



**Politecnico
di Torino**

Vascular Segmentation of Renal Cell Carcinoma

Bioinformatics

Master degree in Data Science and Engineering

Authors: Chiara Tomei s277790 Paola Privitera s277760

Professors: Elisa Ficarra, Alessio Mascolini

June 17, 2022

Contents

1	Project Description	2
1.1	Scope	2
1.2	Project steps	2
1.3	Results and future works	2
2	User Manual and Requirements	3

1 Project Description

1.1 Scope

The main purpose of this project is to perform a Vascular Segmentation of Renal Cell Carcinoma through the support of several neural network architectures. All the models are implemented and evaluated on a dataset composed of 210 images of cancerous cells depicting two types of cancer, Clear cell Renal Cell Carcinoma and Papillary Renal Cell Carcinoma.

1.2 Project steps

Before the training of the different segmentation models, a dataset analysis and preprocessing phase were carried out in order to explore the characteristics of the images. Several techniques of preprocessing were considered but finally the least invasive and least distorting ones were chosen, in order to best retain the original information conveyed by the original biomedical images. In particular, various techniques were chosen to be applied, such as *Histogram Equalization*, *CLAHE*, *Stain Normalization*, creation of patches and resizing of the original images.

The used segmentation models follow a logic of complexity, starting from the baseline of an Autoencoder until testing the properties of Adversarial Loss in more complex networks.

In details, the study involved the use of:

1. Standard Autoencoder (baseline)
2. U-Net (state of the art for segmentation tasks)
3. Pix2Pix GAN (U-Net Generator + Patch GAN Discriminator + our personal variation regarding the use of Jaccard Loss)

Finally, a study was carried out on the different types of losses and metrics suitable for the evaluation of such models, and the use of *IoU* and *Dice* scores, which are particularly recommended for evaluating image segmentation, was chosen.

1.3 Results and future works

With regard to the preprocessing phase, it was seen that the best results were obtained through *Stain Normalization*, which increased performance by several percentage points of IoU-coefficient.

The best model was U-Net, performing well on both tumor types, specifically with a 57.3% IoU on pRCC and a 56.1% IoU on ccRCC. Lower performance, as expected, were reached through Autoencoder, which stands at 53.4% IoU for pRCC and 54.8% IoU for ccRCC. The desired results were not achieved with the more complex Pix2Pix architecture, reaching a score below 45% IoU for both classes. However, it is the only model that performs better with the full dataset (pRCC+ccRCC), achieving 47% IoU, a symptom of the need, for such a complex network, to have much more data available to achieve adequate performance.

Finally, some future works are proposed related to the difficulties we found in this study and to fully exploit the potential of some models. For example, future works proposed include denoising the dataset by removing cells that overlap with the vascular network; using larger patches to be able to retain the information related to the vascular network but, at the same time, to provide more data to more complex models; removing insignificant patches that unbalance the model.

2 User Manual and Requirements

Instructions for training: all the algorithmic models are inside the **Code** folder of the delivered zip-file. In the **Dataset_numpy.rar** (700MB) file, available at this link (https://drive.google.com/file/d/1pjmroiWvpyq-e_P5rtIsg6t30pJReSrc/view?usp=sharing), you can find a preprocessed version of all the datasets used during the model training phases and during the different experiments. The delivered codes often refer to these .npy files, however, it is also possible to directly access the original datasets provided by simply changing the various directories to which the model points.

The folder **Code** contains all the Colab notebooks with the algorithms related to:

- Preprocessing (loading original datasets, image manipulation, patches, resize, preprocessing tasks, saving to numpy-array)
- Autoencoder
- U-Net
- Pix2Pix_Jaccard (GAN modified with our changes to loss and activation function)
- Pix2Pix_Original (original GAN of the Pix2Pix model)
- Graphs (display of final results and plots useful for graphical representation of experiments)

At the current stage, the models have been run with the hyperparameters set to the best performance achieved. However, in the *Parameters* section of each model, it is possible to vary them in order to carry out further investigations.

It is also possible to save the models after the training phase in order to study the results without having to run the entire model each time.

All necessary libraries and packages are listed in the *Import* section of each notebook. All experiments have been performed with Python version 3.7.13, 12GB RAM and GPU.