

PROJECT REPORT  
MILESTONE ONE AGNOR

ALEXANDER VAPTSAROV  
COMPUTER SCIENCE AND ARTIFICIAL INTELLIGENCE  
IMAGE UNDERSTANDING  
TECHNISCHE HOCHSCHULE INGOLSTADT

SUPERVISORS:  
JONATHAN GANZ

APRIL 2024

# Contents

1	Introduction	3
2	Dataset	4
3	Conclusion	5

## INTRODUCTION

---

**Argyrophilic nucleolar organizing region (AgNORs)** are specific regions within the nucleus of a cell that are involved in ribosomal RNA transcription. These regions contain proteins with a high affinity for silver, allowing them to be visualized using silver-based staining techniques in histological tissue sections. AgNORs are used as a marker for cell proliferation and are particularly relevant in cancer research. The number of AgNORs per nucleus has been linked to the rate of tumor growth, with more malignant tumors often exhibiting a higher number of smaller AgNORs compared to benign or less malignant tumors.

**AgNOR images** are thin slices of tissue samples that are prepared for microscopic examination. These sections are typically obtained from biopsy or tissue samples taken from patients. Once the tissue is sliced into thin sections (**histological sections**), these sections are mounted on glass slides, stained using AgNOR staining. By examining histological sections under a microscope, researchers can gain valuable insights into the cellular activity and pathology of the tissue sample.

**Datasets** containing AgNOR images play a crucial role in advancing research in automated AgNOR scoring and histopathological analysis. These datasets are used for developing and validating algorithms, as well as training machine learning models. Expert annotations in AgNOR image datasets include the location, size, shape, and intensity of AgNORs within cell nuclei. This data serves as ground truth for algorithms, improving their accuracy in detecting and quantifying AgNORs.

AgNOR images and datasets are essential for studying cellular proliferation, tumor biology, and disease progression. Quantifying AgNOR characteristics offers insights into molecular disease mechanisms, aiding in the development of advanced diagnostic tools. Automated analysis using machine learning improves evaluation efficiency, accuracy, and enables high-throughput analysis in research and clinical settings.

## DATASET

---

In this work, a total of 27 images for the automated assessment of AgNOR scores in histopathology.

In the study, all nuclei present in the images were annotated by a pathologist, where the number of identifiable AgNORs served as the label for each nucleus. This annotation process led to a total of 19,734 bounding box annotations categorized into twelve classes. The twelfth class specifically includes all nuclei where more than ten AgNORs were identifiable.

Annotations per Class: 0: 4461 | 1: 8152 | 2: 4003 | 3: 1628 | 4: 734 | 5: 356 | 6: 193 | 7: 78 | 8: 47 | 9: 28 | 10: 26 | 11: 28

## CONCLUSION

---

Based on the analysis of the dataset and the challenges mentioned in the report, several problems may arise when solving the AgNOR assessment problem using deep learning:

The dataset is skewed towards classes with fewer AgNORs per nucleus, which can lead to biased model predictions and difficulty in accurately detecting classes with higher AgNOR counts.