

	<h2>Tutorial 5: Biomedical Image Analysis in Python and R using SimpleITK Jupyter Notebooks</h2> <p>Organizers: Hans Johnson, University of Iowa, USA Bradley Lowekamp, National Institutes of Health and MSC LLC, USA Ziv Yaniv, National Institutes of Health and TAJ Technologies Inc., USA</p>
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Overview

In this tutorial, we will use a hands-on approach utilizing Jupyter notebooks to explore and experiment with various SimpleITK features in the Python and R programming languages. Participants will follow along using their personal laptops, enabling them to explore the effects of code changes and parameter settings not covered by the instructors.

We will start by introducing the toolkit's two basic data elements, Images and Transformations. We will then explore the various features available in the toolkit's registration framework including: optimizer selection, the use of linear and deformable transformations, the embedded multi-resolution framework, self-calibrating optimizers and the use of callbacks for registration progress monitoring. We will then show how to use SimpleITK as a data augmentation tool for deep learning via spatial and intensity transformations and its use for segmentation evaluation. Finally, we will show how to set up a collaborative development environment using Jupyter Notebooks, with convenient remote data downloads and regression testing.

Topics

1. SimpleITK basics: images, transformations, resampling, and filters.
2. ITKv4 registration framework: initialization, rigid, and nonrigid registration (FFD, and the Demons set of algorithms).
3. Data augmentation for deep learning and segmentation evaluation.
4. Collaborative Jupyter notebook environment with regression testing.

Audience

The intended audience are students, researchers and engineers involved in biomedical image analysis with the need for convenient image IO, image registration and image manipulation using spatial and intensity transformations.

Knowledge of the Python or R programming language is assumed.