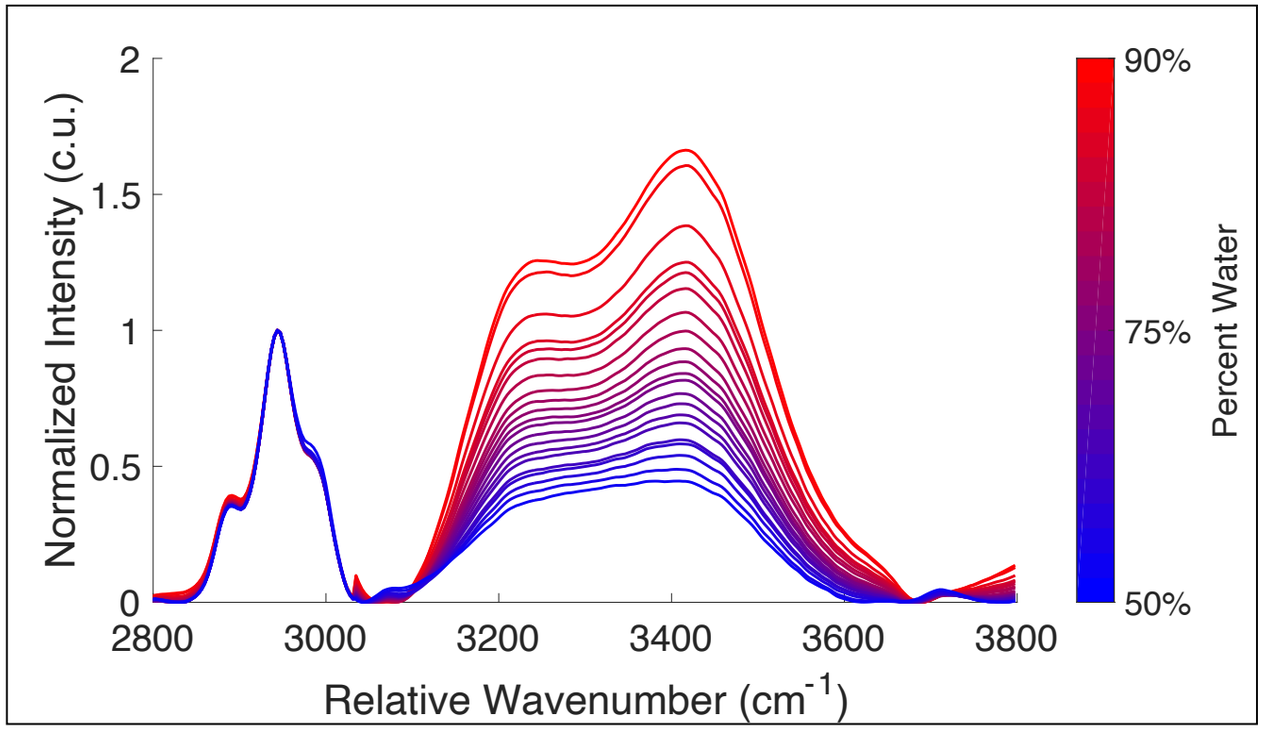
BME 3015

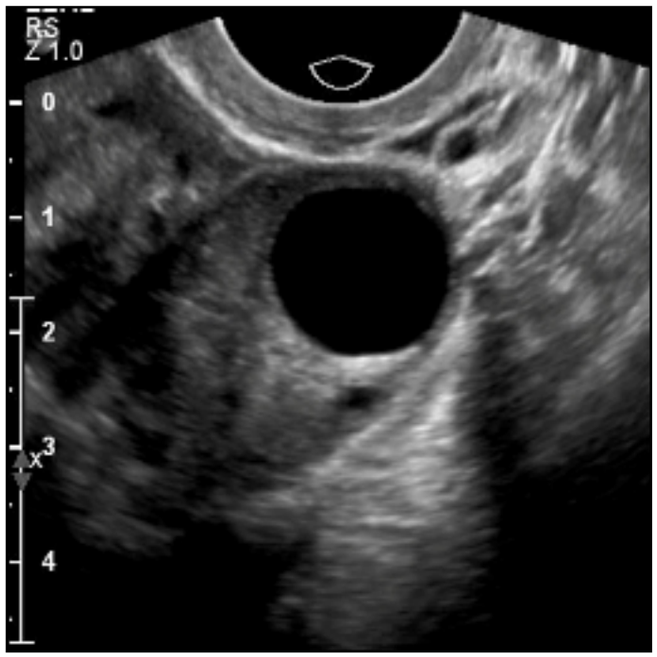
BME3015 Computational Lab: Image Analysis

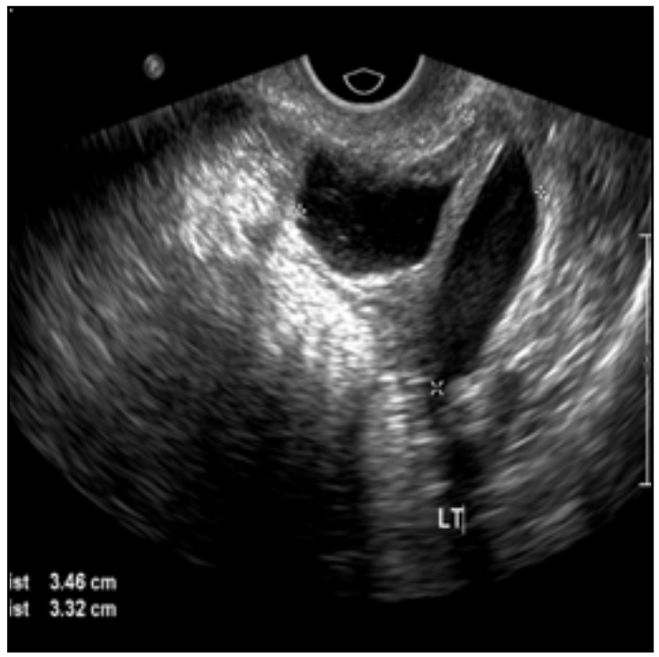


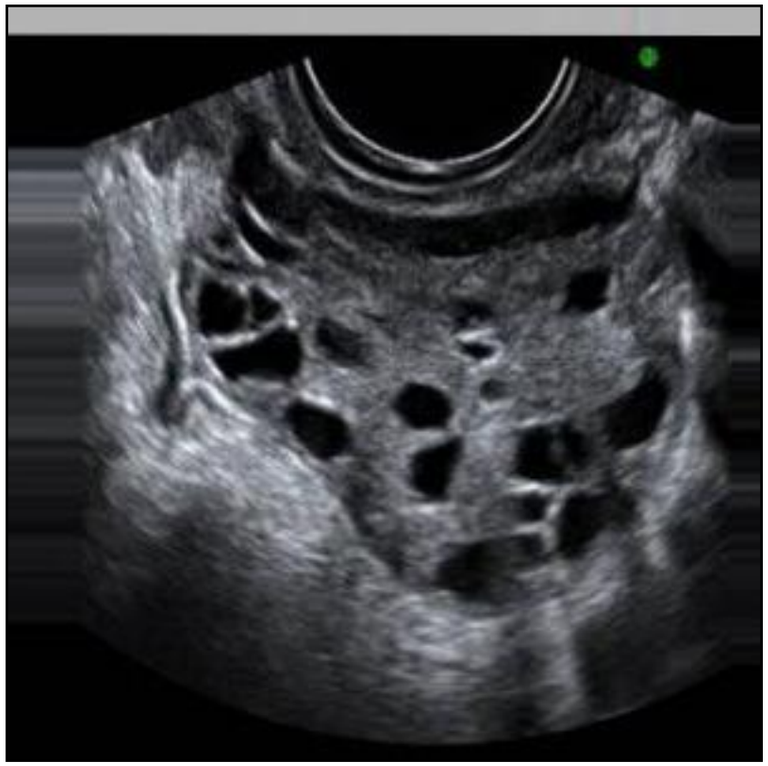
Patricia Widder

CHAPTER 1

Computational Lab: AI-Driven Follicular Monitoring







In this lab, you will develop a pipeline to segment and measure ovarian follicles from 2D ultrasound scans to assess reproductive health markers.

Project Introduction and Instructions

This project will develop over the remaining weeks of the semester, with milestone submissions along the way.

You will develop a pipeline to segment and measure ovarian follicles from 2D ultrasound scans to assess reproductive health markers.

We will use Python tools, segmenting tools, and U-Net, the industry standard for AI-based medical image segmentation.

Project Introduction: AI-Driven Quantitative Folliculometry

In the field of reproductive medicine, ultrasound imaging serves as the primary "window" into the physiological state of the patient. Whether monitoring a patient undergoing In Vitro Fertilization (IVF) or diagnosing Polycystic Ovary Syndrome (PCOS), the ability to accurately count and measure ovarian follicles is a critical clinical requirement.

Traditionally, this task, known as folliculometry, relies on manual tracing and measurement by skilled sonographers. However, manual measurement is inherently subjective, prone to inter-observer variability, and time-intensive, creating a need for automated, quantitative computational tools that can provide standardized results.

The technical challenge of automating this process lies in the physics of the imaging modality itself. Ultrasound images are characterized by *speckle noise*, a granular interference pattern caused by the constructive and destructive interference of backscattered acoustic waves. Furthermore, follicles appear as anechoic (fluid-filled, dark) regions with "fuzzy" boundaries due to the *Partial Volume Effect*, where a single voxel contains both fluid and the surrounding echogenic stroma. Developing an algorithm that can navigate this noise to extract precise physiological dimensions requires a deep understanding of both digital signal processing and advanced computer vision.

Over the next several weeks, you will transition from classical image processing to the cutting edge of medical AI. You will build a complete computational pipeline using the U-Net architecture, a state-of-the-art deep learning model designed specifically for medical image segmentation. Beyond simply "training a model," you will grapple with the realities of medical data engineering: creating "ground truth" through manual and AI-assisted annotation, implementing morphological post-processing to separate crowded follicles, and converting digital pixel data into physical units (mm) to support clinical decision-making.

The ultimate goal of this project is to move beyond the "Black Box" of AI. By employing interpretability tools like Grad-CAM, you will audit your model to ensure it is making decisions based on

relevant physiological features (such as the follicle wall) rather than imaging artifacts.

By the end of this lab, you will have developed a robust, clinically-aware system that can take a raw ultrasound frame and output a quantitative report on ovarian reserve, demonstrating the power of AI as a collaborator in quantitative physiology.

Pre-lab Preparations

The Dataset

We will be working with a public-domain ultrasound image dataset from Kaggle.

The ovarian ultrasound image dataset used for ovarian disorder classification comprises five major diagnostic categories representing distinct ovarian conditions: healthy ovary, dominant follicle, polycystic ovary (poly_cyst), simple cyst, and complex cyst. The dataset demonstrates a balanced class distribution, ensuring that each category contributes a comparable number of samples for effective training and evaluation of deep learning models.

The dataset includes:

Healthy ovary: 1,465 images

Dominant follicle: 1,297 images

Polycystic ovary: 1,423 images

Simple cyst: 1,326 images

Complex cyst: 1,368 images

In total, the dataset contains 6,879 ultrasound images, each depicting high-resolution grayscale ovarian scans. The images were collected from clinical ultrasound examinations, capturing variations in follicular size, cystic morphology, and tissue echotexture — key diagnostic indicators for ovarian abnormalities. Each image is labeled by medical experts to ensure accurate ground truth classification.

Download the dataset here:

https://www.kaggle.com/datasets/ucimachinelearning/ovarian-ultrasound-image-dataset

The Working Environment

Instructions will be given in Python, though you can use other coding platforms. You can work in Jupyter Notebooks or another IDE if you wish.

Instructions and starter code are given in a Jupyter notebook file, which you can use or not use. However, you should make sure you are able to import and run without errors the libraries and packages found in env_check.py or env_check.ipynp on Canvas.

Part 1: Fundamentals of Image Pre-processing

Medical AI is only as good as the data provided to it. We need to understand both our imaging modality (ultrasound) and the capabilities of our digital processing system.

Goals of this part:

- Understand why ultrasound images are difficult for standard computer vision.
- Implement a Python pipeline to "clean" raw ultrasound frames.
- Quantify the Contrast-to-Noise Ratio (CNR) before and after processing.

Physiological Context

In reproductive medicine, ultrasound is used to monitor follicular development. A follicle appears as an *anechoic* (black/dark) circular region within the more *echogenic* (grey) ovarian stroma, as in Figure 1.1.

Ultrasound suffers from *Speckle Noise*, a granular interference pattern caused by the constructive and destructive interference of backscattered echoes. Unlike Gaussian noise, speckle is multiplicative:

$$I(x,y)=J(x,y)\cdot S(x,y)$$

Where:

- I(x,y) is the observed pixel intensity.
- J(x,y) is the "true" underlying tissue signal.
- S(x,y) is the speckle noise component.

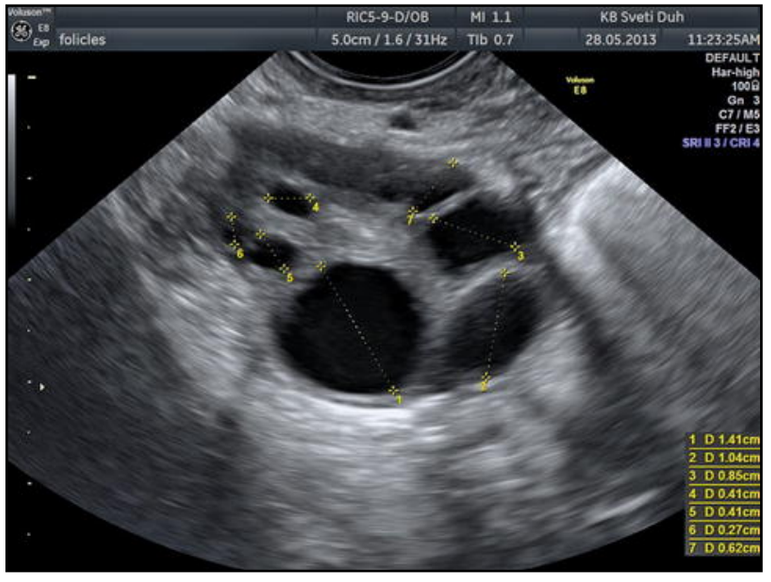


Figure 1.1 Transvaginal image of a normal ovary with dominant follicle.

Go to the Jupyter Notebook labeled “Part 1 template” and follow the instructions there. When you have calculated your Contrast-to-Noise ratios for the pre-processed image files of a single dominant follicle image, return here.

$$CNR = \frac{|\mu_f - \mu_s|}{\sqrt{\sigma_f{}^2 + \sigma_s{}^2}}$$

Part 1 Report

Create a short formatted report, as follows:

Introduction

Begin with a short introductory section that introduces the lab and its goals. Explain why ultrasound images are difficult for standard computer vision. Describe the source and characteristics of the dataset we are using, the filters being applied as part of pre-processing, and the expected outcomes.

Results

Discuss the applied filters, including the final chosen parameters, and why those parameters were chosen. Show visualizations of your selected dominant follicle image, with raw, final median filtered, and final median+CLAHE images side by side. These should be part of a single figure, clearly labeled.

Create a labeled table showing the mean, standard deviation, and CNR of your three images.

Discussion

Discuss the measured changes in CNR from raw to filtered to filtered+enhanced. Discuss the benefits of a high CNR for future analysis, and the tradeoffs between preserving the follicle boundary vs achieving a perfectly smooth image.