# File converter from .PDB to Slicer compatible file format using ITK

# Project Proposal

Protein Data Bank(PDB) is a widely used tool in the protein research community. It contains both the protein structures determined from experimental methods like X-ray, Nuclear magnetic resonance spectroscopy (NMR) and predicted models from computational methods. Models built from computational methods need to compare with those created with experiments for various reasons. For example, to evaluate the current predicted model, or to find template for homologues modelling. And the most common file format PDB uses is .PDB files, which contains atoms position information and other information. Various visualization and analysis tool including Pymol, Chimera is used to build the model and analyses data from .PDB files.

Meanwhile, Slicer and ITK are both strong tools in image processing community. Slicer is an open-source data visualization and processing tool mainly for medical image processing. It allows manipulating 3D models in different ways, as well as making new modules by users. ITK is a C++ library that has many powerful image processing functions and its output can be integrated into Slicer. Some tasks in protein community maybe solved in Slicer using ITK. For example, protein structure-structure alignment is essentially the surface registration problem in image processing field. So if we can use Slicer and ITK to analyze protein data structure, interesting facts may be found.

The challenge is, however, Slicer takes images format mostly generated from medical equipment, such as CT scan, MRI and the common file formats are .nrrd, nii and etc. Thus it is meaningful to create an ITK converter that converts .PDB file to file formats accepted by Slicer.