Analysis of the meiotic spindle is an essential but time-consuming step in the research of the effects of the oocyte-meiosis regulating proteins. In this thesis, we propose a method for automated computation of the spindle volume as a step towards a more efficient analysis pipeline.

The proposed method is based on convolutional neural networks. It consists of two steps: segmentation of the spindle on a microscopic image and calculation of its volume. The segmentation is performed by a modified 3D U-Net architecture, which is trained on an augmented dataset of volumetric images.

The choice of architecture is supported by an in-depth analysis of the current state-of-the-art methods for image segmentation with a focus on biomedical images and volumetric data. The hyperparameters are tuned for the best performance on the dataset.

The model is evaluated on the testing dataset with respect to the segmentation quality and the volume estimation accuracy. The results demonstrate the feasibility of the proposed approach.