# Cycle-GANs for Magnetic Resonance Spectroscopy: Data Augmentation and Denoising

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## Problem Definition

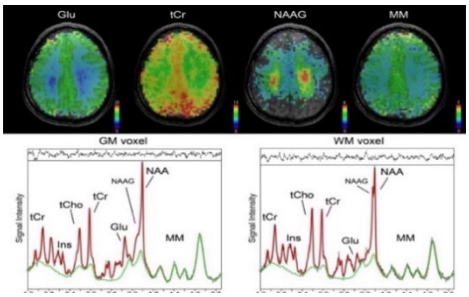


*Figure 1: Example of metabolic maps and MRS spectra, from M. Považan et al. (2015)*

Magnetic Resonance Spectroscopy (MRS) is a powerful non-invasive technique for studying metabolic changes in tissues. However, the application of Deep Learning (DL) to MRS is hindered by the limited availability of large, high-quality datasets. This scarcity arises from privacy concerns, the high cost of data acquisition, and the time-intensive nature of MRS scans. Simulated data can help alleviate this issue, but physics-based simulations struggle to accurately model complex phenomena such as macromolecular baselines and scan imperfections. These limitations reduce the realism and utility of synthetic data for training DL models. Generative Adversarial Networks (GANs), particularly Cycle-Consistent GANs (Cycle-GANs), offer a promising data-driven alternative. Cycle-GANs can learn to translate data between domains without requiring paired samples, making them ideal for transforming simulated MRS data into more realistic, in-vivo-like signals. Additionally, the reverse transformation path can be leveraged for denoising and preprocessing real MRS data, potentially improving metabolite quantification.

## Objectives

This project aims to explore the application of Cycle-GANs in MRS data processing, focusing on two key challenges:

1. **Data Augmentation**: Transforming simulated MRS data into realistic in-vivo-like data to enrich training datasets.
2. **Data Preprocessing**: Using the reverse Cycle-GAN path to denoise and clean real MRS data, enhancing the quality of downstream analysis.

## Methodology

The student will:

- **Curate and prepare datasets:** generate MRS spectra using simulation tools, and incorporate in-vivo data for training, validation, and testing.
- **Develop and implement a Cycle-GAN architecture** in Python, including model training, tuning, and optimization for the MRS application.
- **Design evaluation metrics** to assess both the realism of generated spectra and the effectiveness of the denoising process (e.g., quantitative spectral similarity measures, performance of metabolite quantification pipelines).
- **Conduct experiments and comparative analyses** to benchmark the Cycle-GAN approach against baseline methods (e.g., standard preprocessing, purely simulated data).
- **Document and communicate findings**, providing insights into the benefits and limitations of Cycle-GANs for MRS.

This project therefore combines programming and machine learning with domain knowledge of MRS and critical evaluation of DL-based methods for medical data.