List of Code Files:

**Run\_Model\_Example.m** – This file will load exported Simbiology model and baseline population, then simulate steady state for healthy, Crohn’s disease, and ulcerative colitis. Finally the code will plot for a few key proteins, CRP, FCP, IL8, and IL12.

**GutInflammation.xml** – This is the exported Simbiology model in sbml format.

**VPop\_Baseline.csv** – Matrix (csv format) of virtual patient kinetic parameters and weights (parameter by virtual patient).

**SimulateModel.m** – This file runs model for given exported model, parameter vector, and weights (fold changes on specific parameters). Output is amount species converted to weight and/or cells (X\_converted), time (T), species list, and amount species not converted (OutDYDT).

**FindSteadyState.m** – This file calculates steady state for an exported Simbiology model.

**ParametersToVary.m** – This file creates a vector of parameters in the model.

**ParametersToWeight.m** – This file lists parameters that are varied with weights.

**ConvertUnits.m** – This file converts units from pmole to pg.

**Species\_Location.m** – This file determines species locations in the model.