**1. Subroutines**

**1.1 subsystem.m**

*Description:* Defines the **class** ‘subsystem’ that contains information about SimBiology objects required for definition of the subsystem representing a specific biomolecular circuit and makes these objects easily accessible.

Properties:

1. ModelObject Nominal skin permeability
2. SubsystemType Rate of pathogen eradication by innate immune response

Output variables:

1. par: Vector of parameters

**1.2 BioSIMI\_add\_subsystem.m**

*Description:* In conjunction with SystematicBifurcationAnalysisAD.m plots points into healthy subspace of bifurcation diagram with kappa\_P and alpha\_I (starting from healthy equilibrium point).

Input variables:

1. x\_range
2. y\_range
3. Par\_Healthy\_G\_off
4. Par\_Healthy\_G\_on
5. Par\_Unhealthy\_G\_off
6. Par\_Unhealthy\_G\_on

Output variables:

1. None

**2. Subsystems**

**1.2 BioSIMI\_add\_subsystem.m**

*Description:* Calculation of the effect of various Pathogen stimulus strength and Duration on the final state of the bistable genotype system and plotting as the appropriate color map which code produces as figures. We do not consider treatment in this model. Possible final states are:

* No Flare
* AD Flare
* Allergic Sensitization
* Transfer to Unhealthy Basin of Attraction.

User needs to define the following:

1. t\_ODE: Integration time for the set of ODEs
2. IS\_S: Matrix of strengths of continuous single-pulse Pathogen stimuli

IS\_S = [*min. strength of stimulus, max. strength of stimulus, No. of points*]

1. AT\_S: Matrix of durations of continuous single-pulse Pathogen stimuli

AT\_S = [*min. duration of stimulus, max. duration of stimulus, No. of points*]