visualization in the medical imaging research community. The effort is focused on developing ParaView plug-ins for managing VTK structures from 3D Slicer MRML scenes and encapsulating ITK filters for deployment in ParaView. In this paper, we present KWScene, an open source cross-platform library that is being developed to support implementation of these types of plugins. We describe the overall design of the library and provide implementation details and conclude by presenting a concrete example that demonstrates the use of the KWScene library in computational anatomy research at Johns Hopkins Center for Imaging Science.