Basic ODD for HFSP ABM model - Strain level ABM  
(going by <https://www.sciencedirect.com/science/article/abs/pii/S0304380006002043>)

**1.1 Purpose and patterns:**

Build a model comparable to the ODEs and the empiric experiments. Meaning 2 plasmid strings, 8 bacteria strings, encapsulating the same set of events (death, division, segregation, conjugation, antibiotics death)

**1.2 state variables and scales:**

low-level entities:

Sub Population of Strains - 16 entities. 24 entities with 2 plasmids

Plasmids - implicit agents

Higher-level entities:

Strains - abundance

Environment carrying capacity

Scales:

Time step length - minutes? Half an hour.

Time horizon - two weeks? (as with the empirical experiment)

**1.3 process overview and scheduling:**

Individual processes in the model:

Population Growth - each strain

Death (including death by antibiotics)

Segregation

Conjugation

Scheduling:

How is time modelled? Timestep? Continuous?

**2. Design concepts:**

*Emergence*: Which system-level phenomena truly emerge from individual traits, and which phenomena are merely imposed?

*Adaptation*: no adaptation for now

*Fitness*: Is fitness-seeking modelled explicitly or implicitly? implicit

*Prediction*: In estimating future consequences of their decisions, how do individuals predict the future conditions they will experience? Individuals do not predict the future

*Sensing*: What internal and environmental state variables are individuals assumed to sense or “know” and consider in their adaptive decisions? The presence of other strains, the abundance of the current strain’s sub population.

*Interaction*: What kinds of interactions among individuals are assumed? HGF

*Stochasticity*: Is stochasticity part of the model? What are the reasons? No stochasticity for now

*Collectives*: Are individuals grouped into some kind of collective, e.g. a social group? No

*Observation*: How is data collected from the IBM for testing, understanding, and analyzing it? Saving the abundance values for each subpopulation in each timestamp.

**3.1 Initialization:**

The initial values of the state variables are set using ampirical data. They are fixed among simulations. Initially the competition between the strains should be randomly decided until we get the empirical data.

**3.2 Input**

* Environmental selection pressure (simulate antibiotics)
* Bacteria trait matrix
* Plasmid trait matrix
* Abundances
* Competition matrix (a\_ij)
* Plasmid-bacteria hosting matrix (H\_ij)

**3.3 Submodels**

?