# Medical image segmentation for Prostate cancer

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# Problem statement

Diagnosis of Prostate cancer suffers from significant inter-observer variability between pathologists, limiting its usefulness for individual patients.Accurately detecting PCa on images of prostate tissue samples is very important for patients to avoid risk of missing cancers or unnecessary treatment.

In this project, I will create a pixel-wise mask of each object in the images to segmentation of PCa structures. In other word we want to identify the location and sizes of different Pca in the biopsies

# Data

**Data:Kaggle**

https://www.kaggle.com/c/prostate-cancer-grade-assessment/data

The dataset includes the original image, mask and csv files.

Almost each image has an associated mask with label information, which indicate which parts of tissue are healthy or cancerous, that will help on localization of samples.The mask values has two data provider:Radboud;Karolinsk.

# Image Visualization

Radboud: Prostate glands are individually labelled, Valid values are:

0: background (non tissue) or unknown

1: stroma (connective tissue, non-epithelium tissue)

2: healthy (benign) epithelium

3: cancerous epithelium (Gleason 3)

4: cancerous epithelium (Gleason 4)

5: cancerous epithelium (Gleason 5)

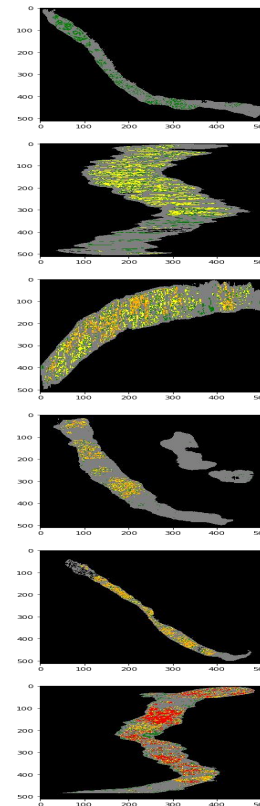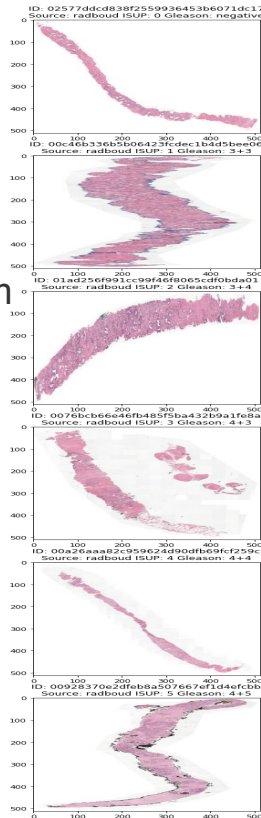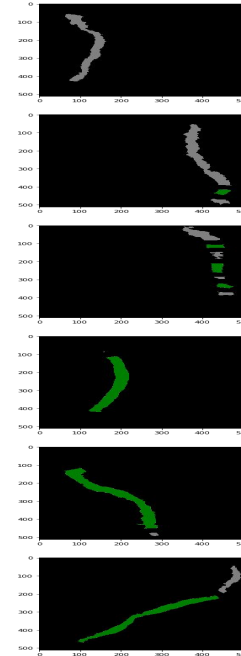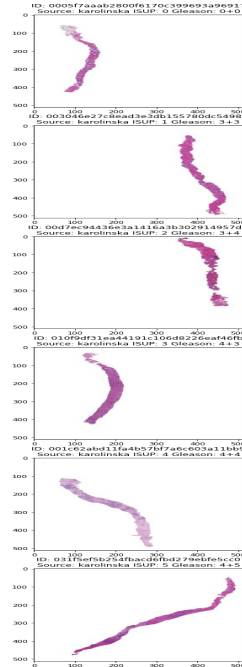# Image Visualization

Karolinska: Regions are labelled, Valid values are:
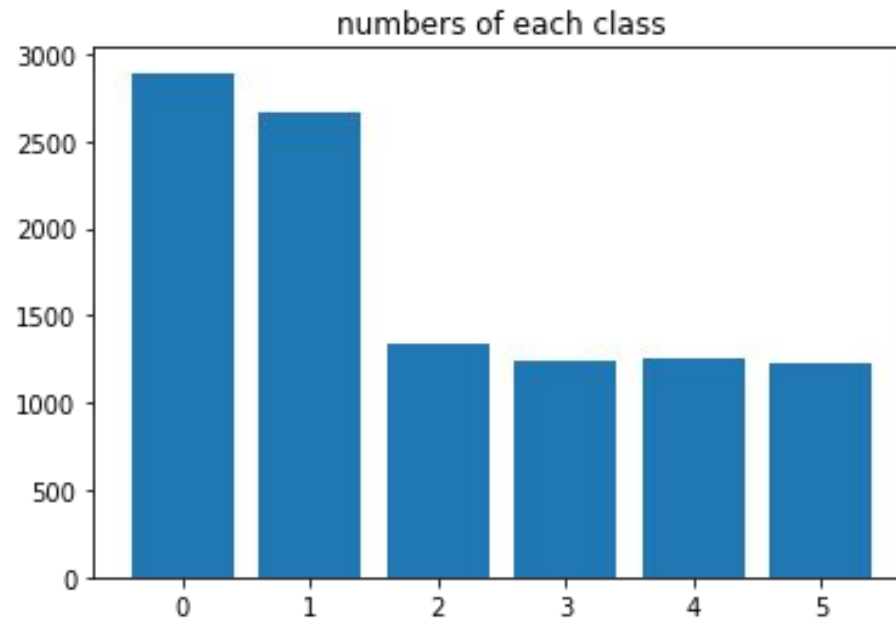
    1: background (non tissue) or unknown

    2: benign tissue (stroma and epithelium combined)

    3: cancerous tissue (stroma and epithelium combined)

# Label Distribution

# Summary

- Our dataset is a large and unbalanced image dataset,
- It has two different label systems.
- We will use the ranboud center grading system, since it includes extra information on the severity of cancer.
- Unet might be a good semantic segmentation model for this, since it has the advantage of using fewer images to obtain good results
- training the data using the highest level class sample(since those samples most likely include all 6 labels) might be good enough.

# Image Segmentation

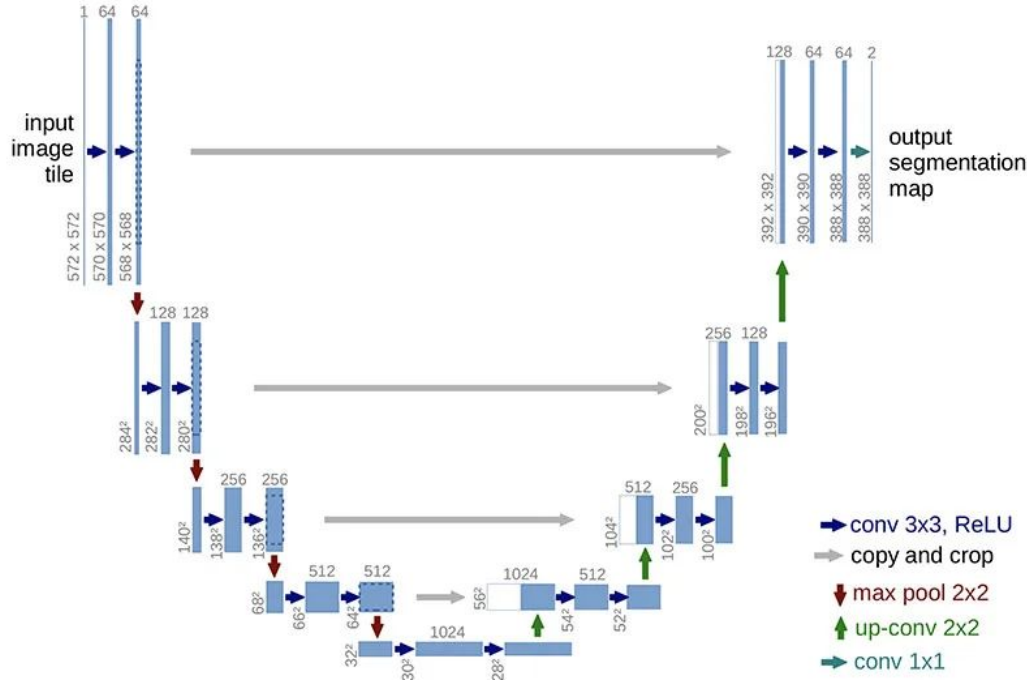label *each pixel* of an image with a corresponding ***class*** of what is being represented



| | |
|---|---|
| Input Image | Segmentation labels |

# U-net Structure

Advantage of requiring fewer training samples and Precise segmentation
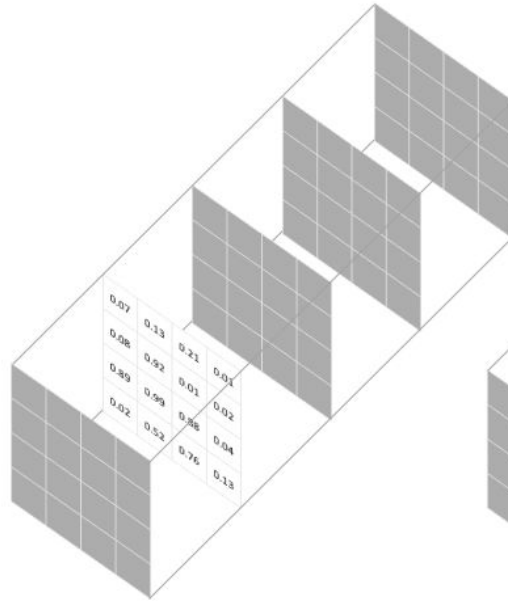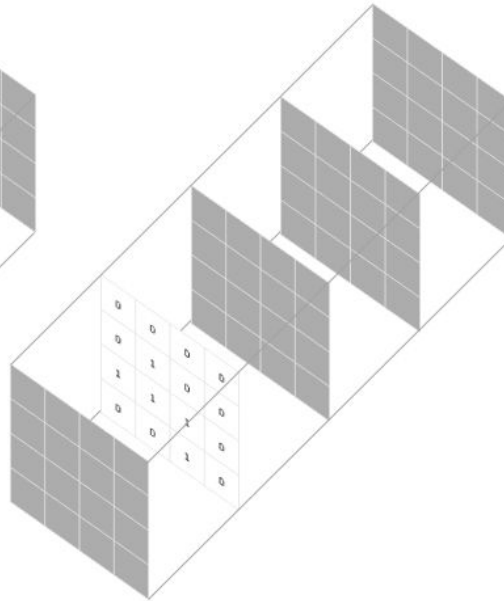


The architecture contains two paths:

Contraction path (encoder) which is used to capture the context in the image.

Symmetric expanding path (decoder) which is used to enable precise localization using transposed convolutions.

# Soft Dice Coefficient



Prediction for a selected class
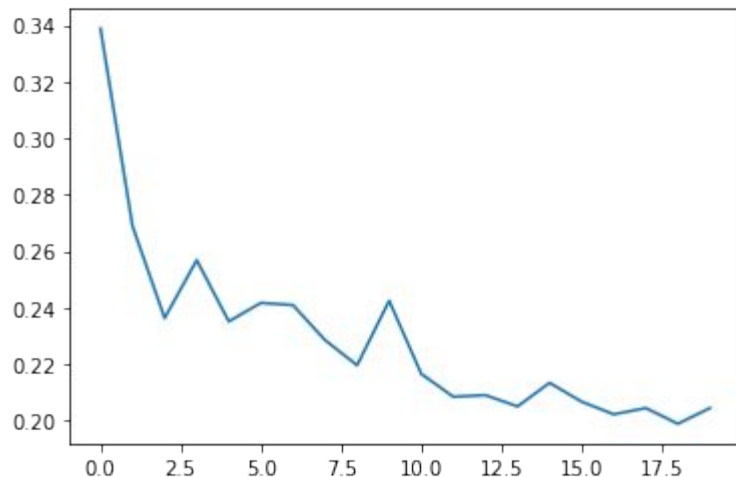
Target for the corresponding class

Soft Dice coefficient is calculated for each class mask

$$1 - \frac{2\sum\limits_{pixels} y_{true} y_{pred}}{\sum\limits_{pixels} y_{true}^2 + \sum\limits_{pixels} y_{pred}^2}$$
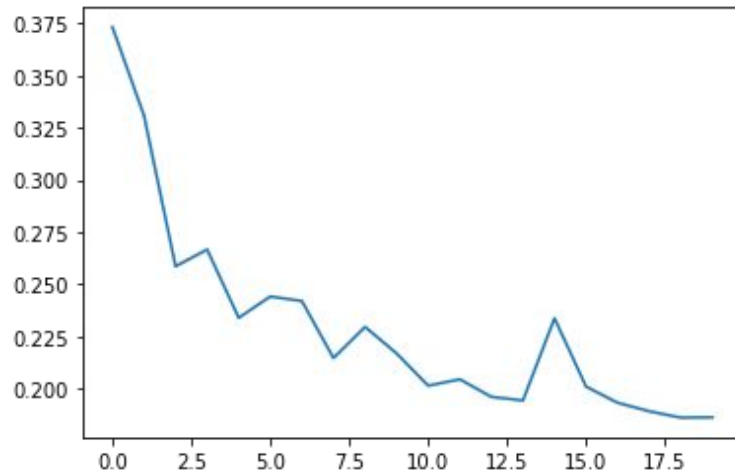
This scoring is repeated over all **classes** and averaged

# Training Loss plot :dataset grader vs grade5



grader(all data from r center)

grade5(only level 5 data)

Both dataset perform quite similar. grader(running_Loss 0.22823013762801225) performing is a little bit better than grade5(0.22823013762801225) for the valid set.
That Is probably because the validate dataset  is from the grader testset which is more similar to the grader training set, they has the same distribution.

# Visualization : Ground truth vs Model prediction
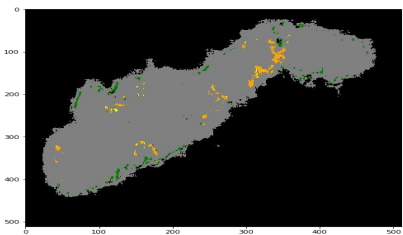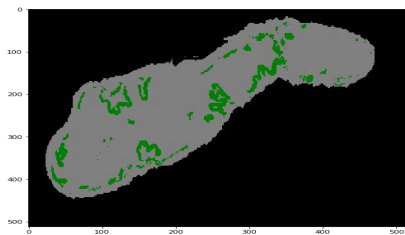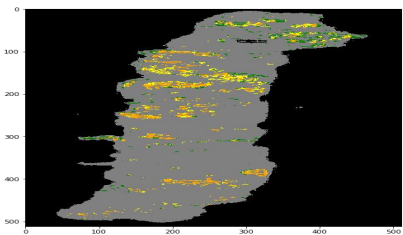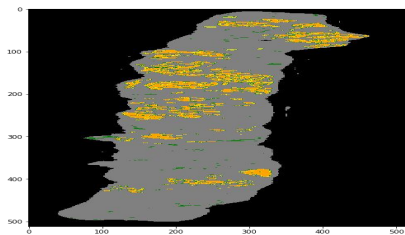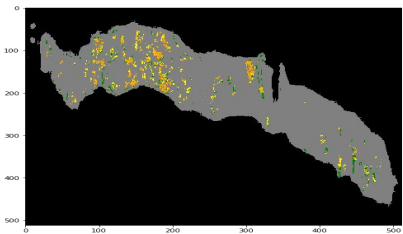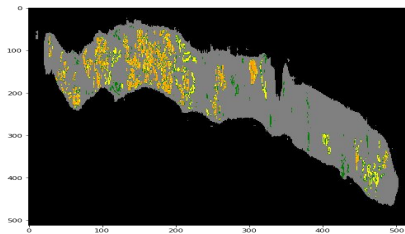
# Evaluation Metrics

Accuracy: 0.960995
Precision: 0.950707
Recall: 0.960995
f1_score: 0.954715
Soft Dice loss :0.830966999828632)
Confusion matrix

```
[[223114  1676    0    0    0    0]
 [  864 27963   29   13   399    0]
 [    0  1004   46   17   172    0]
 [    0   731   27   10   261    0]
 [    0   895   49   15   786    0]
 [    0   858  169   31  3015    0]]
```

# **Final thought**:

since we use resized dataset, if we use high resolution data , may get better results