

# Disease modeling with EMOD

---

Advanced modeling workshop,  
ASTMH 2019

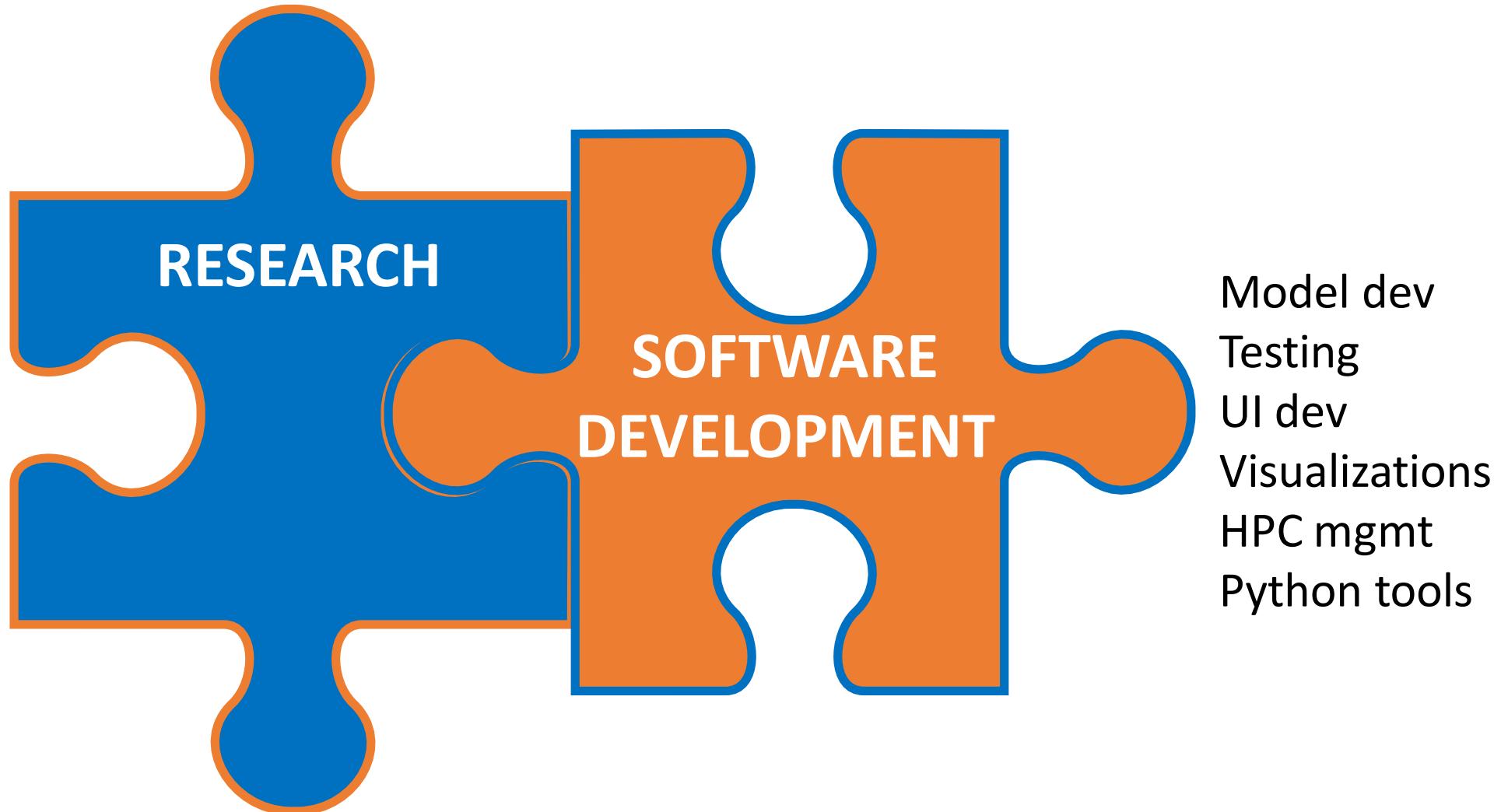
# Our motivation

The collage includes:

- A map of Africa on the left.
- A PLoa article titled "The Great Global Health Perspective" by Bocar Kouyaté, published June 2017, with a subtitle "Household clustering".
- A diagram at the top showing two columns: "LOW IMPORTATION" and "HIGH IMPORTATION". Each column has a green box labeled "enhanced" and an orange box labeled "maintain".
- A section titled "a" with the text "DA" above it.
- A section titled "b" with the text "S/I" above it.
- A section titled "c" with the text "elimination very unlikely" above it.
- The IDM Institute for Disease Modeling logo and text: "IDM INSTITUTE FOR DISEASE MODELING".
- A statement: "IDM shapes global efforts to eradicate infectious disease and to achieve permanent improvements in the health of those most in need."
- A statement: "By developing, using, and freely sharing computational modeling tools, we advise policymakers, promote quantitative decision-making, and advance scientific methodologies."
- A statement: "IDM is an institute within the Global Good Fund, a collaboration between Intellectual Ventures and Bill and Melinda Gates."
- A section titled "Africa Suggests It May Be" with a quote from Gerardin et al. 2017.
- A "NPf" logo.
- A photograph of a dense, colorful hillside settlement.

# About IDM

Malaria  
Polio  
TB  
HIV  
Typhoid  
Cholera  
Epidemics  
Vaccine Econ  
Family Planning  
Applied Math



# GOALS!

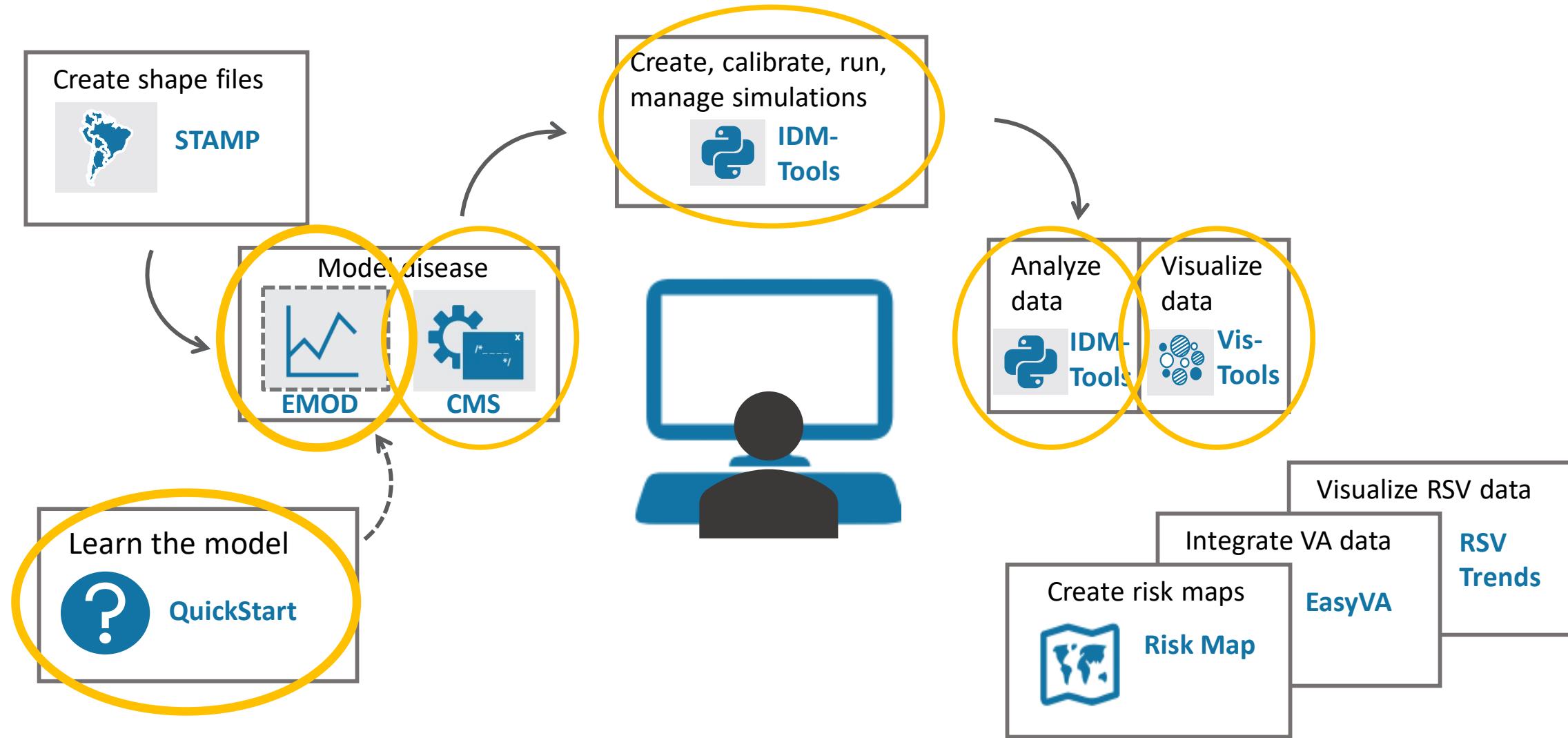
## **What you should get out of the workshop:**

- Increased understanding of computational methodologies for use in epidemiology
- Training on open-source, readily-available modeling tools
- The foundation to use EMOD in your own research
- Resources to answer questions and increase your expertise
- Neat swag and a free dinner!

## **What we are getting out of the workshop:**

- An opportunity to connect with members of the global health community, and a chance to increase understanding of infectious disease modeling
- More users for our software: the more it gets used, the more we can refine it, and the better it gets!

# IDM modeling tools



# Overview

## (Already done, pre-workshop)

- Tech troubleshooting & making sure you can boot from the thumb drive

## Part 1: Getting started

- Quick intro to epi models
- Adding detail
- Heterogeneity and stochasticity
- Introduction to EMOD
- EMOD: IndividualProperties (IPs)
- QuickStart exercise: IPs

## Part 2: Diving into modeling with EMOD

- EMOD simulation scenarios
- Advanced EMOD features: HINT
  - EMOD HINT exercise 1-3
- Additional EMOD features:
  - Cascade of care
  - Disease-specific
- How to use EMOD in your research (including information about using the software)

*Please join us this evening for an IDM-hosted dinner at Rosa Mexicano, following the conclusion of this session at 6:00 pm!*

# Part 1: Getting started with disease modeling

# About compartmental models

For more information, see:

★ Keeling, M. J., & Rohani, P. (2011). *Modeling infectious diseases in humans and animals*. Princeton University Press.

★ Bjørnstad, Ottar N. (2018) *Epidemics: models and data using R*.

Anderson, R. M., & May, R. M. (1992). *Infectious diseases of humans: dynamics and control*. Oxford university press.

Diekmann, O., Heesterbeek, H., & Britton, T. (2012). *Mathematical tools for understanding infectious disease dynamics*. Princeton University Press.

# Compartmental models



$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

*A Contribution to the Mathematical Theory of Epidemics.*

By W. O. KERMACK and A. G. MCKENDRICK.

(Communicated by Sir Gilbert Walker, F.R.S.—Received May 13, 1927.)

(From the Laboratory of the Royal College of Physicians, Edinburgh.)

## Compartmental models



$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

$$S(t) + I(t) + R(t) = 1$$

## Compartmental models



$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

$$\frac{dI}{dt} \approx I(\beta - \gamma)$$

$\Rightarrow \frac{dI}{dt} < 0 \text{ if } \beta < \gamma \quad \frac{dI}{dt} > 0 \text{ if } \beta > \gamma$

$$\Rightarrow \frac{dI}{dt} < 0 \text{ if } \frac{\beta}{\gamma} < 1 \quad \frac{dI}{dt} > 0 \text{ if } \frac{\beta}{\gamma} > 1$$

# Compartmental models



$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Basic reproductive number

$$R_0 = \frac{\beta}{\gamma}$$

Pathogen	$R_0$
Influenza	3 – 4
Ebola	1.5 – 3
Measles	16 – 18

## Compartmental models



$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Basic reproductive number

$$R_0 = \frac{\beta}{\gamma}$$

If we can vaccinate a population such that at most  $1/R_0$  percent of the individuals are still susceptible, the pathogen cannot subsist. **I.e.,  
vaccinate at least  $1 - \frac{1}{R_0}$  percent of the population**

# Compartmental models



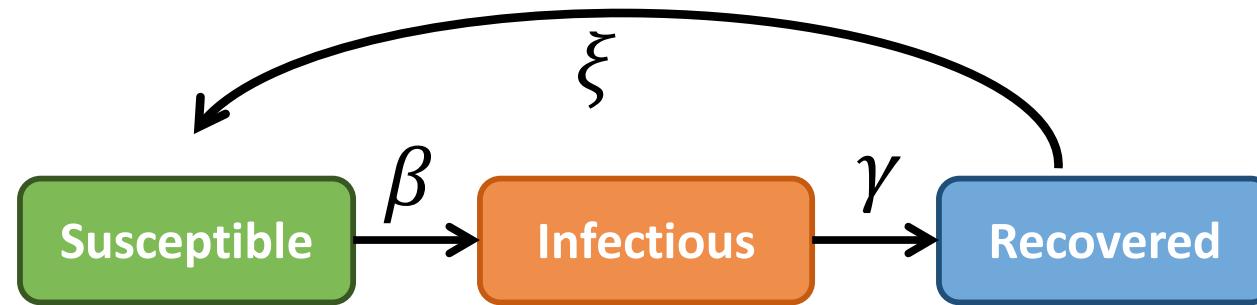
$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

```
##### SIR - Euler
SIRE <- function(Days,i_0,beta,gamma,dt){
  S <- I <- R <- rep(0,round(Days/dt))
  I[1] <- i_0
  S[1] <- 1-i_0
  time <- dt
  if (length(s)>1){
    for (t in 2:length(s)){
      StoI <- S[t-1] * I[t-1] * beta * dt
      ItoR <- I[t-1] * gamma * dt
      time <- c(time,time[t-1] + dt)
      #
      S[t] <- S[t-1] - StoI
      I[t] <- I[t-1] + StoI - ItoR
      R[t] <- R[t-1] + ItoR
    }
  }
  return(cbind(time,S,I,R))
}
```

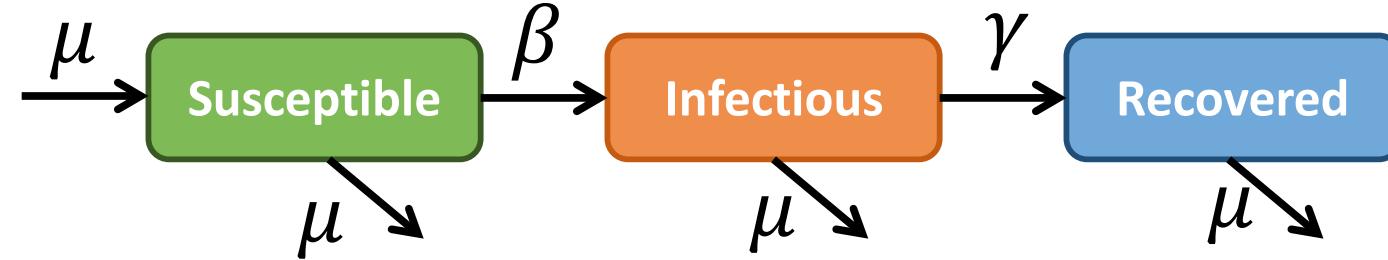
## Extensions of the SIR model: SIRS



Temporary / waning immunity

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI + \xi R \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I - \xi R\end{aligned}$$

## Extensions of the SIR model



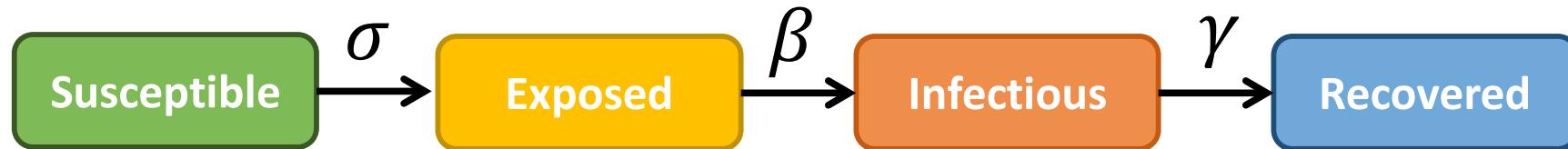
Demography

$$\frac{dS}{dt} = \mu - \beta SI - \mu S$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

## Extensions of the SIR model: SEIR



Pathogen incubation

$$\frac{dS}{dt} = -\beta SI$$

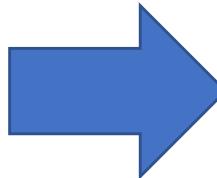
$$\frac{dE}{dt} = \beta SI - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

# Extensions of the SIR model

```
##### SIR - Euler
SIRE <- function(Days,i_0,beta,gamma,dt){
  S <- I <- R <- rep(0,round(Days/dt))
  I[1] <- i_0
  S[1] <- 1-i_0
  time <- dt
  if (length(s)>1){
    for (t in 2:length(s)){
      StoI <- S[t-1] * I[t-1] * beta * dt
      ItoR <- I[t-1] * gamma * dt
      time <- c(time,time[t-1] + dt)
      #
      S[t] <- S[t-1] - StoI
      I[t] <- I[t-1] + StoI - ItoR
      R[t] <- R[t-1] + ItoR
    }
  }
  return(cbind(time,S,I,R))
}
```



```
##### SEIRS
SEIRS <- function(Days,i_0,beta,gamma,sigma,delta){
  dt <- 0.01
  S <- E <- I <- R <- rep(0,round(Days/dt))
  I[1] <- i_0
  S[1] <- 1-i_0
  time <- dt
  if (length(s)>1){
    for (t in 2:length(s)){
      StoE <- S[t-1] * I[t-1] * beta * dt
      EtoI <- E[t-1] * sigma * dt
      ItoR <- I[t-1] * gamma * dt
      Rtos <- R[t-1] * delta * dt
      time <- c(time,time[t-1] + dt)
      #
      S[t] <- S[t-1] - StoE + Rtos
      E[t] <- E[t-1] + StoE - EtoI
      I[t] <- I[t-1] + EtoI - ItoR
      R[t] <- R[t-1] + ItoR - Rtos
    }
  }
  return(cbind(time,S,E,I,R))
}
```

# Drawbacks of differential equation models

(Some) limitations of these models:  
(not in order of importance!)

- Deterministic & has “fractional” people
- Homogeneous populations
- Well-mixed populations
- Difficult to include realistic interventions

## Drawbacks of differential equation models

**Problem:** Model is deterministic & has “fractional” people

**Solution:** Reformulate in terms of probabilities

$$X(t + \Delta t) - X(t) = -\frac{\beta X(t)Y(t)}{N} * \Delta t$$

## Drawbacks of differential equation models

**Problem:** Model is deterministic & has “fractional” people

**Solution:** Reformulate in terms of probabilities

$$\text{Number of new infections} = X(t) * \left( \frac{\beta Y(t)}{N} * \Delta t \right)$$

## Drawbacks of differential equation models

**Problem:** Model is deterministic & has “fractional” people

**Solution:** Reformulate in terms of probabilities

$$\text{Number of new infections} = X(t) * \left( \frac{\beta Y(t)}{N} * \Delta t \right)$$

We can re-imagine the number of susceptible people who become infected as a realization from a Binomial draw where the probability of “infection” is

$$\frac{\beta Y(t)}{N} * \Delta t$$

## Drawbacks of differential equation models

**Problem:** Model is deterministic & has “fractional” people

**Solution:** Reformulate in terms of probabilities

$$\text{Number of new infections} = X(t) * \left( \frac{\beta Y(t)}{N} * \Delta t \right)$$

We can re-imagine the number of susceptible people who become infected as a realization from a Binomial draw where the probability of “infection” is

$$\frac{\beta Y(t)}{N} * \Delta t$$

$$\text{Number of new infections} \sim \text{Binomial} \left( n = X(t), p = \frac{\beta Y(t)}{N} * \Delta t \right)$$

## Drawbacks of differential equation models

**Problem:** Model is deterministic & has “fractional” people

**Solution:** Reformulate in terms of probabilities

$$X(t + \Delta t) = X(t) - \Delta N_i$$

$$Y(t + \Delta t) = Y(t) + \Delta N_i - \Delta N_r$$

$$Z(t + \Delta t) = Z(t) + \Delta N_r$$

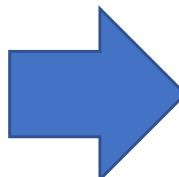
where

$$\Delta N_i \sim \text{Binomial} \left( n = X(t), p = \frac{\beta Y(t)}{N} * \Delta t \right)$$

$$\Delta N_r \sim \text{Binomial}(n = Y(t), p = \gamma * \Delta t)$$

# Drawbacks of differential equation models

```
##### SIR - Euler
SIRe <- function(Days,i_0,beta,gamma,dt){
  S <- I <- R <- rep(0,round(Days/dt))
  I[1] <- i_0
  S[1] <- 1-i_0
  time <- dt
  if (length(S)>1){
    for (t in 2:length(S)){
      StoI <- S[t-1] * I[t-1] * beta * dt
      ItoR <- I[t-1] * gamma * dt
      time <- c(time,time[t-1] + dt)
      #
      S[t] <- S[t-1] - StoI
      I[t] <- I[t-1] + StoI - ItoR
      R[t] <- R[t-1] + ItoR
    }
  }
  return(cbind(time,S,I,R))
}
```



```
##### SIR - stochastic
StochSIR <- function(Days,i_0,beta,gamma,popN, simN){
  dt <- 0.01
  S <- I <- R <- matrix(0,simN,floor(Days/dt))
  I[,1] <- round(popN * i_0)
  S[,1] <- popN - I[,1]
  time <- dt
  if (length(S)>1){
    for (t in 2:length(S[,1])){
      StoIRate <- pmin(I[,t-1] * beta * dt / popN,1)
      ItoRRate <- pmin(gamma * dt,1)
      StoI <- rbinom(simN,S[,t-1],prob=StoIRate)
      ItoR <- rbinom(simN,I[,t-1],prob=ItoRRate)
      time <- c(time,time[t-1] + dt)
      #
      S[,t] <- S[,t-1] - StoI
      I[,t] <- I[,t-1] + StoI - ItoR
      R[,t] <- R[,t-1] + ItoR
    }
  }
  return(cbind(time,t(S),t(I),t(R)))
}
```

## Drawbacks of differential equation models

**Problem:** Populations are homogenous

**Solution:** Introduce even more equations...

## Drawbacks of differential equation models

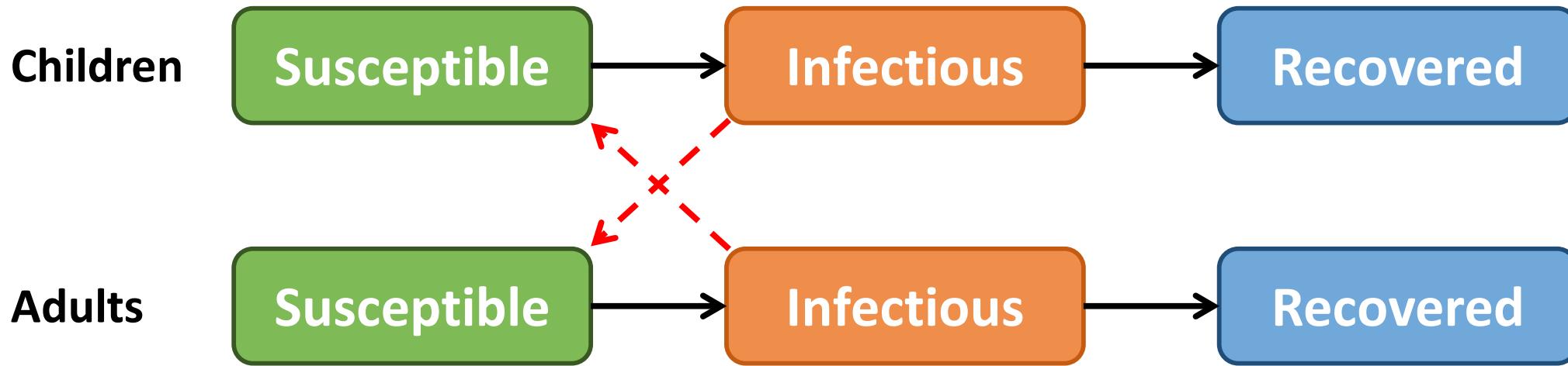
Children



Adults



## Drawbacks of differential equation models



$$\frac{dS_c}{dt} = -S_c(\beta_{cc}I_c + \beta_{ac}I_a) - \delta S_c$$

$$\frac{dI_c}{dt} = S_c(\beta_{cc}I_c + \beta_{ac}I_a) - \gamma_c I_c - \delta I_c$$

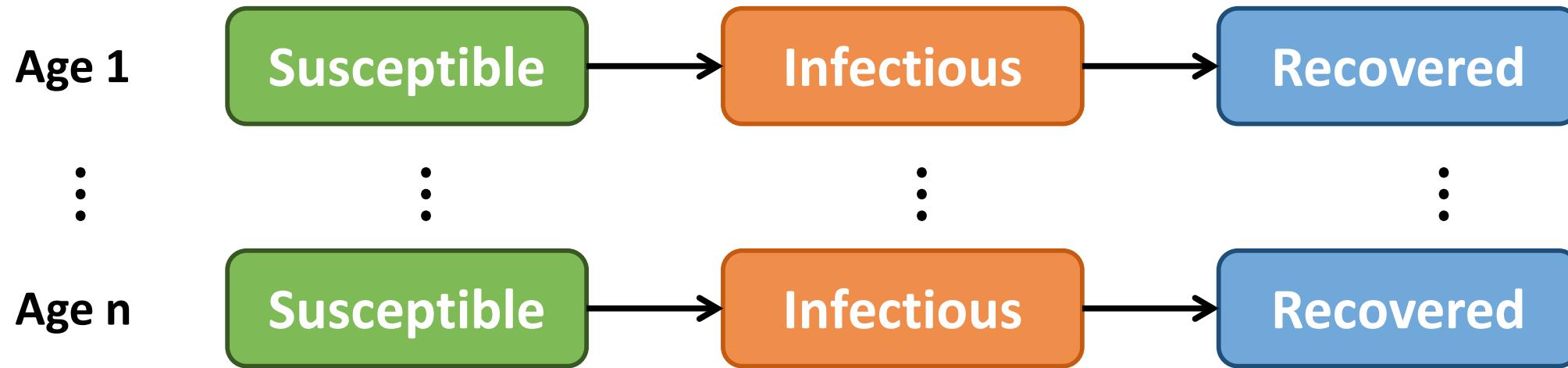
$$\frac{dR_c}{dt} = \gamma_c I_c - \delta R_c$$

$$\frac{dS_a}{dt} = -S_a(\beta_{ca}I_c + \beta_{aa}I_a) + \delta S_c$$

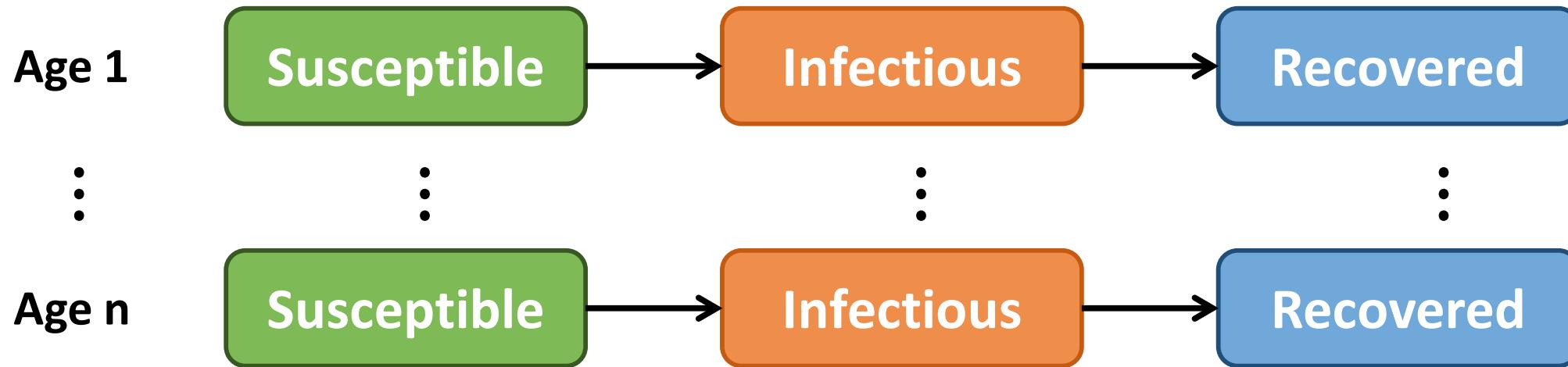
$$\frac{dI_a}{dt} = S_a(\beta_{ca}I_c + \beta_{aa}I_a) - \gamma_a I_a + \delta I_c$$

$$\frac{dR_a}{dt} = \gamma_a I_a + \delta R_c$$

## Drawbacks of differential equation models



# Drawbacks of differential equation models



$$\frac{dS_i}{dt} = \delta S_{i-1} - \delta S_i - S_i * \sum_{j=1}^n \beta_{j,i} I_j$$

$$\frac{dI_i}{dt} = \delta I_{i-1} - \delta I_i + S_i * \sum_{j=1}^n \beta_{j,i} I_j - \gamma_i I_i$$

$$\frac{dR_i}{dt} = \delta R_{i-1} - \delta R_i + \gamma_i I_i$$

## Drawbacks of differential equation models

**Problem:** Populations are well-mixed

**Solution:** Introduce more equations...

**Solution 2:** Account for sub-populations

# Drawbacks of differential equation models

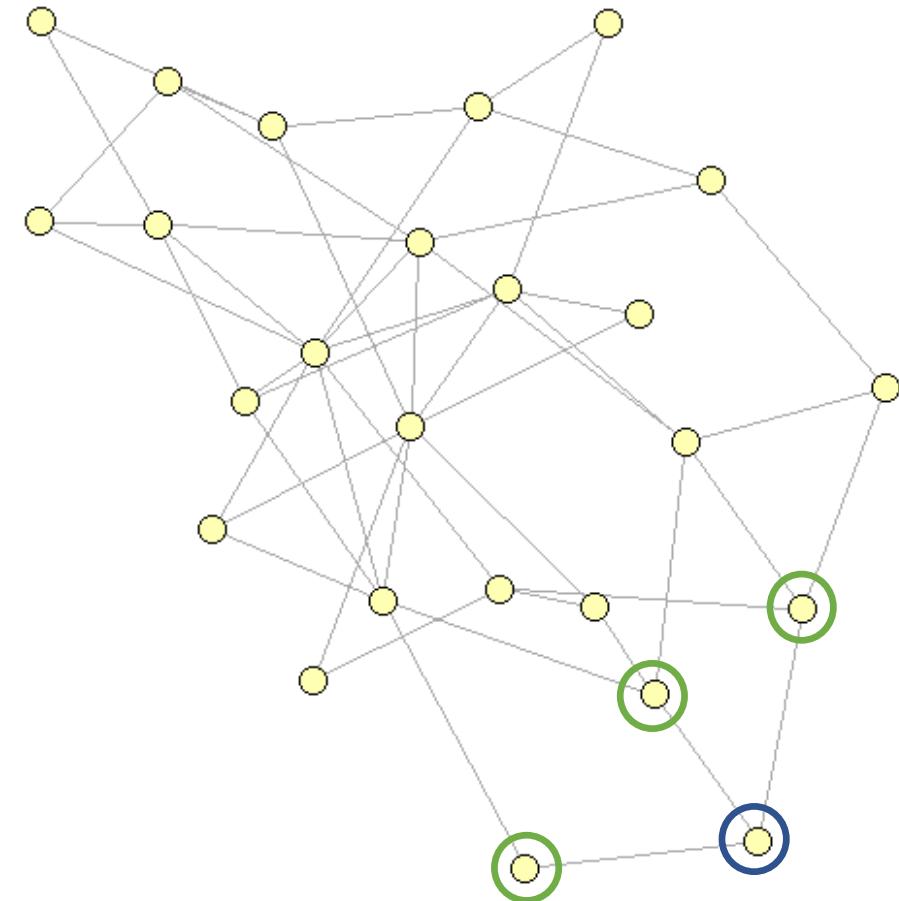
**Problem:** Populations are well-mixed

**Solution:** Introduce more equations...

**Solution 2:** Account for sub-populations

As an example, imagine a population of 25 sub-populations (e.g., neighborhood, or individual).

Assume further, that we know something about contact patterns. For sub-population  $i$ , let  $C_i$  be the set of all other sub-populations they interact with.



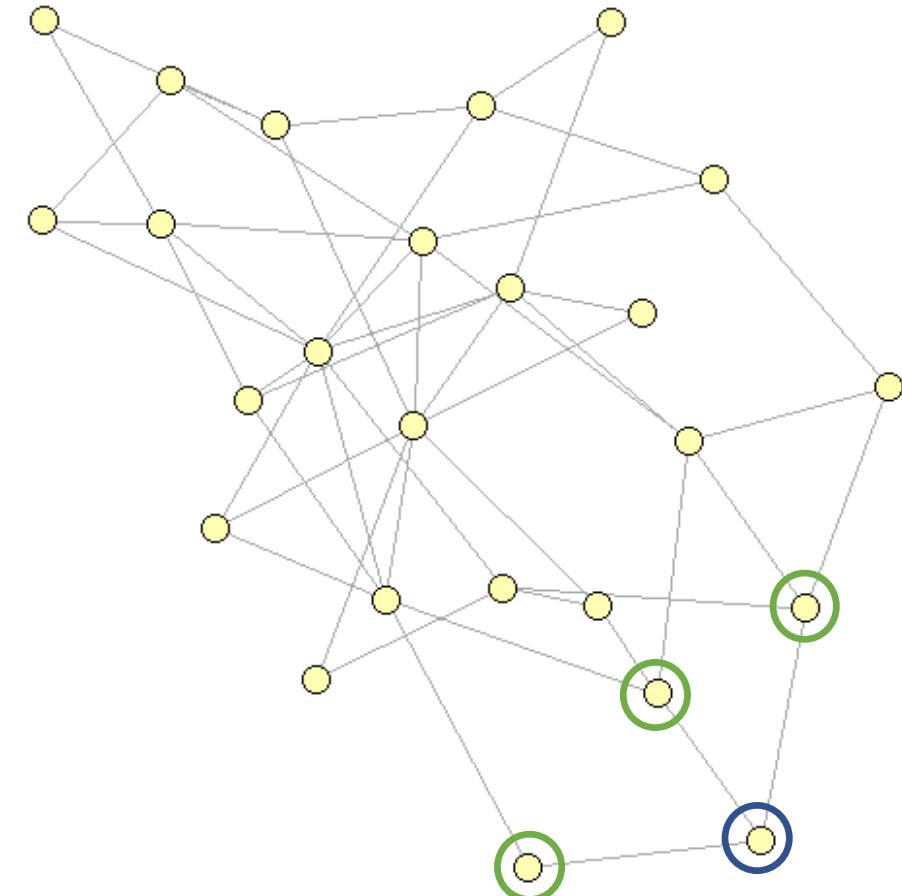
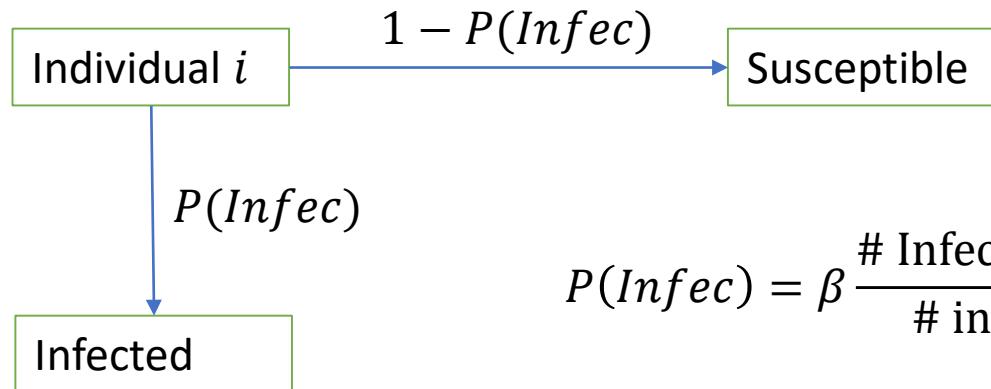
# Drawbacks of differential equation models

**Problem:** Populations are well-mixed

**Solution:** Introduce more equations...

**Solution 2:** Account for sub-populations

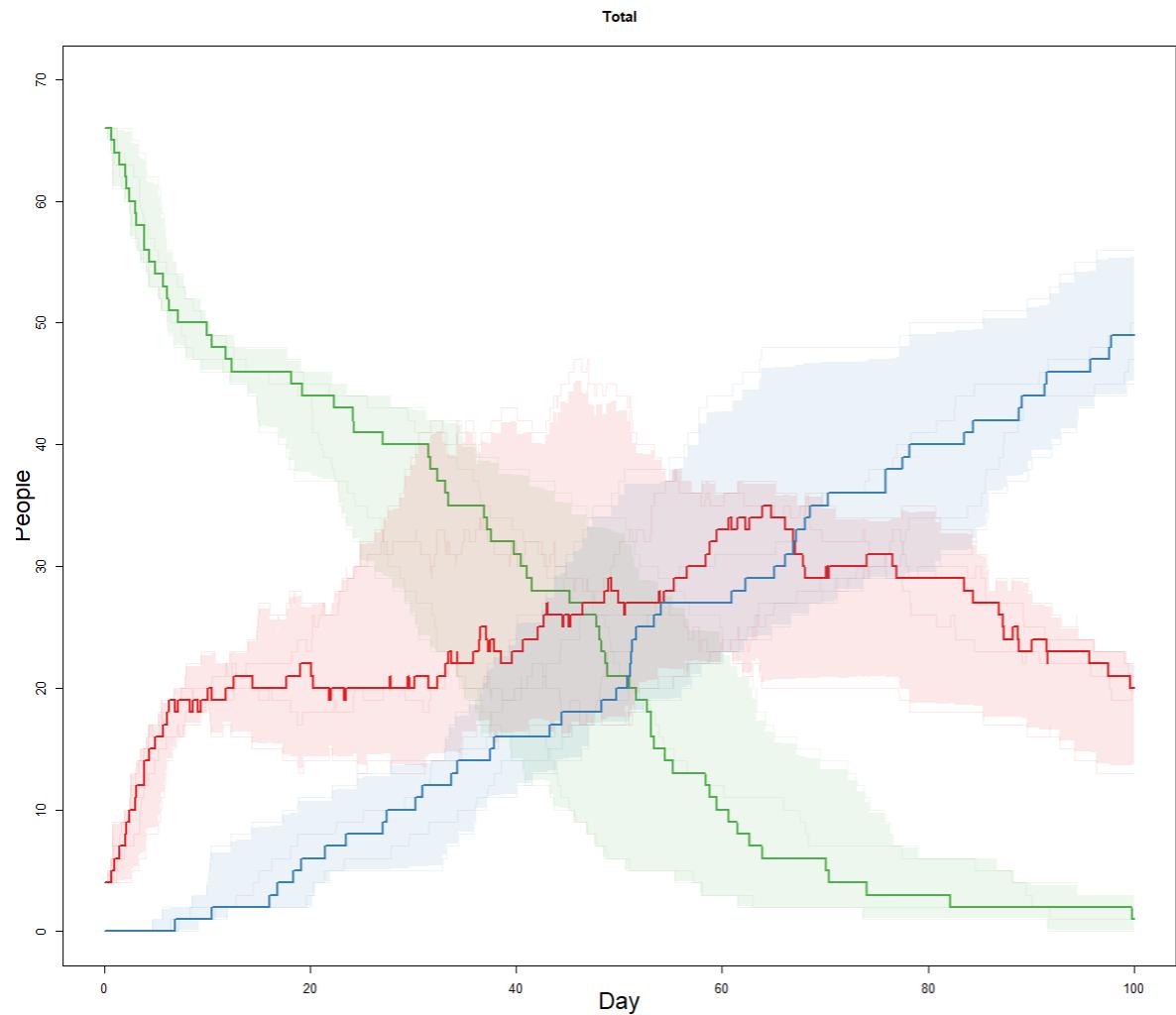
Now, for individuals in a sub-population, their probability of being infected is a function of the number of people they interact with.



# Adding heterogeneity to compartmental models

## Heterogeneous transmission questions:

1. Without selecting any additional heterogeneities and without cutting them off from other groups, create an outbreak where group 3 never sees an infection across simulations (hint: try running the same values several times...stochasticity!)
2. With 2 populations and as many heterogeneities as you'd like, create an outbreak that appears to have two phases: one, a quick rise in infecteds followed by a relatively flat but slightly increasing fraction of the population infectious over time.



[Heterogeneous models in Shiny](#)

## Drawbacks of differential equation models

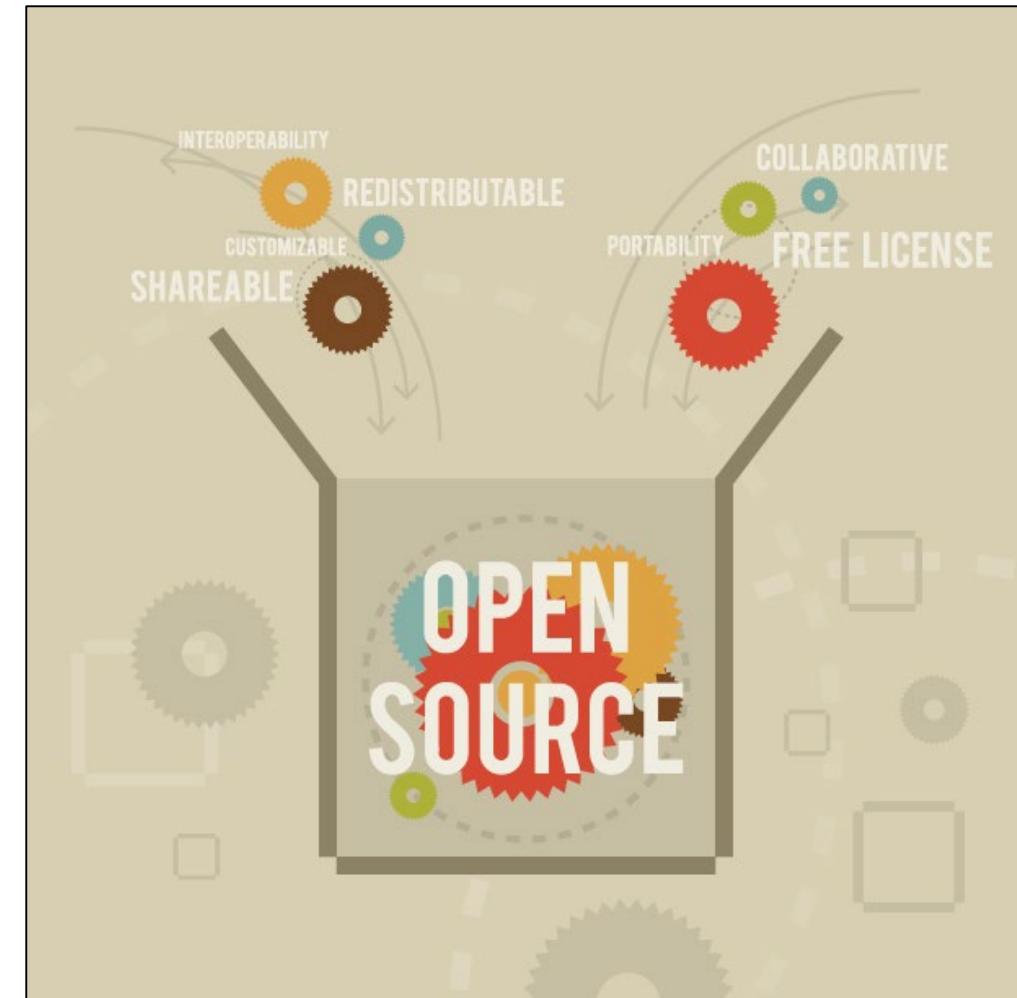
**Problem:** Difficult to include realistic interventions

**Solution:** Give up and use ABMs!

# About EMOD

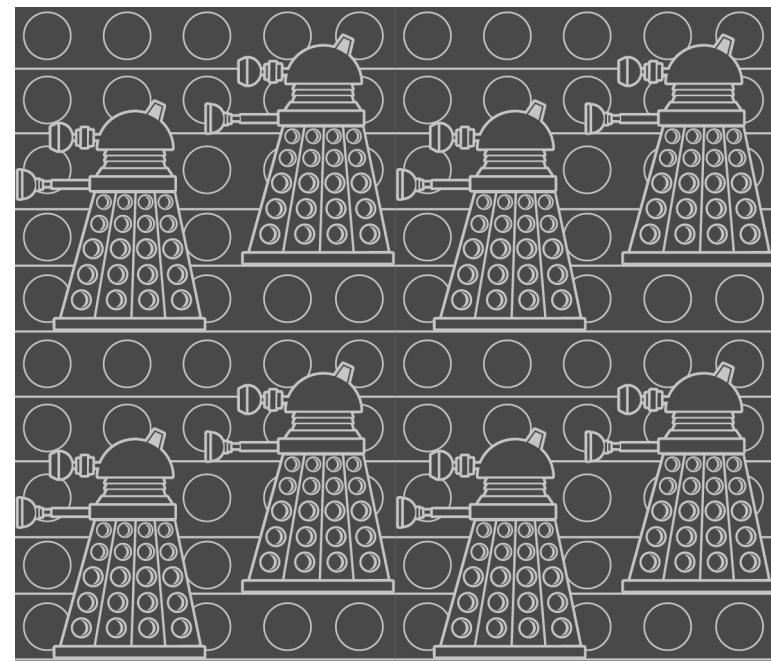
# About EMOD

- Free, open-source software (*freely use without listing IDM as a co-author*)
- Available on GitHub  
<https://github.com/InstituteforDiseaseModeling/EMOD>
- Stochastic, agent-based model
- Rigorously tested for quality and scientific accuracy

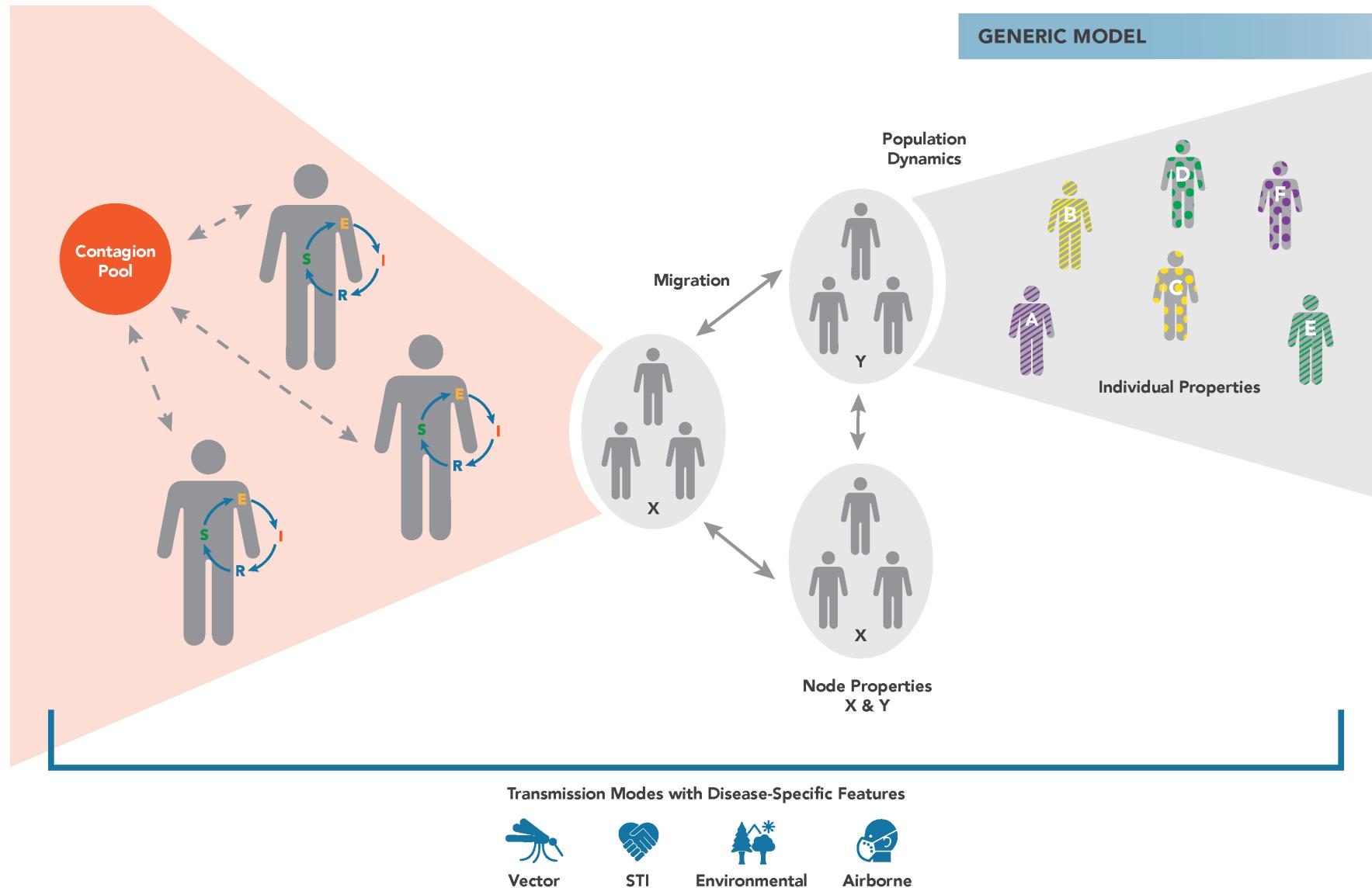


# About EMOD

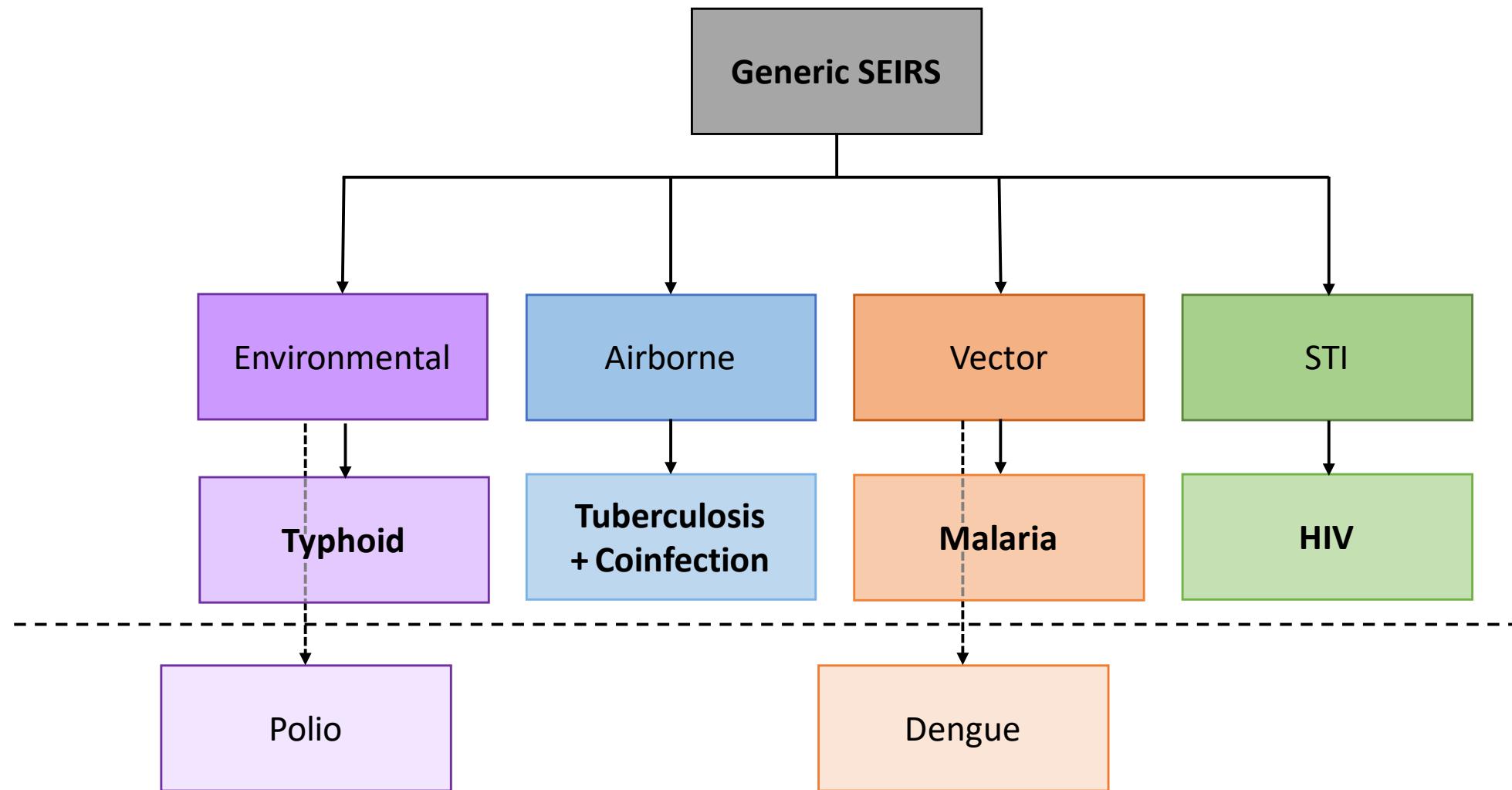
- Examine the effects of interventions to create actionable plans:
  - Conditions necessary for eradication
  - Predicted outcomes of particular strategies
  - Include complex cascade of care systems
- Flexible framework:
  - Test theoretical conditions, create simulated data
  - Simulate realistic strategies in actual locations



# About EMOD



# EMOD simulation types



# Interacting with EMOD

```
1 {  
2   "Metadata": {  
3     "DateCreated": "Sun Sep 25 23:19:55 2011",  
4     "Tool": "convertdemog.py",  
5     "Author": "jsteinkraus",  
6     "IdReference": "SampleContent",  
7     "NodeCount": 1,  
8     "Resolution": 150  
9   },  
10  "Defaults": {}  
11  },  
12  "Nodes": [  
13    {  
14      "NodeID": 1,  
15      "NodeAttributes": {  
16        "Latitude": 0,  
17        "Longitude": 0,  
18        "Altitude": 0,  
19        "Airport": 0,  
20        "Region": 1,  
21        "Seaport": 0,  
22        "InitialPopulation": 10000,  
23        "BirthRate": 0.0000548  
24      },  
25      "IndividualAttributes": {  
26        "AgeDistributionFlag": 3,  
27        "AgeDistribution1": 0.000118,  
28        "AgeDistribution2": 0,  
29        "PrevalenceDistributionFlag": 0,  
30        "PrevalenceDistribution1": 0.0,  
31        "PrevalenceDistribution2": 0.0,  
32        "ImmunityDistributionFlag": 0,  
33        "ImmunityDistribution1": 1,  
34        "ImmunityDistribution2": 0,  
35        "RiskDistributionFlag": 0,  
36        "RiskDistribution1": 1,  
37        "RiskDistribution2": 0,  
38        "MigrationHeterogeneityDistributionFlag": 0,  
39        "MigrationHeterogeneityDistribution1": 1,  
40        "MigrationHeterogeneityDistribution2": 0,  
41        "MortalityDistribution": {  
42          "NumDistributionAxes": 2,  
43          "AxisNames": [ "gender", "age" ],  
44          "AxisUnits": [ "male=0,female=1", "years" ],  
45          "AxisScaleFactors": [ 1, 365 ],  
46          "NumPopulationGroups": [ 2, 1 ],  
47          "PopulationGroups": [  
48            [ 0, 1 ],  
49            [ 0 ]  
50          ],  
51          "ResultUnits": "deaths per day",  
52          "ResultScaleFactor": 1,  
53          "ResultValues": [  
54            [ 0.0000548 ],  
55            [ 0.0000548 ]  
56          ]  
57        }  
58      }  
59    }  
60  ]  
61 }  
62 }
```

```
1 ▼ {  
2   "parameters": {  
3     "Age Initialization Distribution Type": "DISTRIBUTION_SIMPLE",  
4     "Animal_Reservoir_Type": "NO_ZOONOSIS",  
5     "Base_Incubation_Period": 0,  
6     "Base_Individual_Sample_Rate": 1,  
7     "Base_Infectious_Period": 50000,  
8     "Base_Infectivity": 0.0003653,  
9     "Base_Mortality": 0,  
10    "Base_Population_Scale_Factor": 1,  
11    "Birth_Rate_Dependence": "POPULATION_DEP_RATE",  
12    "Birth_Rate_Time_Dependence": "NONE",  
13    "Campaign_Filename": "campaign.json",  
14    "Climate_Model": "CLIMATE_OFF",  
15    "Config_Name": "SI",  
16    "Custom_Reports_Filename": "",  
17    "Death_Rate_Dependence": "NONDISEASE_MORTALITY_BY_AGE_AND_GENDER",  
18    "Default_Geography_Initial_Node_Population": 1000,  
19    "Default_Geography_Torus_Size": 10,  
20    "Demographics_Filenames": [  
21      "generic_scenarios_demographics.json"  
22    ],  
23    "Enable_Aging": 1,  
24    "Enable_Birth": 1,  
25    "Enable_Default_Report": 1,  
26    "Enable_Demographics_Birth": 0,  
27    "Enable_Demographics_Builtin": 0,  
28    "Enable_Demographics_Gender": 1,  
29    "Enable_Demographics_Report": 1,  
30    "Enable_Disease_Mortality": 0,  
31    "Enable_Heterogeneous_Intranode_Transmission": 0,  
32    "Enable_Immune_Decay": 0,  
33    "Enable_Immunity": 0,  
34    "Enable_Immunity_Distribution": 0,  
35    "Enable_Initial_Prevalence": 1,  
36    "Enable_Interventions": 1,  
37    "Enable_Maternal_Infection_Transmission": 0,  
38    "Enable_Maternal_Protection": 0,  
39    "Enable_Natural_Mortality": 1,  
40    "Enable_Property_Output": 0,  
41    "Enable_Skipping": 0,  
42    "Enable_Spatial_Output": 0,  
43    "Enable_Superinfection": 0,  
44    "Enable_Susceptibility_Scaling": 0,  
45    "Enable_Vital_Dynamics": 1  
46  }
```

```
1 ▼ {  
2   "Campaign_Name": "Initial Seeding",  
3   "Events": [  
4     {  
5       "Event_Coordinator_Config": {  
6         "Demographic_Coverage": 0.05,  
7         "Intervention_Config": {  
8           "Antigen": 0,  
9           "Genome": 0,  
10          "Outbreak_Source": "PrevalenceIncrease",  
11          "class": "OutbreakIndividual"  
12        },  
13        "Target_Demographic": "Everyone",  
14        "class": "StandardInterventionDistributionEventCoordinator"  
15      },  
16      "Event_Name": "Outbreak",  
17      "Nodeset_Config": {  
18        "class": "NodeSetAll"  
19      },  
20      "Start_Day": 30,  
21      "class": "CampaignEvent"  
22    }  
23  ],  
24  "Use_Defaults": 1  
25 }  
26  
27 }
```

Running EMOD involves looking at files in JSON format...

# Interacting with EMOD

```
1 {  
2   "Metadata": {  
3     "DateCreated": "Sun Sep 25 23:19:55 2011",  
4     "Tool": "convertdemog.py",  
5     "Author": "jsteinkraus",  
6     "IdReference": "SampleContent",  
7     "NodeCount": 1,  
8     "Resolution": 150  
9   },  
10  "Defaults": {},  
11  "Nodes": [  
12    {  
13      "NodeID": 1,  
14      "NodeAttributes": {  
15        "Latitude": 0,  
16        "Longitude": 0,  
17        "Altitude": 0,  
18        "Airport": 0,  
19        "Region": 1,  
20        "Seaport": 0,  
21        "InitialPopulation": 10000,  
22        "BirthRate": 0.0000548  
23      },  
24      "IndividualAttributes": {  
25        "AgeDistributionFlag": 3,  
26        "AgeDistribution1": 0.000118,  
27        "AgeDistribution2": 0,  
28        "PrevalenceDistributionFlag": 0,  
29        "PrevalenceDistribution1": 0.0,  
30        "PrevalenceDistribution2": 0.0,  
31        "ImmunityDistributionFlag": 0,  
32        "ImmunityDistribution1": 1,  
33        "ImmunityDistribution2": 0,  
34        "RiskDistributionFlag": 0,  
35        "RiskDistribution1": 1,  
36        "RiskDistribution2": 0,  
37        "MigrationHeterogeneityDistributionFlag": 0,  
38        "MigrationHeterogeneityDistribution1": 1,  
39        "MigrationHeterogeneityDistribution2": 0,  
40        "MortalityDistribution": {  
41          "NumDistributionAxes": 2,  
42          "AxisNames": [ "gender", "age" ],  
43          "AxisUnits": [ "male=0,female=1", "years" ],  
44          "AxisScaleFactors": [ 1, 365 ],  
45          "NumPopulationGroups": [ 2, 1 ],  
46          "PopulationGroups": [  
47            [ 0, 1 ],  
48            [ 0 ]  
49          ],  
50          "ResultUnits": "deaths per day",  
51          "ResultScaleFactor": 1,  
52          "ResultValues": [  
53            [ 0.0000548 ],  
54            [ 0.0000548 ]  
55          ]  
56        }  
57      }  
58    }  
59  ]  
60 }  
61 }
```

```
1 ▼ {  
2   "parameters": {  
3     "Age Initialization Distribution Type": "DISTRIBUTION_SIMPLE",  
4     "Animal_Reservoir_Type": "NO_ZOONOSIS",  
5     "Base_Incubation_Period": 0,  
6     "Base_Individual_Sample_Rate": 1,  
7     "Base_Infectious_Period": 50000,  
8     "Base_Infectivity": 0.0003653,  
9     "Base_Mortality": 0.8,  
10    "Base_Population_Scale_Factor": 1,  
11    "Birth_Rate_Dependence": "POPULATION_DEPENDENT",  
12    "Birth_Rate_Time_Dependence": "NONE",  
13    "Campaign_Filename": "campaign.json",  
14    "Climate_Model": "CLIMATE_OFF",  
15    "Config_Name": "SI",  
16    "Custom_Reports_Filename": "",  
17    "Disease_Heterogeneity": "HOMOGENEOUS_HOMOPATHIC_BY_AGE_AND_GENDER"  
18  }  
19  "Base_Infectivity": 0.0003653,  
20  "Base_Mortality": 0.8,  
21  "Base_Population_Scale_Factor": 1,  
22  "Birth_Rate_Dependence": "POPULATION_DEPENDENT",  
23  "Birth_Rate_Time_Dependence": "NONE",  
24  "Enable_birth": 1,  
25  "Enable_Default_Report": 1,  
26  "Enable_Demographics_Birth": 0,  
27  "Enable_Demographics_Builtin": 0,  
28  "Enable_Demographics_Gender": 1,  
29  "Enable_Demographics_Report": 1,  
30  "Enable_Disease_Mortality": 0,  
31  "Enable_Heterogeneous_Intranode_Transmission": 0,  
32  "Enable_Immune_Decay": 0,  
33  "Enable_Immunity": 0,  
34  "Enable_Immunity_Distribution": 0,  
35  "Enable_Initial_Prevalence": 1,  
36  "Enable_Interventions": 1,  
37  "Enable_Maternal_Infection_Transmission": 0,  
38  "Enable_Maternal_Protection": 0,  
39  "Enable_Natural_Mortality": 1,  
40  "Enable_Property_Output": 0,  
41  "Enable_Skipping": 0,  
42  "Enable_Spatial_Output": 0,  
43  "Enable_Superinfection": 0,  
44  "Enable_Susceptibility_Scaling": 0,  
45  "Enable_Vital_Dynamics": 1  
46 }  
47 }
```

```
1 ▼ {  
2   "Campaign_Name": "Initial Seeding",  
3   "Events": [  
4     {  
5       "Event_Coordinator_Config": {  
6         "Demographic_Coverage": 0.05,  
7         "Intervention_Config": {  
8           "Antigen": 0,  
9           "Genome": 0,  
10          "Outbreak_Source": "PrevalenceIncrease",  
11          "class": "OutbreakIndividual"  
12        },  
13        "Target_Demographic": "Everyone",  
14        "class": "StandardInterventionDistributionEventCoordinator"  
15      },  
16      "Event_Name": "Outbreak",  
17      "Nodeset_Config": {  
18        "class": "NodeSetAll"  
19      },  
20      "Start_Day": 30,  
21      "class": "CampaignEvent"  
22    }  
23  ],  
24  "Use_Defaults": 1  
25 }  
26  
27 }
```

Running EMOD involves looking at files in JSON format... but we have a more fun way to learn the model!

# EMOD's QuickStart: overview

quickstart.idmod.org

The screenshot shows the 'QuickStart to Disease Modeling' interface. It features a grid of 12 modules, each with an icon and a brief description:

- GENERAL**: QuickStart Introduction
- PROGRAMMING GENERAL**: JSON and programming
- GENERAL EPIDEMIOLOGY**: SIR models
- GENERAL EPIDEMIOLOGY**: Comparing EMOD to SIR models
- DEMOGRAPHICS**: Population initialization
- DEMOGRAPHICS**: Vital dynamics
- EPIDEMIOLOGY**: Intradust infection
- CAMPAIGN**: Interventions
- PROGRAMMING GENERAL**: Explore input files

**Modular lessons to explore particular aspects of the model**

Explore the function of related sets of parameters

The screenshot shows the 'Configure births' section of the EMOD configuration interface.

**Configure births**

In the demographics file, you will set the birth rate across the entire population. However, until births are enabled (by setting `Enable_Birth` to 1 in the configuration file), this birth rate will not be used.

EMOD also provides the capability of configuring the fertility rate distribution for the population, but fertility is not covered in this lesson. However, fertility rate distribution can be set up in much the same way as mortality distribution, which is covered below.

**EXERCISE**

**BirthRate**

After you enable births by setting `Enable_Birth` to 1, you can set several other parameters in the configuration file to determine how the birth rate set in the demographics file is used. For example, you can scale the rate up or down or make it dependent upon other characteristics like fertility rate, maternal age, or population size.

Keeping the birth rate in the demographics file, separate from the configuration parameters that indicate how to use that rate enables you to easily create multiple configuration files to model different scenarios while maintaining the same demographics file for a particular region.

**Enable\_Birth**

<code>x_Birth</code>	300
<code>Birth_Rate_Time_Dependence</code>	NONE
<code>Birth_Rate_Dependence</code>	FIXED_BIRTH_RATE

**Chart these values**

**Enable aging**

Unless aging is enabled in the configuration file, individuals in a simulation will remain the same age throughout the simulation. When aging is turned on, their age will be incremented automatically at each time step and those that reach the maximum age (125 years) will die.

**Enable Aging**

**Enable mortality**

In the configuration file, you can enable deaths in the simulation and indicate how the mortality rates set in the demographics file will be used. Depending on this setting, the simulated daily mortality rate can be adjusted based on age and gender or age and year for each gender. In this

**Graphs update dynamically**

**JSON files**

Config file Campaign file Demographics file COMPS

**JSON code**

```
1. {
2.   "parameters": {
3.     "Age_Initialization_Distribution_Type": "DISTRIBUTION_SIMPLE",
4.     "Animal_Reservoir_Type": "NO_ZOONOSIS",
5.     "Base_Population_Scale_Factor": 1,
6.     "Birth_Rate_Boxcar_Forcing_Amplitude": 0,
7.     "Birth_Rate_Boxcar_Forcing_End_Time": 0,
8.     "Birth_Rate_Boxcar_Forcing_Start_Time": 0,
9.     "Birth_Rate_Dependence": "FIXED_BIRTH_RATE",
10.    "Birth_Rate_Sinusoidal_Forcing_Amplitude": 0,
11.    "Birth_Rate_Sinusoidal_Forcing_Phase": 0,
12.    "Birth_Rate_Time_Dependence": "NONE",
13.    "Death_Rate_Dependence": "NONDISEASE_MORTALITY_BY_AGE_AND_GENDER",
14.    "Enable_Birth": 1,
15.    "Enable_Demographics_Birth": 0,
16.    "Enable_Demographics_Gender": 1,
17.    "Enable_Demographics_Other": 0,
18.    "Enable_Demographics_Risk": 0,
19.    "Enable_Immunity_Distribution": 0,
20.    "Enable_Initial_Prevalence": 0,
21.    "Enable_Maternal_Transmission": 0,
22.    "Enable_Vital_Dynamics": 1,
23.    "Immune_Threshold_For_Downsampling": 0,
24.    "Maternal_Transmission_Probability": 0,
25.    "Population_Scale_Type": "USE_INPUT_FILE",
26.    "x_Birth": 1000,
27.    "x_Other_Mortality": 1
28.  }
```

**JSON input files update dynamically**

**Population** Deaths/Day Deaths/Mo Births/Day Births/Mo

Population

COUNT DAYS

515  
512.5  
510  
507.5  
505  
502.5  
500  
497.5

# QuickStart lessons

## Lesson 1: Population initialization

<https://quickstart.idmod.org/#PopulationInitialization>

- **Exercises:**
  - Change the Age\_Initialization\_Distribution\_Type to “DISTRIBUTION\_SIMPLE.” Now you have the option for changing the type of distribution the population follows with the AgeDistributionFlag parameter. Spend time going through each of the distribution types. Does the graph reflect what you expect the population to look like?

# QuickStart lessons

## Lesson 2: Using interventions

<https://quickstart.idmod.org/#intervention>

- The event (when and where) and event coordinator (who) is static
- Change only the intervention itself
- Exercises:
  - Can you make the intervention prevent 50% of infections?
  - Play with the WaningEffect parameters. Note how much of an impact waning efficacy has on the number of infections.

## EMOD features: Individual properties

Recall some of the limitations of compartmental models. It is very difficult to:

- Add heterogeneity or individual attributes
- Target population groups for interventions

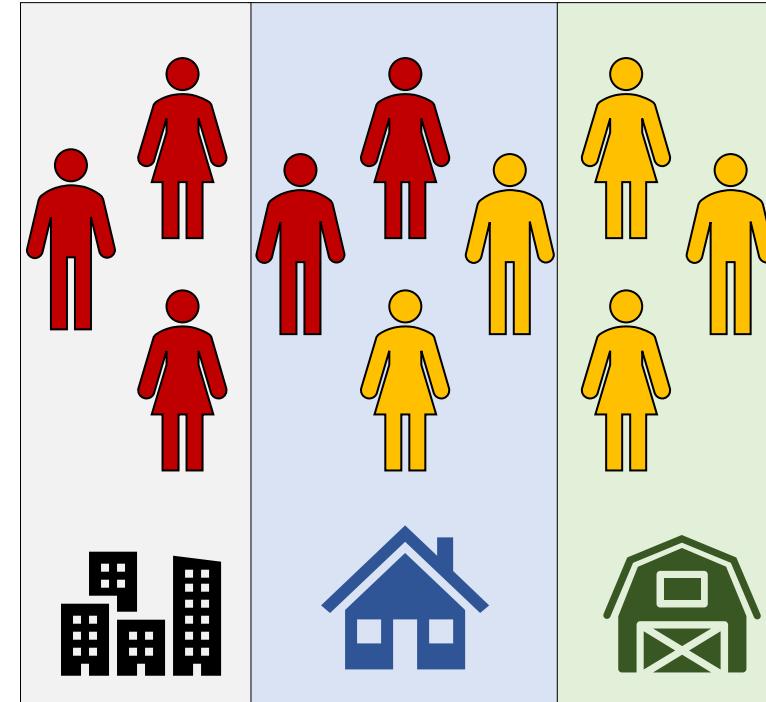
For example, can you model differences in efficacy of interventions if someone has nutrient deficiencies?

YES you can! EMOD is very good at doing these tasks: its power and flexibility stems from a feature called **individual properties**! You can add properties to individuals without modifying code or requiring new parameters.

# EMOD features: Individual properties

## What are **individual properties**:

- Define groups & target individuals:
  - Risk level
  - Place/geography
  - Socioeconomic status
  - Proximity to health centers
  - **ETC!**
- Multiple purposes:
  - Targeted campaigns and interventions
  - Heterogeneous intranode transmission, or HINT
  - Use for custom output reports



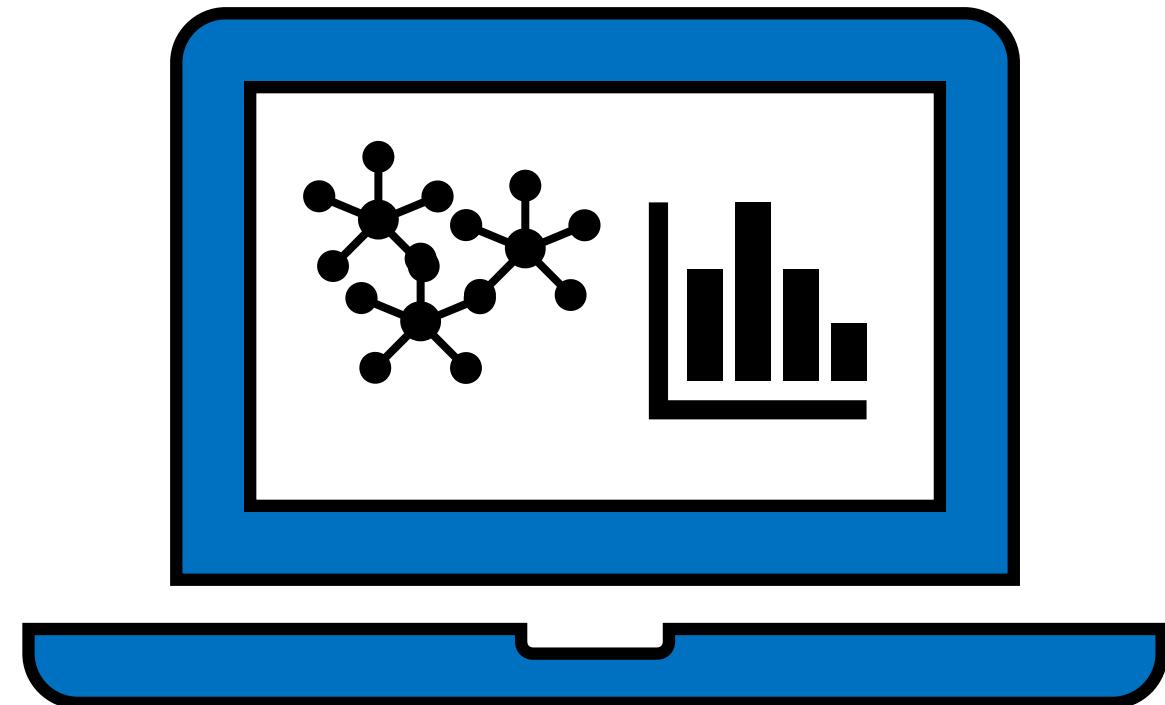
# QuickStart lessons

## Lesson 3: Using individual properties

<https://quickstart.idmod.org/#individualproperties>

- Assigning and targeting based on individual properties
- Use to create targeted campaigns
- **Exercises:**
  - How would you target high-risk individuals who receive high quality care?
  - How would you target anyone who is high risk **or** receives high quality care?

## Part 2: Diving into EMOD



# EMOD simulation scenarios

## Included on your IDM thumb drive:

- To log-in, the username is “research” and the password is “IDM”
- All input files needed to run simulations for 30+ scenarios that demonstrate EMOD capabilities, including those for different disease models
  - Double click on scripts to run the scenario or plot results
  - README files that describe each scenario
- R wrappers provided for all scenarios that will be used during this workshop
  - Run multiple iterations of the simulation (stochasticity!)
  - Change parameter values
  - Plot output

# EMOD simulation scenarios

## Requirements to run EMOD simulations:

- Windows (local runs):
  - Prerequisites: Microsoft packages and R
  - Thumb drive with scenario files and R wrapper
  - (Optional) Python 3.6 or 3.7: Python plotting scripts are provided for all 30+ scenarios
- Booting from the thumb drive will enable you to run EMOD locally with NO software installation!

# EMOD simulation scenarios: SEIR model

**Objective:** Using an R script to alter EMOD and visualize output, familiarize yourself with the options for a basic SEIR model.

Using the R script '**SEIR.r**', you can alter the duration of infectiousness.

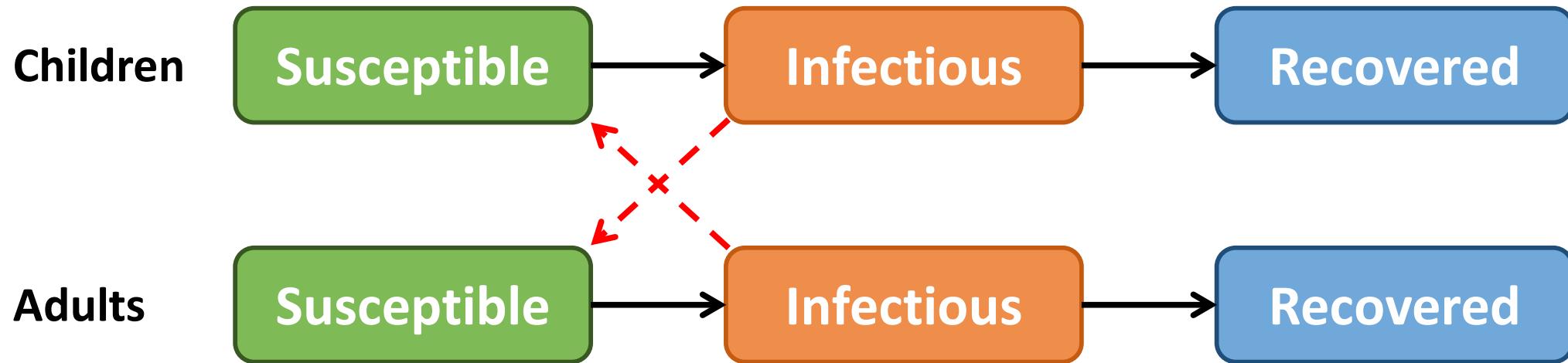
First, change Base\_Incubation\_Period to Incubation\_Period\_Constant, and  
Base\_Infectious\_Period to Infectious\_Period\_Constant.

## Exercises:

1. Can you make there be more people in the infectious category than the exposed category **at the time when the exposed category reaches its maximum?**

This goal can be achieved in multiple ways. You only have to alter the parameters described above, but feel free to try to alter other aspects of EMOD if you feel comfortable.

## Advanced EMOD features: Heterogeneous disease transmission (HINT)



$$\frac{dS_c}{dt} = -S_c(\beta_{cc}I_c + \beta_{ac}I_a) - \delta S_c$$

$$\frac{dI_c}{dt} = S_c(\beta_{cc}I_c + \beta_{ac}I_a) - \gamma_c I_c - \delta I_c$$

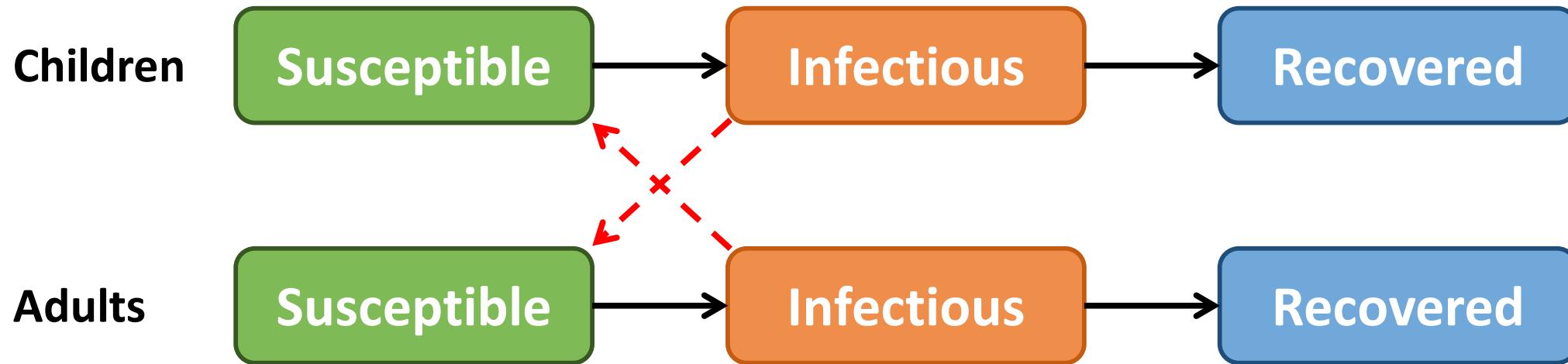
$$\frac{dR_c}{dt} = \gamma_c I_c - \delta R_c$$

$$\frac{dS_a}{dt} = -S_a(\beta_{ca}I_c + \beta_{aa}I_a) + \delta S_c$$

$$\frac{dI_a}{dt} = S_a(\beta_{ca}I_c + \beta_{aa}I_a) - \gamma_a I_a + \delta I_c$$

$$\frac{dR_a}{dt} = \gamma_a I_a + \delta R_c$$

## Advanced EMOD features: Heterogeneous disease transmission (HINT)



$$\frac{dS_c}{dt} = -S_c \beta_0 (\beta_{cc} I_c + \beta_{ac} I_a) - \delta S_c$$

$$\frac{dI_c}{dt} = S_c \beta_0 (\beta_{cc} I_c + \beta_{ac} I_a) - \gamma_c I_c - \delta I_c$$

$$\frac{dR_c}{dt} = \gamma_c I_c - \delta R_c$$

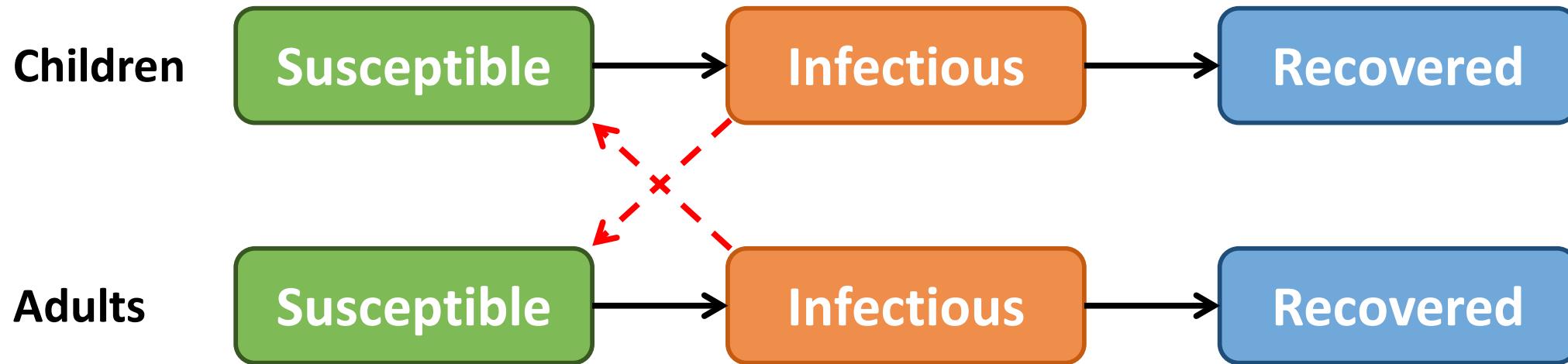
$$\frac{dS_a}{dt} = -S_a \beta_0 (\beta_{ca} I_c + \beta_{aa} I_a) + \delta S_c$$

$$\frac{dI_a}{dt} = S_a \beta_0 (\beta_{ca} I_c + \beta_{aa} I_a) - \gamma_a I_a + \delta I_c$$

$$\frac{dR_a}{dt} = \gamma_a I_a + \delta R_c$$

Now,  $\beta_{cc}$ ,  $\beta_{ca}$ ,  $\beta_{ac}$ , and  $\beta_{aa}$  represents the deviation in infectiousness from baseline

## Advanced EMOD features: Heterogeneous disease transmission (HINT)

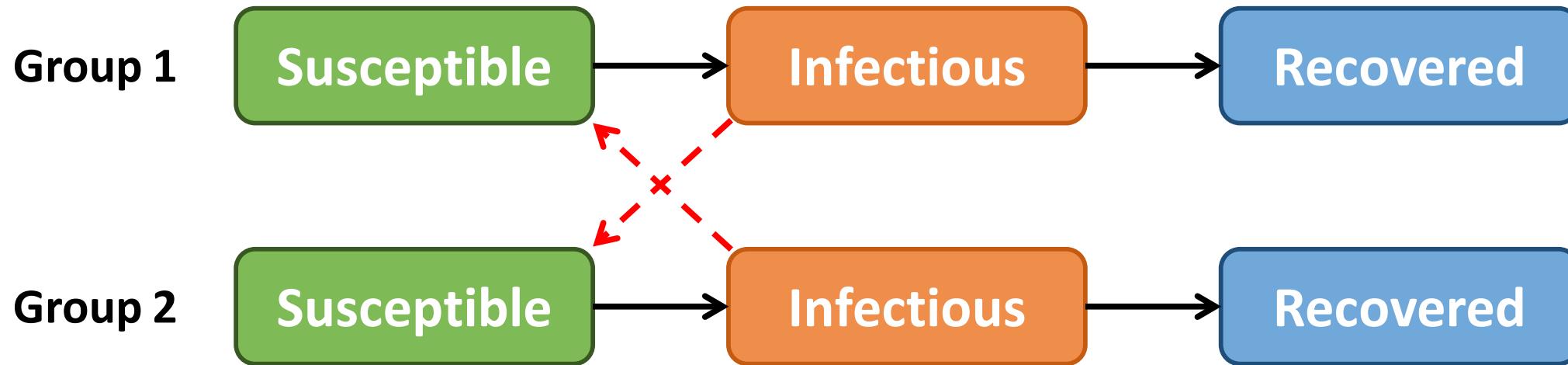


$$\frac{dS_c}{dt} = -S_c \beta_0 (\beta_{cc} I_c + \beta_{ac} I_a) - \delta S_c$$

$$\frac{dI_c}{dt} = S_c \beta_0 (\beta_{cc} I_c + \beta_{ac} I_a) - \gamma_c I_c - \delta I_c$$

$$\frac{dR_c}{dt} = \gamma_c I_c - \delta R_c$$

## Advanced EMOD features: Heterogeneous disease transmission (HINT)

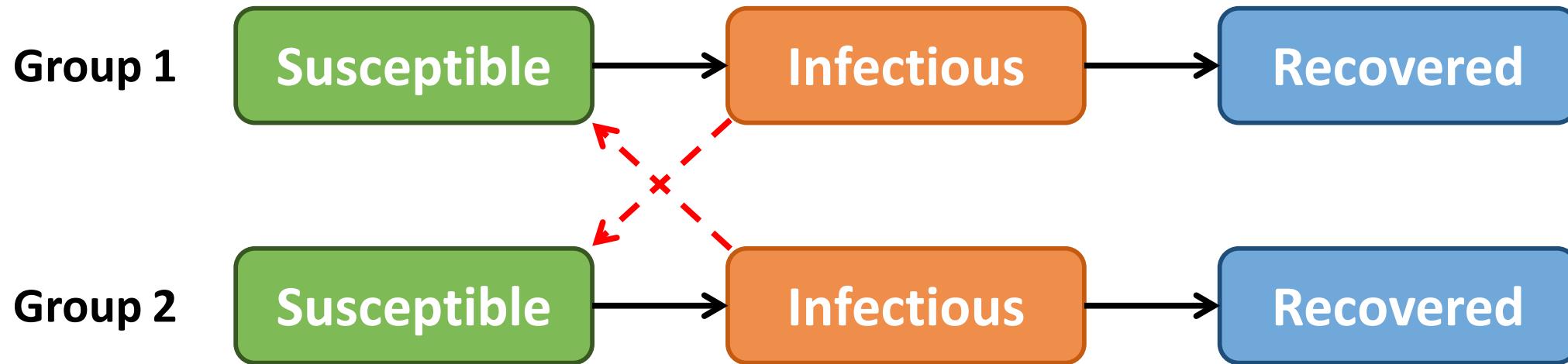


$$\frac{dS_c}{dt} = -S_c \beta_0 (\beta_{cc} I_c + \beta_{ac} I_a) - \delta S_c$$

$$\frac{dI_c}{dt} = S_c \beta_0 (\beta_{cc} I_c + \beta_{ac} I_a) - \gamma_c I_c - \delta I_c$$

$$\frac{dR_c}{dt} = \gamma_c I_c - \delta R_c$$

## Advanced EMOD features: Heterogeneous disease transmission (HINT)

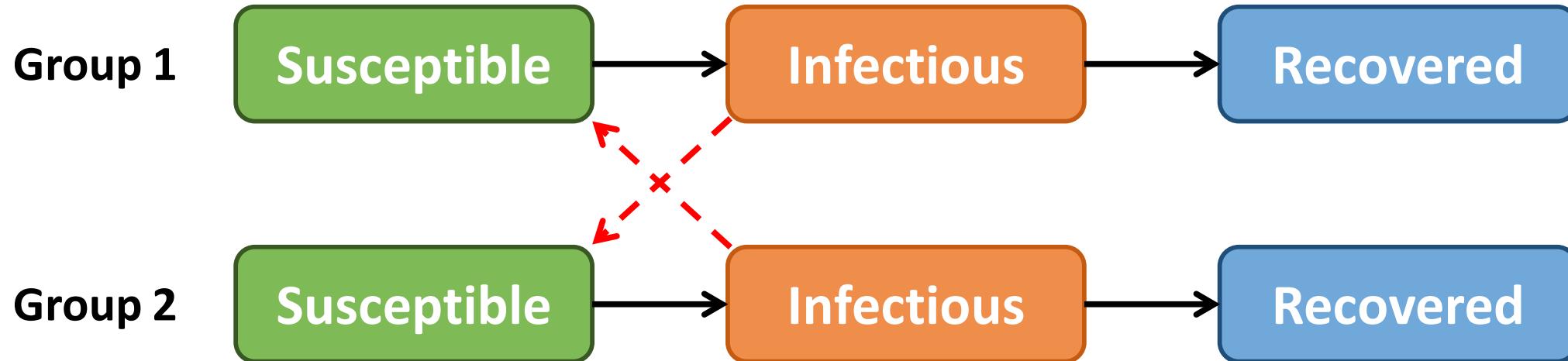


$$\frac{dS_1}{dt} = -S_1\beta_0(\beta_{11}I_1 + \beta_{21}I_2) - \delta S_1$$

$$\frac{dI_1}{dt} = S_1\beta_0(\beta_{11}I_1 + \beta_{21}I_2) - \gamma_1 I_1 - \delta I_1$$

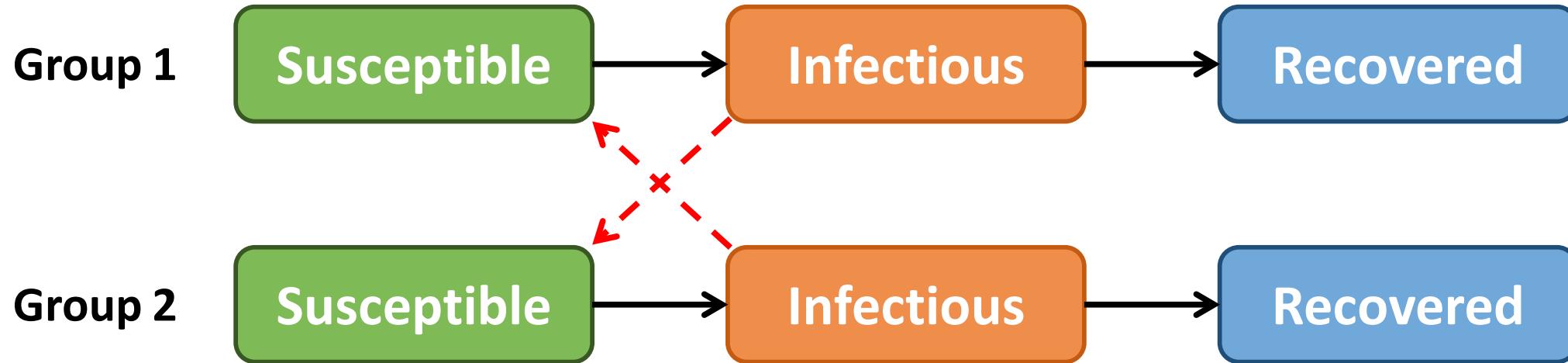
$$\frac{dR_c}{dt} = \gamma_1 I_1 - \delta R_1$$

## Advanced EMOD features: Heterogeneous disease transmission (HINT)



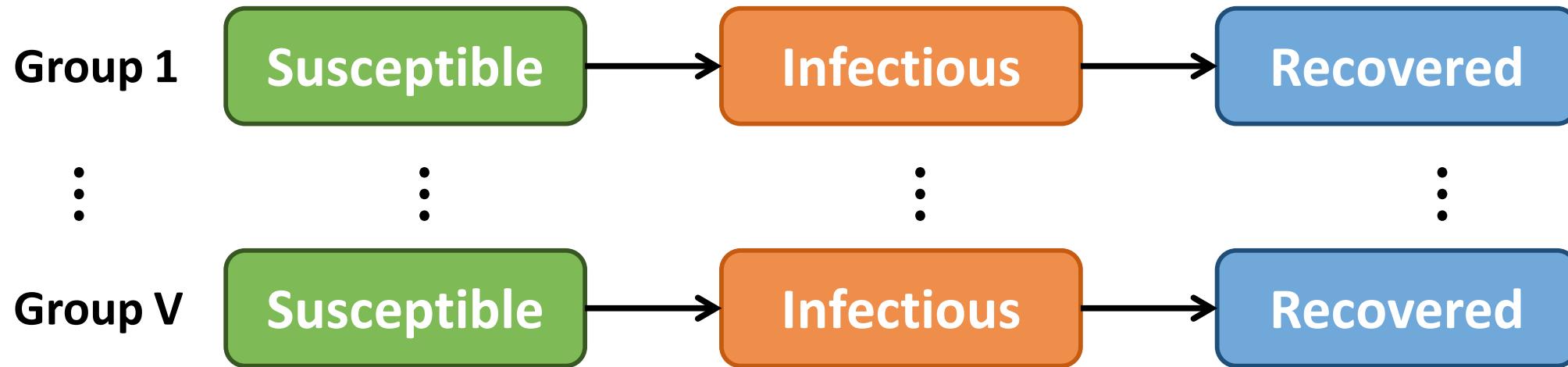
$$\frac{dX_1}{dt} = \nu N - \frac{X_1 \beta_0 (\beta_{11} Y_1 + \beta_{21} Y_2)}{N} - \mu X_1$$
$$\frac{dY_1}{dt} = \frac{X_1 \beta_0 (\beta_{11} Y_1 + \beta_{21} Y_2)}{N} - \gamma_1 Y_1 - \mu Y_1$$
$$\frac{dZ_1}{dt} = \gamma_1 Y_1 - \mu Z_1$$

# Advanced EMOD features: Heterogeneous disease transmission (HINT)



$$\begin{aligned}\frac{dX_i}{dt} &= \nu N - \frac{X_i \beta_0 (\beta_{ii} Y_i + \beta_{ji} Y_j)}{N} - \mu X_i \\ \frac{dY_i}{dt} &= \frac{X_i (\beta_{ii} Y_i + \beta_{ji} Y_j)}{N} - \gamma_i Y_i - \mu Y_i \\ \frac{dZ_i}{dt} &= \gamma_i Y_i - \mu Z_i\end{aligned}$$

# Advanced EMOD features: Heterogeneous disease transmission (HINT)

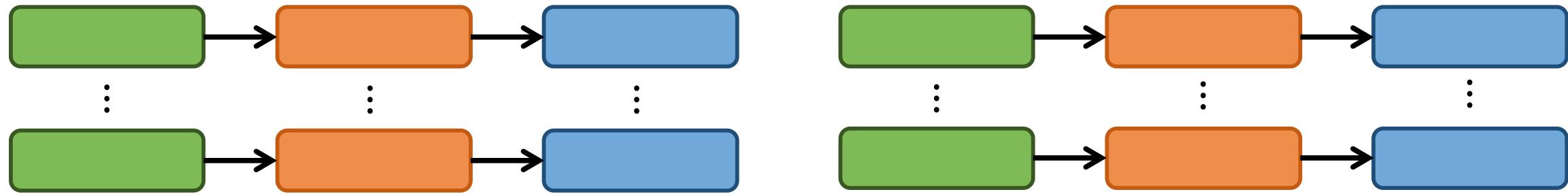


$$\frac{dX_v}{dt} = \nu_v N - \frac{\beta_0 X_v}{N} \sum_{k=1}^V \beta_{jv} Y_k - \mu_v X_v$$

$$\frac{dY_v}{dt} = \frac{\beta_0 X_v}{N} \sum_{k=1}^V \beta_{jv} Y_k - \gamma_v Y_v - \mu_v Y_v$$

$$\frac{dZ_v}{dt} = \gamma_v Y_v - \mu_v Z_v$$

# Advanced EMOD features: Heterogeneous disease transmission (HINT)



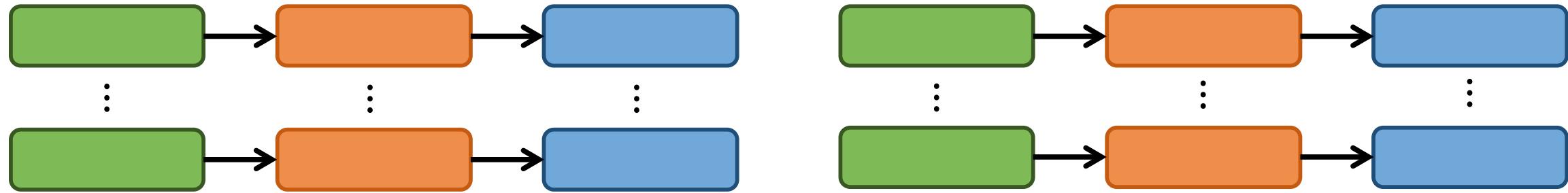
We can have multiple individual properties, each with many levels. If, for property  $p$ , we have a multiplier matrix

$$[\beta^p]_{ij}$$

we can ‘simply’ expand the model

$$\begin{aligned}\frac{dX_\nu}{dt} &= \nu_\nu N - \frac{\beta_0 X_\nu}{N} \sum_{k=1}^V \beta_{j\nu} Y_k - \mu_\nu X_\nu \\ \frac{dY_\nu}{dt} &= \frac{\beta_0 X_\nu}{N} \sum_{k=1}^V \beta_{j\nu} Y_k - \gamma_\nu Y_\nu - \mu_\nu Y_\nu \\ \frac{dZ_\nu}{dt} &= \gamma_\nu Y_\nu - \mu_\nu Z_\nu\end{aligned}$$

# Advanced EMOD features: Heterogeneous disease transmission (HINT)



We can have multiple individual properties, each with many levels. If, for property  $p$ , we have a multiplier matrix

$$[\beta^p]_{ij}$$

we can ‘simply’ expand the model

$$\begin{aligned}\frac{dX_{v_1 v_2}}{dt} &= \nu_{v_1 v_2} N - \frac{\beta_0 X_{v_1 v_2}}{N} \sum_{k_1=1}^{V_1} \sum_{k_2=1}^{V_2} [\beta^{p_1}]_{k_1 v_1} [\beta^{p_2}]_{k_2 v_2} Y_{k_1 k_2} - \mu_{v_1 v_2} X_{v_1 v_2} \\ \frac{dY_{v_1 v_2}}{dt} &= \frac{\beta_0 X_{v_1 v_2}}{N} \sum_{k_1=1}^{V_1} \sum_{k_2=1}^{V_2} [\beta^{p_1}]_{k_1 v_1} [\beta^{p_2}]_{k_2 v_2} Y_{k_1 k_2} - \gamma_{v_1 v_2} Y_{v_1 v_2} - \mu_{v_1 v_2} Y_{v_1 v_2} \\ \frac{dZ_{v_1 v_2}}{dt} &= \gamma_{v_1 v_2} Y_{v_1 v_2} - \mu_{v_1 v_2} Z_{v_1 v_2}\end{aligned}$$

# Advanced EMOD features: Heterogeneous disease transmission (HINT)

**Heterogeneous Intra-Node Transmission (HINT):** enables the user to configure different (heterogeneous) disease transmission between different groups within a node.

- Each group is defined by **IndividualProperties** in the **demographics** file.
- To use HINT:
  - **IndividualProperties** attribute must have a **TransmissionMatrix** (defined in the **demographics** file)
  - **Enable\_Heterogeneous\_Intranode\_Transmission** must be set to 1 (true) in the **config.json** file
  - Set **Base\_Infectivity** in the **config.json** file. The transmission matrix will modify this parameter

# Advanced EMOD features: Heterogeneous disease transmission (HINT)

## Transmission matrix:

- $n \times n$  matrix where  $n$  is the number of groups defined in **IndividualProperties**.
- Each value in the matrix is the transmission rate,  $\beta$ , which will scale the base infectivity,  $\beta_0$  (as set by the config parameter **Base\_Infectivity**).
- Rows represent *from* whom the disease is transmitted and columns represent *to* whom the disease is transmitted

## Example showing transmission between “high-risk” and “low-risk” groups:

```
{  
  "IndividualProperties": [ {  
    "Property": "Risk", ← Property name (“Risk”)  
    "Values": ["High", "Low"], ← The order in which the properties are listed (“High” is “low”)  
    "TransmissionMatrix": {  
      "Route": "Contact",  
      "Matrix": [  
        [10, 0.1], ← high risk → high risk  
        [0.1, 1] ← low risk → high risk  
      ]  
    }  
  }]  
}
```

The order in which the properties are listed (“High” is “low”) determines what the matrix represents:

high risk → high risk      high risk → low risk  
low risk → high risk      low risk → low risk

<https://idmod.org/docs/general/model-hint.html>

# Advanced EMOD features: Heterogeneous disease transmission (HINT)

Multiple properties can be combined to increase heterogeneity in transmission.

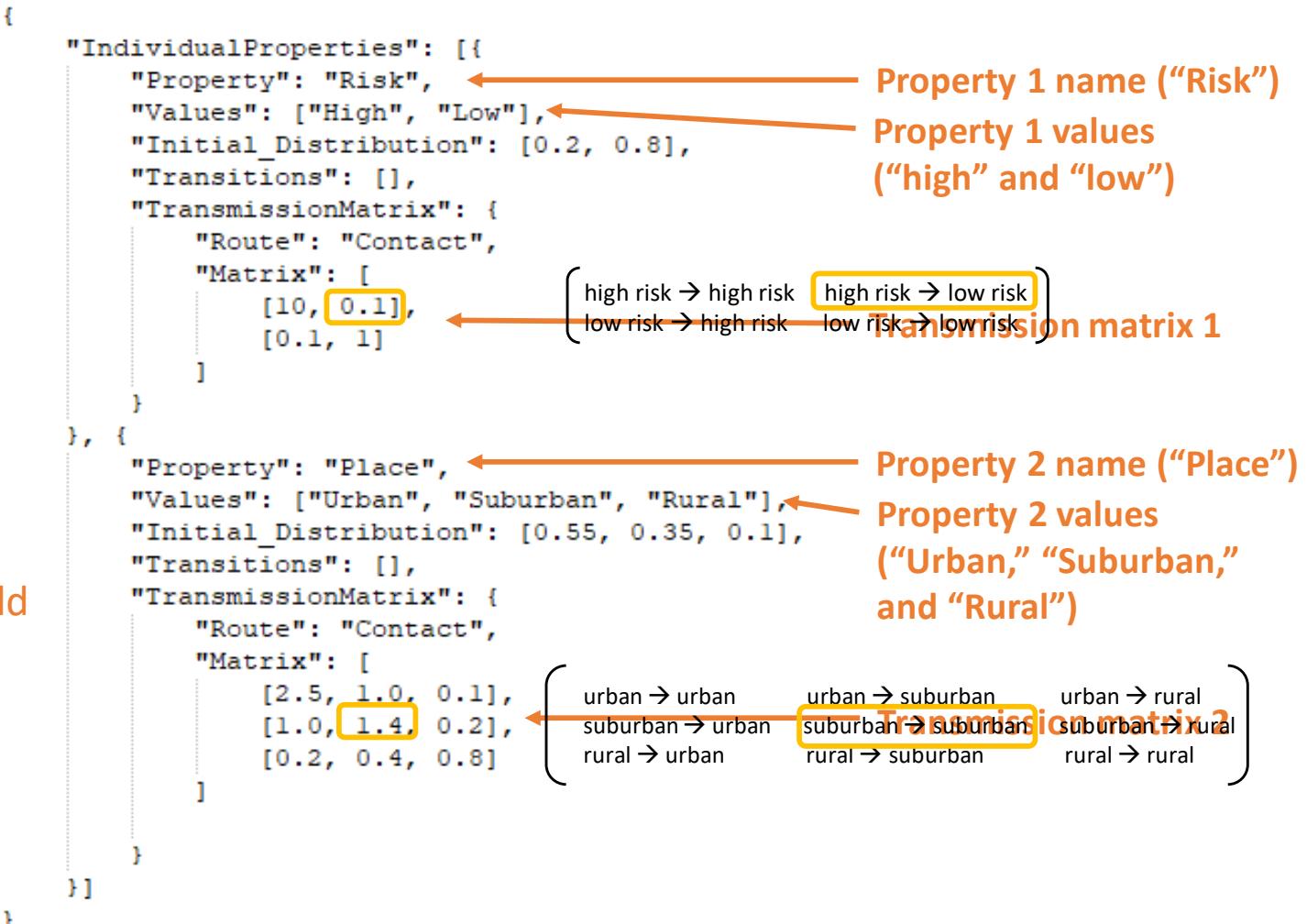
- Effects are combined independently via multiplication

## Example showing transmission with two properties: “Risk” and “Place”

The transmission rate multiplier,  $\beta$ , for someone who is **high risk** and **suburban** when interacting with someone who is **low risk** and **suburban** would be:  $0.1 \times 1.4 = 0.14$

**high risk → low risk = 0.1**

**suburban → suburban = 1.4**



# EMOD simulation scenarios: HINT model

**Objective:** Using a R script to alter EMOD and visualize output, familiarize yourself with the options for the more advanced HINT model.

Using the R script '**HINT\_A.r**', you can now alter the transmission matrices as well as **Base\_Infectivity**. First, change Base\_Incubation\_Period to Incubation\_Period\_Constant, and Base\_Infectious\_Period to Infectious\_Period\_Constant.

## Exercises:

1. Can you prevent the outbreak from ever reaching one of the groups?
2. Try to achieve the largest gap in time between the peak of the outbreak in the earliest group and the peak of the outbreak in the latest group. For this exercise, define “peak of the outbreak” for a group as when “percent infectious” is at its maximum.

Both of these goals can be achieved in multiple ways. You only have to alter the parameters described above, but feel free to try to alter other aspects of EMOD if you feel comfortable.

# EMOD simulation scenarios: HINT model **with interventions**

Using the HINT structure, we can now implement targeted intervention campaigns.

**Objective:** Using a R script to alter EMOD and visualize output, assess the impact of various targeted intervention campaigns on an outbreak.

Using the R script '**HINT\_B.r**', you have all the capabilities of the previous script, plus you can design your own targeted intervention.

## **Exercises:**

1. Try to run a scenario where the intervention is perfect, everyone accepts it, it hits all ages, and starts on day 50. What do you notice about the number of infectious people on day 51 versus day 50 (hint: there is an error in the script)?

Change `Base_Incubation_Period` to `Incubation_Period_Constant`, and `Base_Infectious_Period` to `Infectious_Period_Constant`.

# EMOD simulation scenarios: HINT model **with interventions**

## Exercises:

2. This question will look into the relationship between vaccine intervention campaign and cases averted.
  - a) Run the outbreak with (a) no intervention at all and (b) the ‘perfect’ vaccine intervention from question 1, but implemented at day 20. How many cases were averted?
  - b) Assume a more realistic intervention. Configure the vaccine to be 95% effective and only reach 95% of the targeted population. Finally, assume that you can only reach certain age groups (here, you can reach any 5 consecutive ages). Running this new vaccination campaign at day 15, what is the optimal 5-year age range for the intervention?
  - c) Is the age range you identified the most *efficient*? Here, we calculate efficiency as the number of cases averted per number of vaccines distributed.
  - d) Bonus: repeat b) and c) but you can only vaccinate a single age. What decisions would you make with a limited amount of resources?
  - e) Bonus: Make the pathogen twice as infective (Base\_Infectivity). How does this change your answers?

# EMOD simulation scenarios: HINT model **with interventions**

## Useful code:

```
sum(CumSumIs[, , 1, 365])
TotOut <- sapply(1:30, function(x) sum(CumSumIs[, , x, 365]))
mean(TotOut)
mean(TotOut[TotOut > 0])

output_PR
output_IC
output_IC$Channels$`CampaignCost`$Data[365]
```

## EMOD simulation scenarios: HINT model with interventions (part II)

We can target interventions by numerous individual properties. Let's consider interventions based on access.

**Objective:** Using an R script to alter EMOD and visualize output, assess the impact of targeted intervention campaigns based on access.

Using the R script '**HINT\_C.r**', we can repeat the exercise from before, but now the intervention focuses only on those who are easy to access. It (currently) ignores age.

As before, change `Base_Incubation_Period` to `Incubation_Period_Constant`, and `Base_Infectious_Period` to `Infectious_Period_Constant`.

### Exercises:

1. Vaccinate everyone who is “easy” to access on day 20. How many cases do you avert? How many vaccinations did you use?

# EMOD simulation scenarios: HINT model with interventions (part II)

## Exercises:

2. This advanced question will require you to alter the campaign file more than you have before. This will be in 2 steps.
  1. Within **C\_AccessTargetedVaccines**, create a duplicate **campaign.json** and call it **campaign\_new.json**. Open both this file and the campaign file from **B\_AgeTargetedVaccine**. Find where in the “B” campaign file we are specifying the age range of the intervention. Likewise, find in the “C” new campaign file where we are specifying to vaccinate everyone. Replace the code in the new campaign with the code from the “B” campaign.
  2. Now, within the R script for **HINT\_C**, find where we define the campaign file. Add “\_new” to the appropriate location. Finally, uncomment the lines where we want to alter the age range of the population receiving the intervention.

Run the script to see if this worked. If it fails spectacularly, repeat steps 1 and 2. **Do not** save over any of the original campaign files.

Now, on to the question...

# EMOD simulation scenarios: HINT model with interventions (part II)

## Exercises:

2. We are now prepared to vaccinate subsets of the ‘easy to access’ population. As with the previous exercise, we want to evaluate relative efficiency of different interventions.
  - a) Configure the vaccine to be 95% effective and only reach 95% of the targeted population. Finally, assume that you can only reach certain age groups (now, you can reach any 10 consecutive ages). Running this new vaccination campaign at day 15, what is the optimal 10-year age range for the intervention? Is the age range you identified the most *efficient*? How does it compare to the previous exercise when you could vaccinate all people but only in 5 year age bins?
  - b) Bonus: Knowing the age distribution helps. Using the QuickStart (and the appropriate demographic file), can you change the age distribution to something else? For example, how does everything change if you have a log-Normal age distribution?
  - c) Bonus: See if you can create a cost / benefit curve of interventions as a function of age range start and day of intervention.
  - d) Bonus: Make the pathogen twice as infective (Base\_Infectivity). How does this change your answers?

## Additional advanced EMOD features

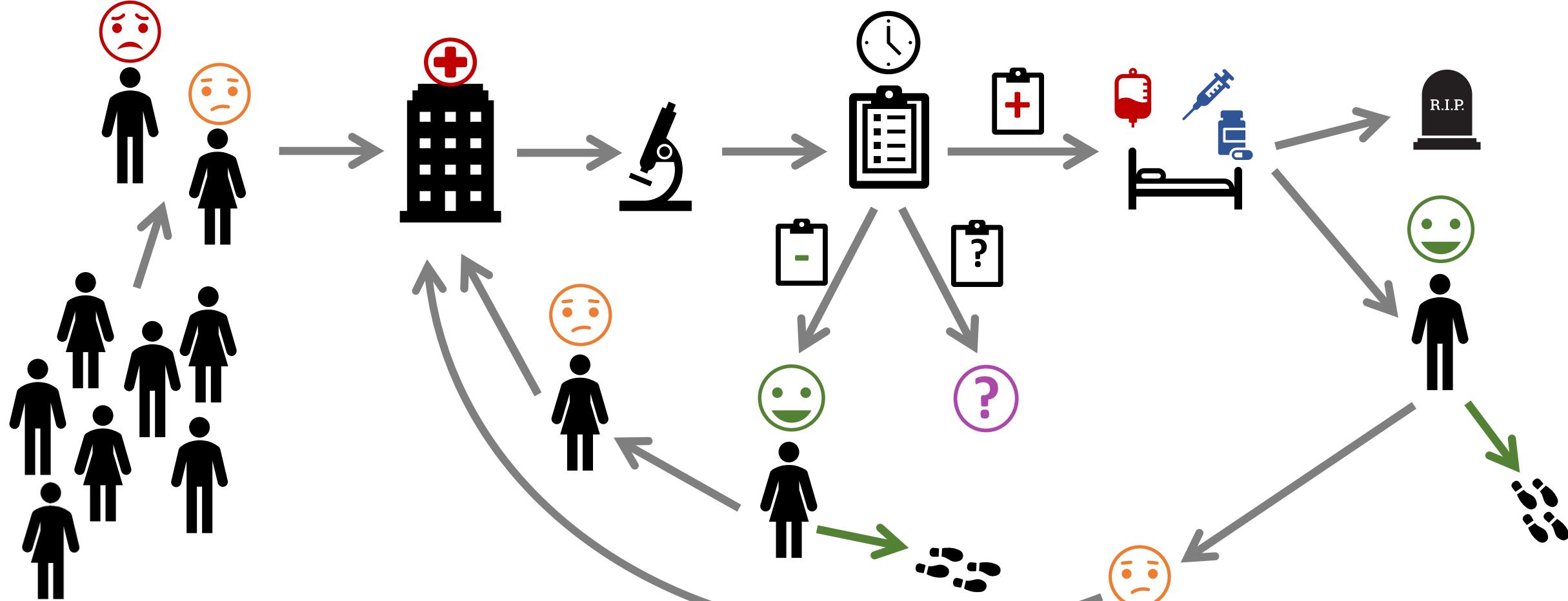
## Additional advanced EMOD features

- Cascade of care & health systems
- Numerous micro-solvers for detailed information on agent behavior
- Integration of climate data into specific simulation types
- Disease-specific features for different transmission modes
- Migration and nodes (including node properties), and the ability to recreate specific geography

## Additional advanced EMOD features

- Cascade of care & health systems
- Numerous micro-solvers for detailed information on agent behavior
- Integration of climate data into specific simulation types
- Disease-specific features for different transmission modes
- Migration and nodes (including node properties), and the ability to recreate specific geography

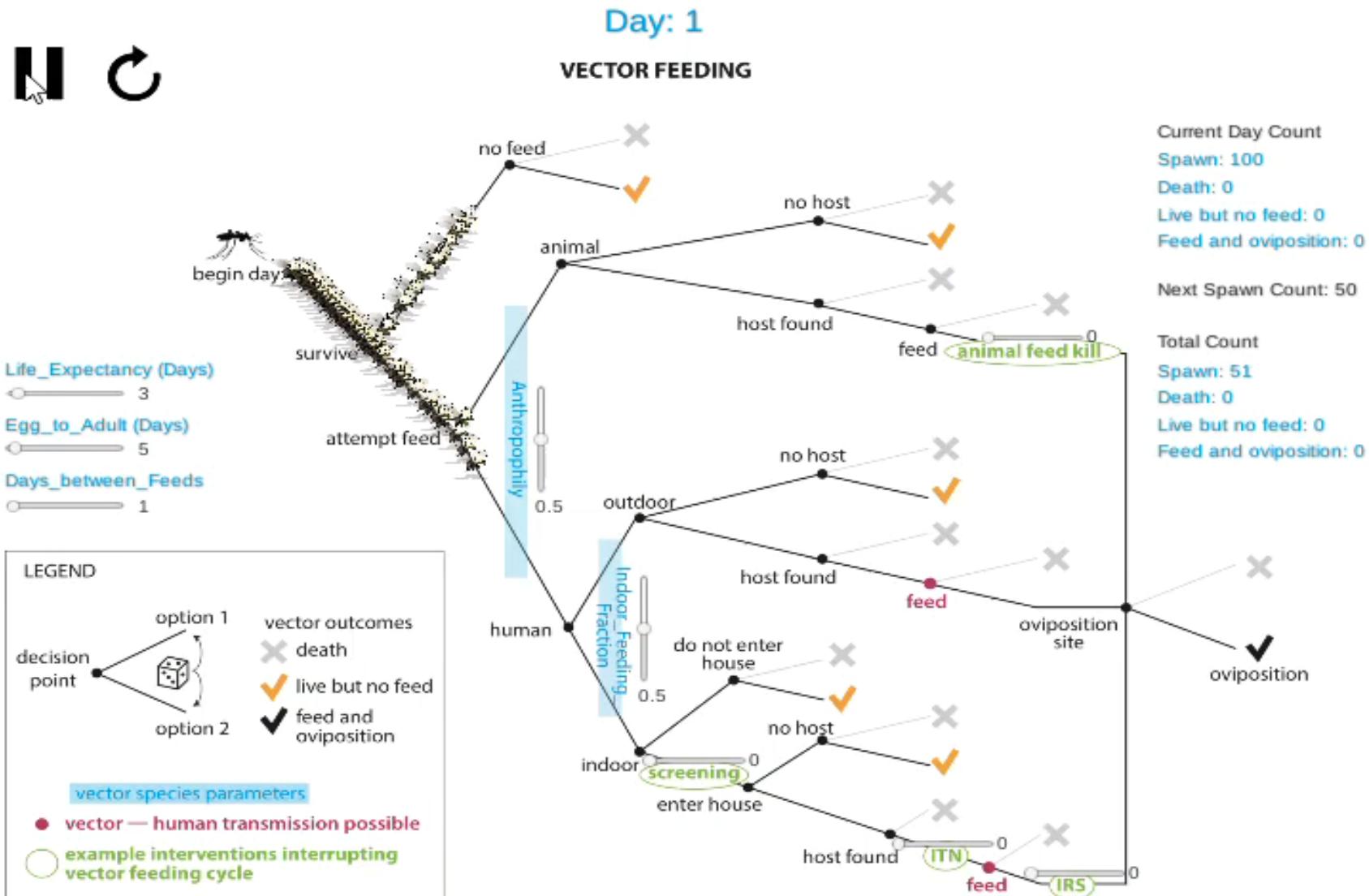
## Advanced EMOD features: Cascade of care



## Additional advanced EMOD features

- Cascade of care & health systems
- Numerous micro-solvers for detailed information on agent behavior
- Integration of climate data into specific simulation types
- Disease-specific features for different transmission modes
- Migration and nodes (including node properties), and the ability to recreate specific geography

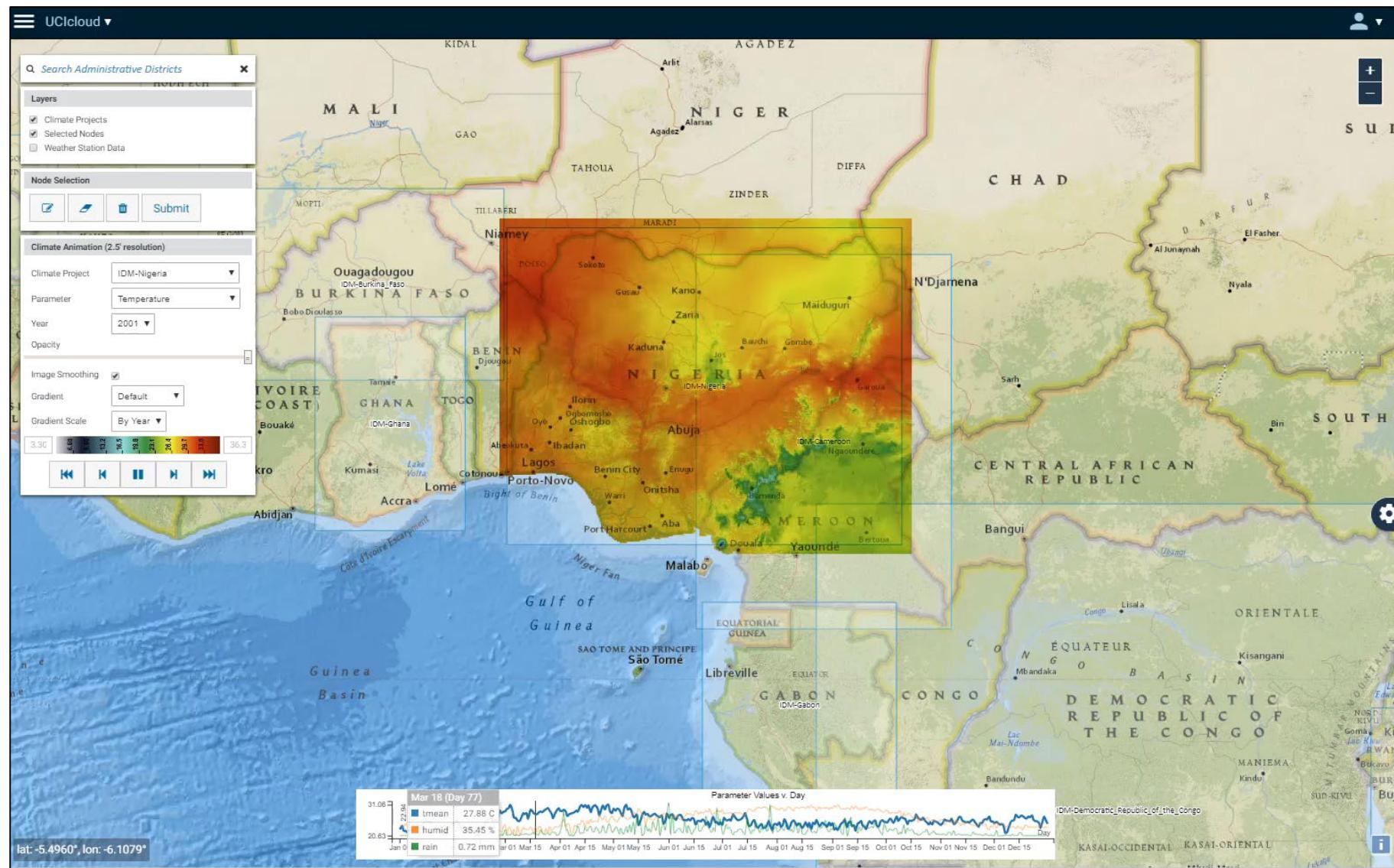
# Advanced EMOD features: Detailed micro-solvers (Ex: vector feeding)



## Additional advanced EMOD features

- Cascade of care & health systems
- Numerous micro-solvers for detailed information on agent behavior
- **Integration of climate data into specific simulation types**
- Disease-specific features for different transmission modes
- Migration and nodes (including node properties), and the ability to recreate specific geography

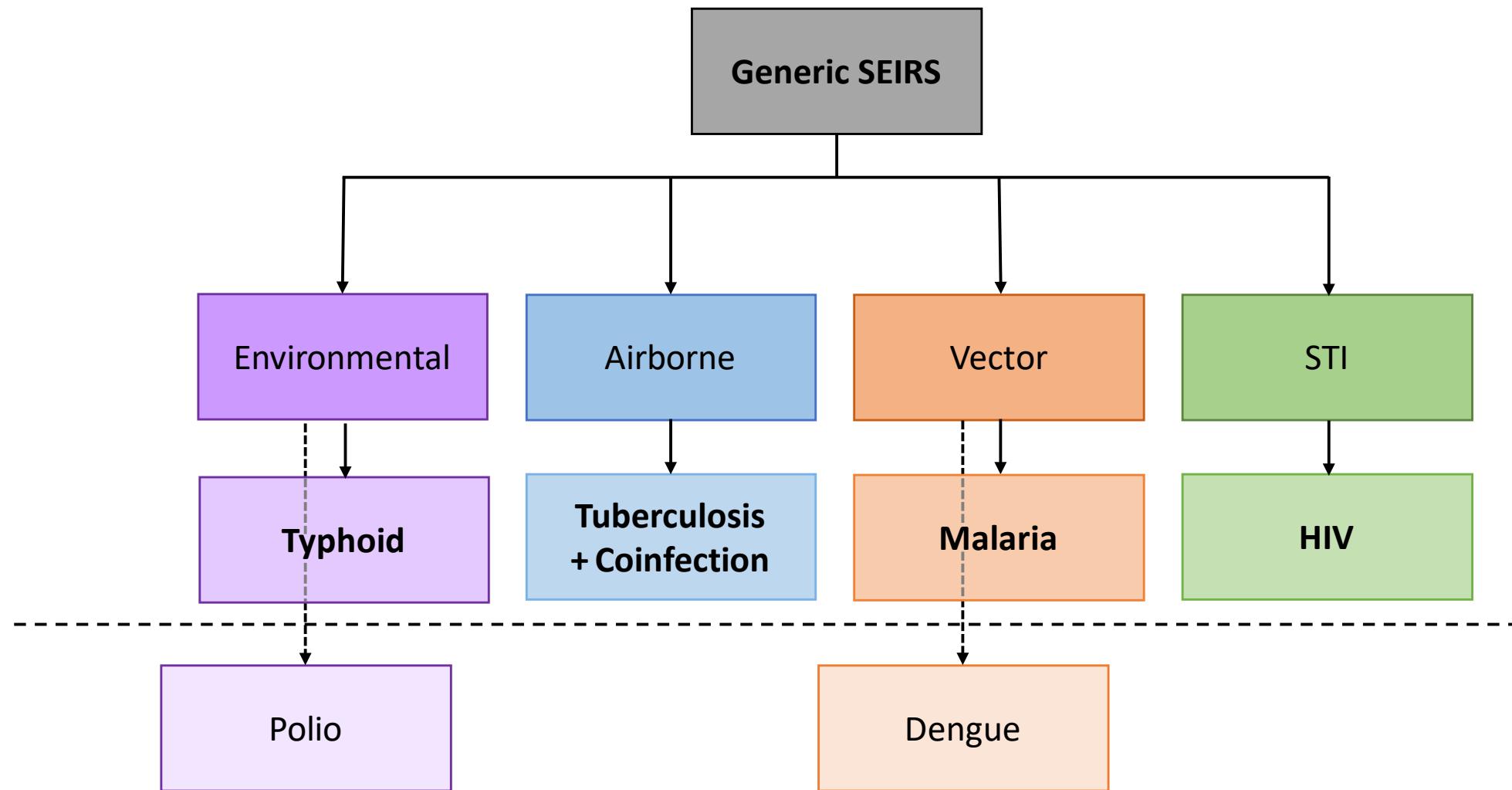
# Advanced EMOD features: Integrate climate data into simulations



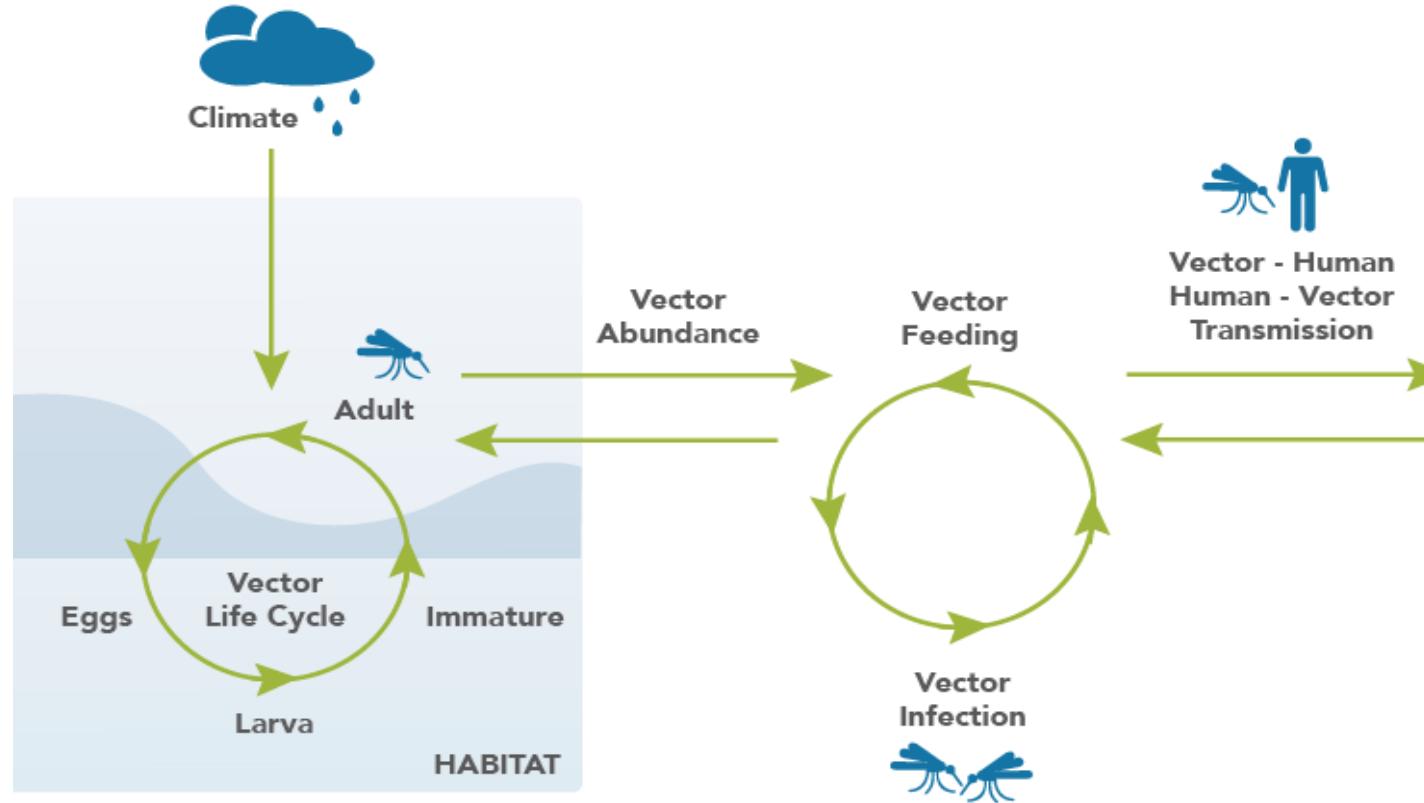
## Additional advanced EMOD features

- Cascade of care & health systems
- Numerous micro-solvers for detailed information on agent behavior
- Integration of climate data into specific simulation types
- Disease-specific features for different transmission modes
- Migration and nodes (including node properties), and the ability to recreate specific geography

# EMOD simulation types

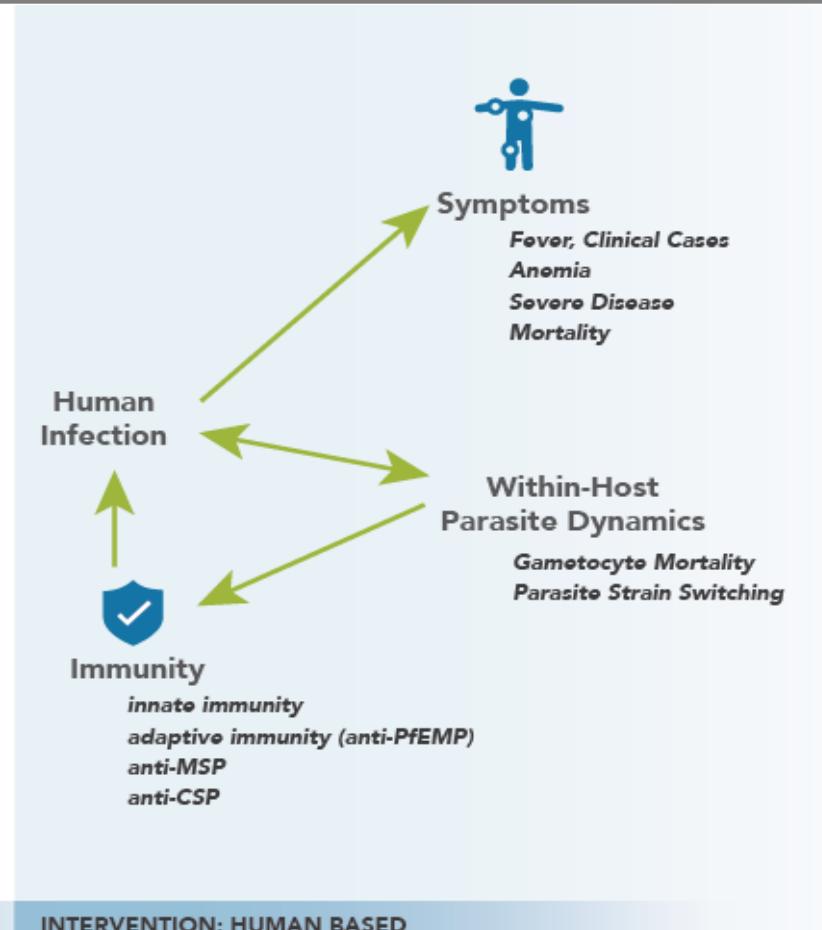


# Advanced EMOD features: Disease-specific functionality - MALARIA



## INTERVENTION: VECTOR CONTROL

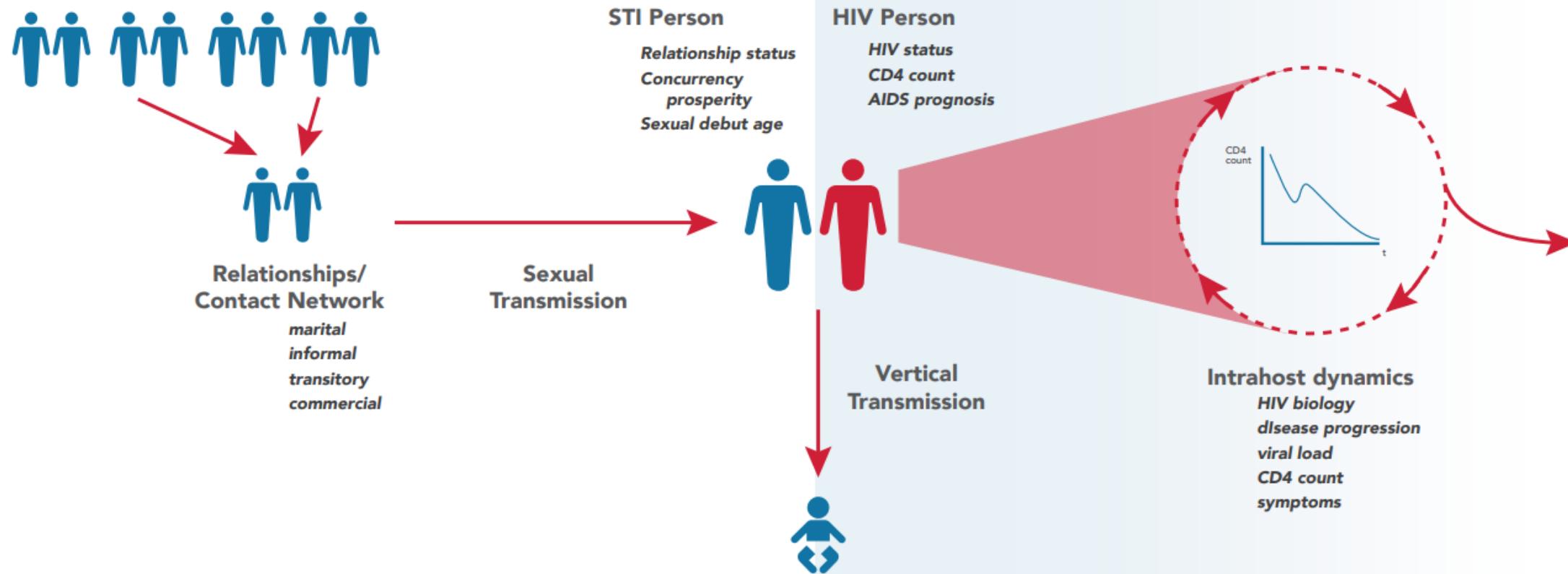
- bed nets
- house screening
- indoor residual spraying
- traps
- larvicides
- larval habitat draining
- mosquito release



## INTERVENTION: HUMAN BASED

- vaccines
- diagnostics
- anti-malarial drugs
- ivermectin

# Advanced EMOD features: Disease-specific functionality - HIV



## INTERVENTION: BEHAVIORAL

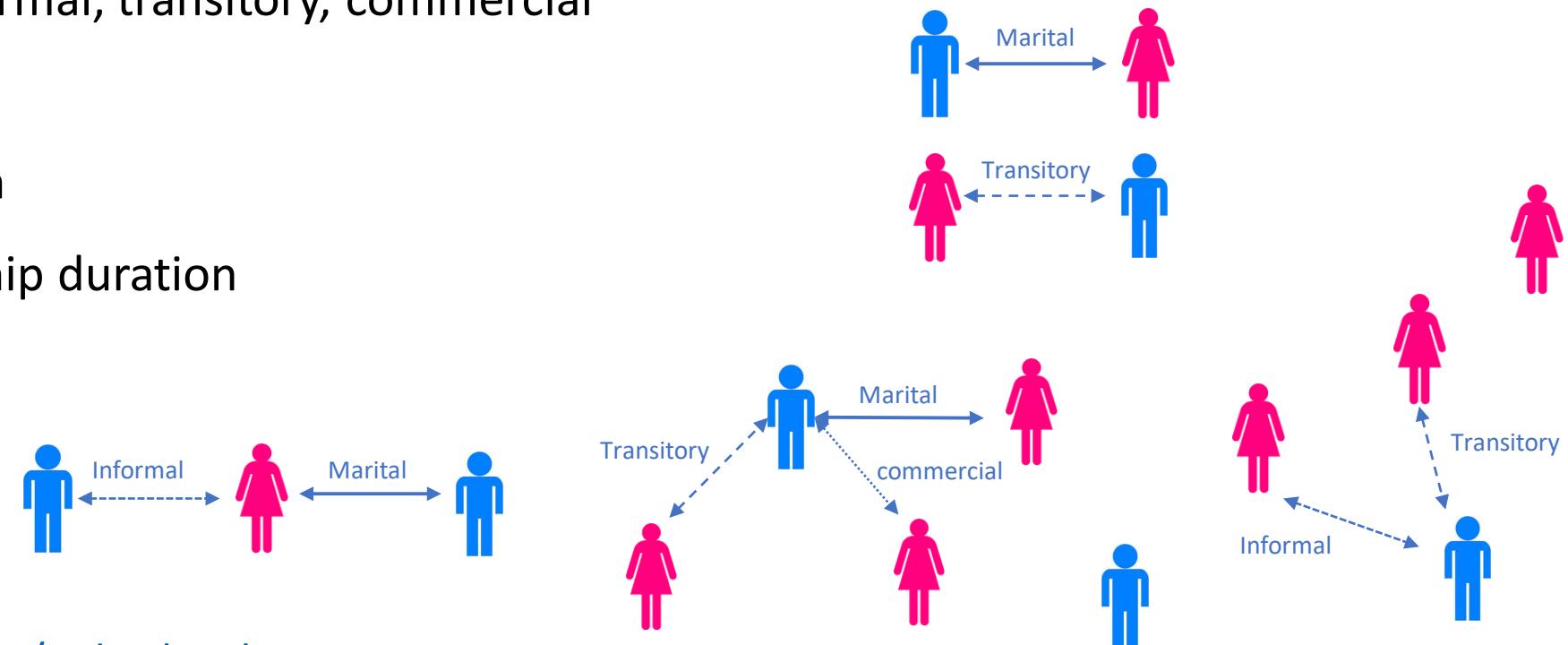
Condom usage  
HIV testing  
Reduction of multiple partnerships  
Sex work

## INTERVENTION: BIOLOGICAL

ART (antiretroviral therapy)  
PMTCT (prevention of mother to child transmission)  
PrEP (pre-exposure prophylaxis)  
Vaccine  
Male medical circumcision

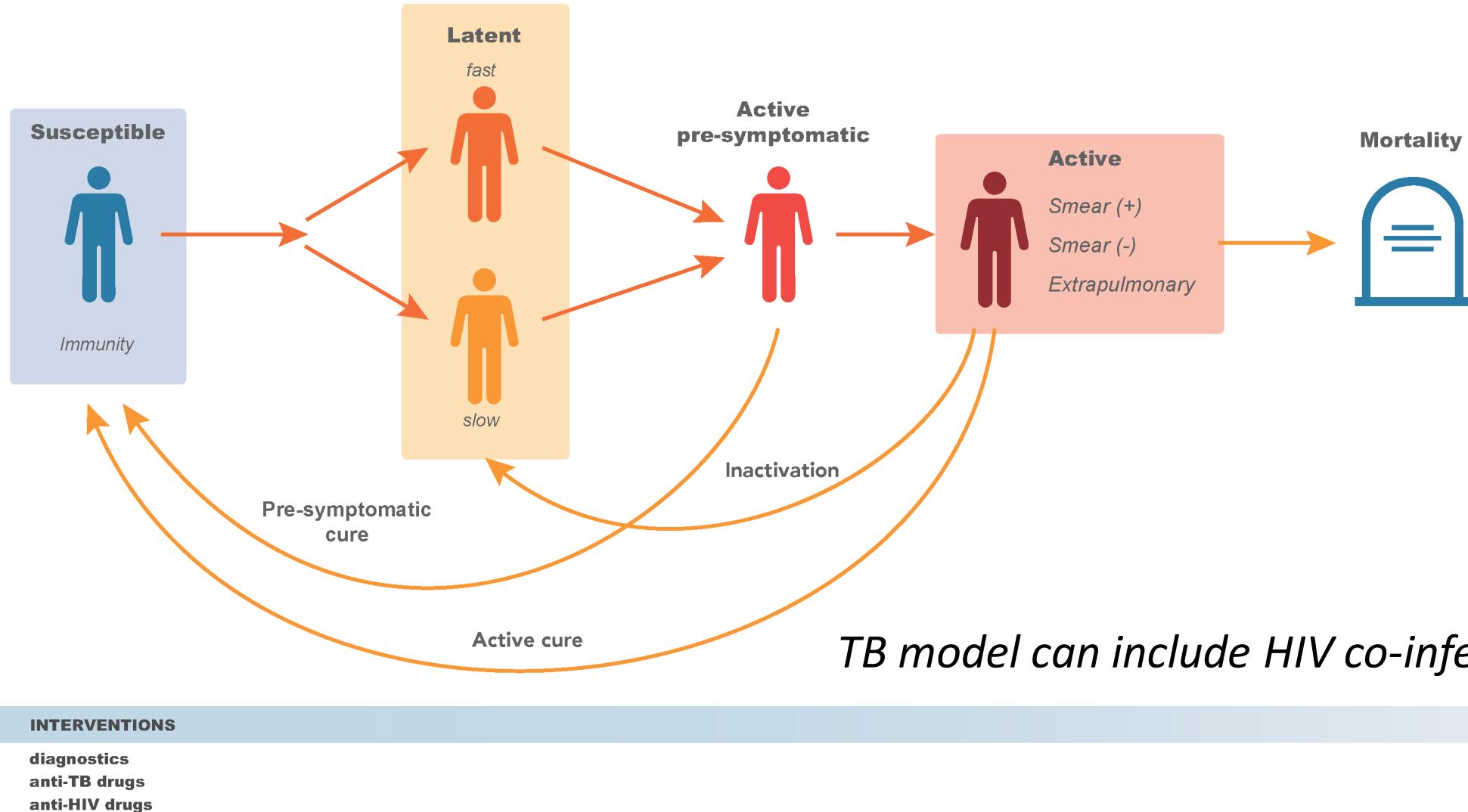
# Advanced EMOD features: Disease-specific functionality – STI/HIV

- Model relies on contact networks
- Relationships within each contact network can change over time
- “Society” params in the **demographics file** govern relationships
  - Type: marital, informal, transitory, commercial
  - Mixing patterns
  - Rates of formation
  - Average relationship duration
  - Participant ages
  - Age gaps
  - Coital patterns



# Advanced EMOD features: Disease-specific functionality - TB

## TUBERCULOSIS DISEASE PROGRESSION IN EMOD



## Additional advanced EMOD features

- Cascade of care & health systems
- Numerous micro-solvers for detailed information on agent behavior
- Integration of climate data into specific simulation types
- Disease-specific features for different transmission modes
- Migration and nodes (including node properties), and the ability to recreate specific geography

# Advanced EMOD features: Nodes and migration

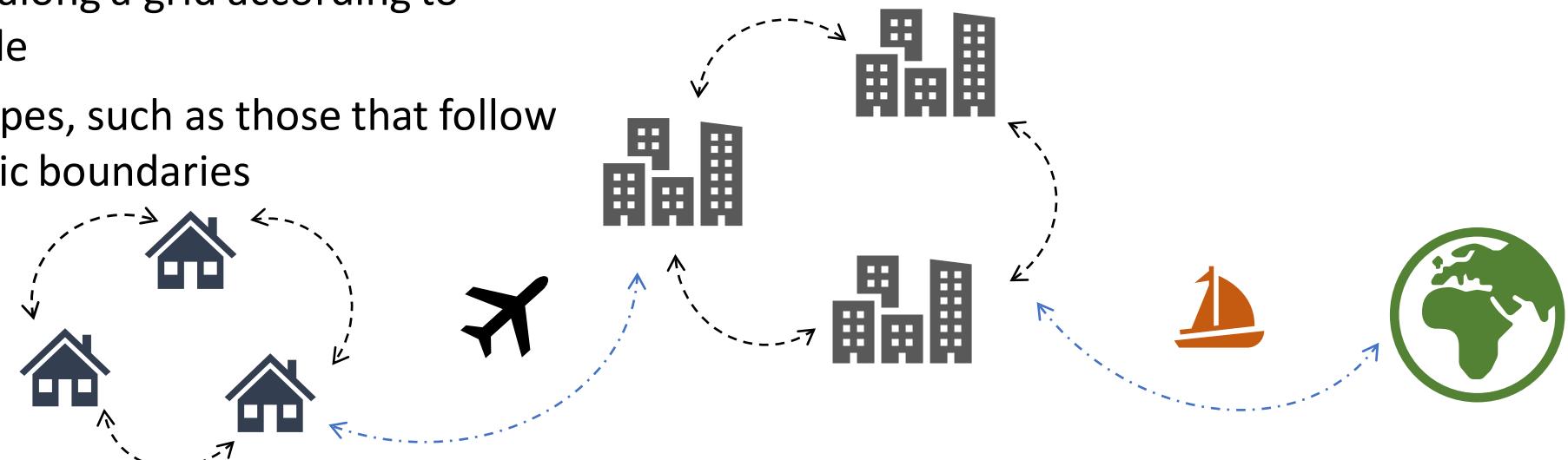
**Node:** a geographic location.

- Defined in the **demographics file**
  - Population size
  - Relevant modes of transportation (airport, seaport, roads, etc)
- Can be at any size & scale: houses in a village, towns in a state, states within a country, etc.
- May be demarcated along a grid according to latitude and longitude
- May be arbitrary shapes, such as those that follow political or geographic boundaries

**Migration:** movement between nodes.

There are 4 basic types:

- Local: foot travel between adjacent nodes
- Regional: migration along a road or rail network
- Air: migration by air travel
- Sea: migration by ship travel



# Features of EMOD: Examples from published work

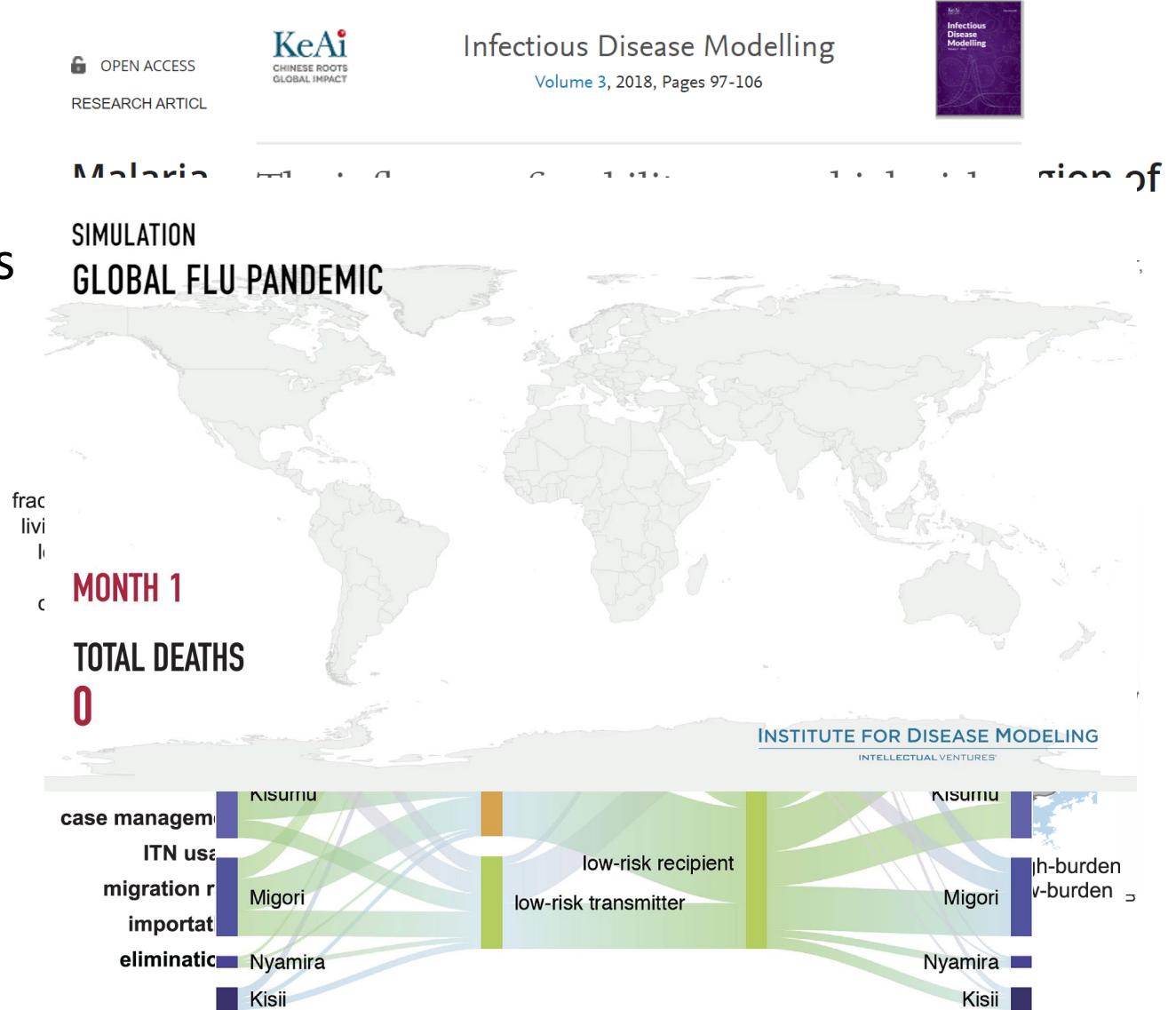
<http://idmod.org/publications>

★ Use EMOD to create generalizable strategies based on location attributes

★ Use EMOD to create detailed strategies for actionable intervention plans

★ Use EMOD to examine how particular populations are at risk

★ Use EMOD to simulate data, to test various potential outcomes (such as outbreak scenarios, or create data to test various strategies)



# Next steps: After the workshop!

## Next steps: After the workshop!

- We will hold office hours during the conference!
- Continue working through QuickStart lessons at your own pace
- Install Python 3.6 and other plotting tools at <http://idmod.org/docs/general/install-overview.html> (to run locally, or keep using your thumb drive)
- Work through remaining scenario simulations
- Review <http://idmod.org/documentation> to learn more about EMOD and our other software tools:
  - CMS: Stochastic compartmental model
  - Vis-Tools: Animated visualizations of spatio-temporal data
- Explore our dashboards
- Check our website for newly released tools! [www.idmod.org/tools](http://www.idmod.org/tools)

# Research at IDM: Opportunities for collaboration!

## Current research areas:

- Household-level modeling for malaria
- Typhoid
- Measles
- Polio
- Network models
- TB
- HIV
- Vaccine distribution economics
- Family planning
- Applied math

## Opportunities to engage:

- Work at IDM:
  - Post-doctoral positions
  - Open research positions
  - Summer internships
- Collaborate!
  - Visiting scholar positions at IDM
  - Joint research projects
- IDM annual Symposium (April! Bellevue, WA)
- **IDM training sessions**
  - On-site at your university
  - On-site at IDM

# Troubleshooting and further information

## Encountering problems? We can help!

1. Use the documentation. Many questions can be answered by using the parameter reference tables. <http://idmod.org/documentation>
2. There is a “troubleshooting” section within the documentation, which can address known issues:  
<http://www.idmod.org/docs/general/troubleshooting.html>
3. Email us! If you are working with a particular researcher, feel free to reach out to them. Otherwise, please email IDM support at [support@idmod.org](mailto:support@idmod.org)
  - Bobby Reiner: [bcreiner@uw.edu](mailto:bcreiner@uw.edu)
  - Mandy Izzo: [mizzo@idmod.org](mailto:mizzo@idmod.org)
  - Jen Schripsema: [jschripsema@idmod.org](mailto:jschripsema@idmod.org)
4. Follow us on Twitter! **@IDMOD\_ORG**



**IDM** INSTITUTE FOR  
DISEASE MODELING

*Don't forget: please join us this evening for an IDM-hosted dinner at Rosa Mexicano, following the conclusion of the advanced session at 6:00 pm!*

## Solutions

The following slides contain solutions to the exercises in this workshop. Note that EMOD is stochastic, so running the same parameter values will often result in different output. Additionally, there may be multiple ways to achieve results; the solutions presented here are simply one method and you may have discovered a different method.

# QuickStart lessons

## Lesson 1: Population initialization

- **Solutions:**
  - *Change the Age\_Initialization\_Distribution\_Type to “DISTRIBUTION\_SIMPLE.” Now you have the option for changing the type of distribution the population follows with the AgeDistributionFlag parameter. Spend time going through each of the distribution types. Does the graph reflect what you expect the population to look like?*
  - The graphs should reflect the appropriate distributions!

# QuickStart lessons: Solutions!

## Lesson 2: Using interventions

### Exercises:

- Can you make the intervention prevent 50% of infections?
  - Change Vaccine\_Take to 0.5. This means that it will have a 50% chance of achieving the set efficacy (which is default to 1).

# QuickStart lessons: Solutions!

## Lesson 3: Using individual properties

### Exercises:

- How would you target high-risk individuals who receive high quality care?
  - Using the “target interventions” section, you will want to set the parameters to select risk AND accessibility. Note the JSON format for this: the properties are in the same array.
- How would you target anyone who is high risk **or** receives high quality care?
  - Using the “target interventions” section, you will want to set the parameters to select risk OR accessibility. Note the JSON format for this: the properties are in different arrays.

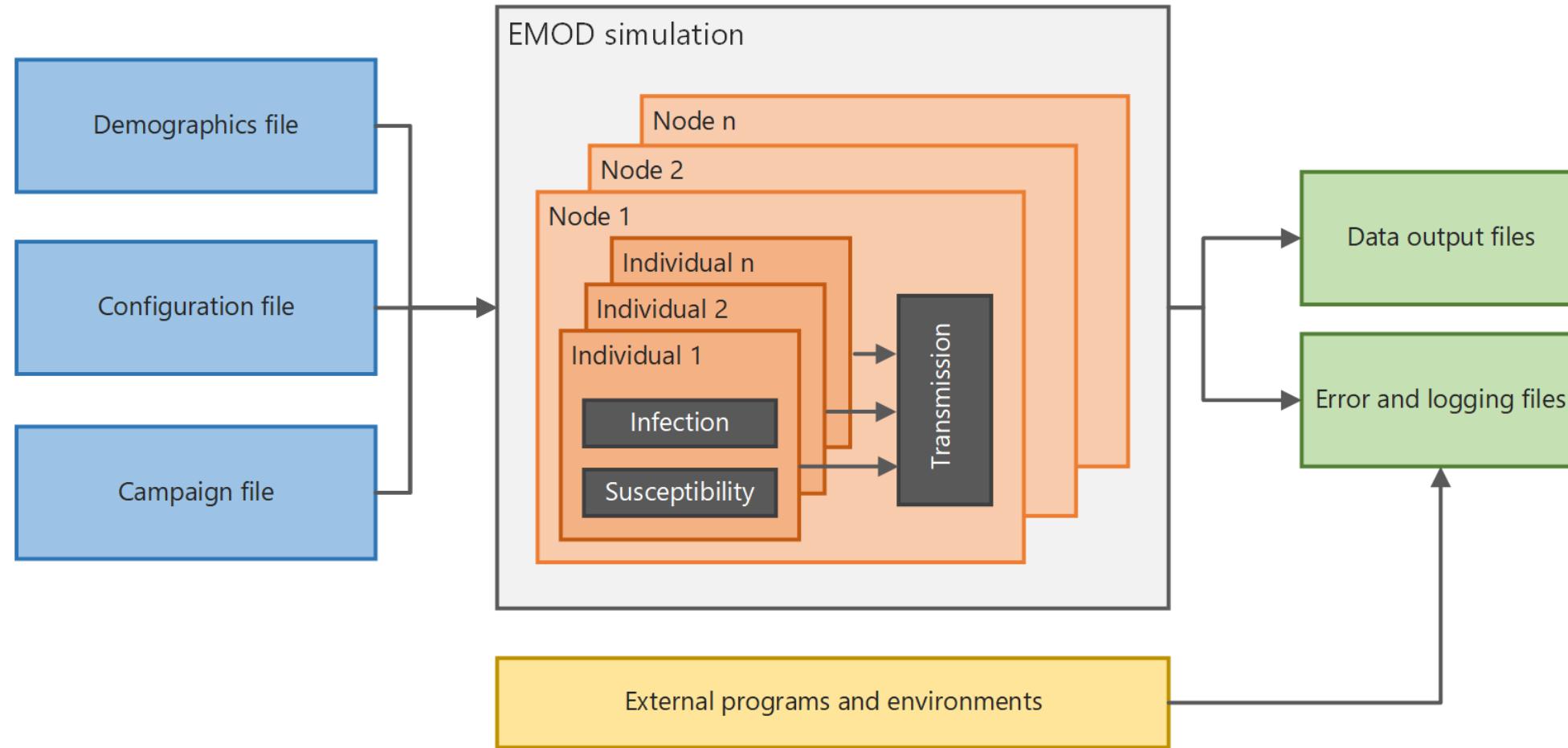
# Using EMOD for your own research

# Using EMOD for your own research

- Install EMOD on your own machine:
  - Instructions and required software install found here:  
<http://idmod.org/docs/general/install-overview.html>
  - Docker image available:  
<https://packages.idmod.org/artifactory/webapp/#/artifacts/browse/tree/General/idm-docker-public>
  - Local install currently supported on Windows and Linux
  - Run locally or connect to your institutions' HPC
  - Use IDM-Tools (suite of Python packages) designed for facilitating job creation, management, and data analysis
  - All scenario files (and today's PPT decks) available here:  
<https://github.com/InstituteforDiseaseModeling/docs-emod-scenarios>

➤ **Discussion: How can EMOD benefit you?**

# EMOD architecture



# EMOD files

- Primary files
  - Demographics: The population and the geographic region
  - Configuration: Disease dynamics, simulation length, and more
  - Campaign: Outbreak events and interventions
- Optional files
  - Migration: Movement of individuals or vectors among nodes
  - Climate: Rainfall, humidity, and temperature
  - Load-balancing: Distribution of computing resources
- All files are in **JSON** format

# EMOD files: JSON file structure

Almost all files that are passed to EMOD to run disease models use JavaScript Object Notation (**JSON**) format. In addition, it can easily be created and parsed using a variety of programming languages, such as Python, MATLAB, R, etc.

## About JSON:

- Uses JavaScript syntax
- All data is key/value pairs, separated by commas
- Keys (parameters) are case-sensitive
- Curly braces hold objects
- Square brackets hold arrays
- Data can be hierarchically organized in nested objects or arrays

```
{  
    "A_Complex_Key": {  
        "An_Array_with_a_Nested_Object_Value": [  
            {  
                "A_Simple_Key": "Value",  
                "A_Simple_Array": [ "Value1", "Value2" ],  
                "An_Array_with_Number_Values": [ 0.1, 0.2 ],  
                "A_Nested_Object": {  
                    "Another_Simple_Key": "Value",  
                    "Nested_Arrays": [  
                        [ 10, 0.1 ],  
                        [ 0.1, 1 ]  
                    ]  
                }  
            }  
        ]  
    }  
}
```

# EMOD demographics files

- Typically named <region>\_demographics.json
- Size, shape, and location of each geographic node
- Age, gender, immunity, etc. for the population in each node
- Node and individual properties initialization
  - Very flexible and powerful feature to add heterogeneity to a simulation
  - Add differences in disease transmission, migration, treatments
- Often use overlay files to target particular parameters

```
1 {  
2     "Metadata": {  
3         "DateCreated": "Sun Sep 25 23:19:55 2011",  
4         "Tool": "convertdemog.py",  
5         "Author": "jsteinkraus",  
6         "IdReference": "SampleContent",  
7         "NodeCount": 1,  
8         "Resolution": 150  
9     },  
10    "Defaults": {  
11    },  
12    "Nodes": [  
13        {  
14            "NodeID": 1,  
15            "NodeAttributes": {  
16                "Latitude": 0,  
17                "Longitude": 0,  
18                "Altitude": 0,  
19                "Airport": 0,  
20                "Region": 1,  
21                "Seaport": 0,  
22                "InitialPopulation": 10000,  
23                "BirthRate": 0.0000548  
24            },  
25            "IndividualAttributes": {  
26                "AgeDistributionFlag": 3,  
27                "AgeDistribution1": 0.000118,  
28                "AgeDistribution2": 0,  
29                "PrevalenceDistributionFlag": 0,  
30                "PrevalenceDistribution1": 0.0,  
31                "PrevalenceDistribution2": 0.0,  
32                "ImmunityDistributionFlag": 0,  
33                "ImmunityDistribution1": 1,  
34                "ImmunityDistribution2": 0,  
35                "RiskDistributionFlag": 0,  
36                "RiskDistribution1": 1,  
37                "RiskDistribution2": 0,  
38                "MigrationHeterogeneityDistributionFlag": 0,  
39                "MigrationHeterogeneityDistribution1": 1,  
40                "MigrationHeterogeneityDistribution2": 0,  
41                "MortalityDistribution": {  
42                    "NumDistributionAxes": 2,  
43                    "AxisNames": [ "gender", "age" ],  
44                    "AxisUnits": [ "male=0,female=1", "years" ],  
45                    "AxisScaleFactors": [ 1, 365 ],  
46                    "NumPopulationGroups": [ 2, 1 ],  
47                    "PopulationGroups": [  
48                        [ 0, 1 ],  
49                        [ 0 ]  
50                    ],  
51                    "ResultUnits": "deaths per day",  
52                    "ResultScaleFactor": 1,  
53                    "ResultValues": [  
54                        [ 0.0000548 ],  
55                        [ 0.0000548 ]  
56                    ]  
57                }  
58            }  
59        }  
60    }  
61}  
62}
```

# EMOD configuration files

- Typically named config.json
- Mostly a flat list of key:value pairs
- Controls many aspects of the simulation:
  - Names of additional files to use
  - Enable/disable features
  - Simulation-wide demographics, climate, migration
  - General disease attributes: infectivity, immunity, mortality, etc.
  - Specific disease attributes such as treatment efficacy
  - Output reports to produce

```
1 ▼ {  
2 ▼   "parameters": {  
3     "Age_Initialization_Distribution_Type": "DISTRIBUTION_SIMPLE",  
4     "Animal_Reservoir_Type": "NO_ZOONOSIS",  
5     "Base_Incubation_Period": 0,  
6     "Base_Individual_Sample_Rate": 1,  
7     "Base_Infectious_Period": 50000,  
8     "Base_Infectivity": 0.0003653,  
9     "Base_Mortality": 0,  
10    "Base_Population_Scale_Factor": 1,  
11    "Birth_Rate_Dependence": "POPULATION_DEPENDENT",  
12    "Birth_Rate_Time_Dependence": "NONE",  
13    "Campaign_Filename": "campaign.json",  
14    "Climate_Model": "CLIMATE_OFF",  
15    "Config_Name": "SI",  
16    "Custom_Reports_Filename": "",  
17    "Death_Rate_Dependence": "NONDEISEASE_MORTALITY_BY_AGE_AND_GENDER",  
18    "Default_Geography_Initial_Node_Population": 1000,  
19    "Default_Geography_Torus_Size": 10,  
20    "Demographics_Filenames": [  
21      "generic_scenarios_demographics.json"  
22    ],  
23    "Enable_Aging": 1,  
24    "Enable_Birth": 1,  
25    "Enable_Default_Report": 1,  
26    "Enable_Demographics_Birth": 0,  
27    "Enable_Demographics_Builtin": 0,  
28    "Enable_Demographics_Gender": 1,  
29    "Enable_Demographics_Report": 1,  
30    "Enable_Disease_Mortality": 0,  
31    "Enable_Heterogeneous_Intranode_Transmission": 0,  
32    "Enable_Immune_Decay": 0,  
33    "Enable_Immunity": 0,  
34    "Enable_Immunity_Distribution": 0,  
35    "Enable_Initial_Prevalence": 1,  
36    "Enable_Interventions": 1,  
37    "Enable_Maternal_Infection_Transmission": 0,  
38    "Enable_Maternal_Protection": 0,  
39    "Enable_Natural_Mortality": 1,  
40    "Enable_Property_Output": 0,  
41    "Enable_Skipping": 0,  
42    "Enable_Spatial_Output": 0,  
43    "Enable_Superinfection": 0,  
44    "Enable_Susceptibility_Scaling": 0,  
45    "Enable_Vital_Dynamics": 1.  
}
```

# EMOD campaign files

- Typically named campaign.json
- Hierarchically nested:
  - Campaign event (when/where)
  - Event coordinator (who); nested within campaign event
  - Intervention (what)
- Controls many aspects of disease eradication efforts:
  - When, how, and who to test for disease
  - When, how, and who to distribute treatments to
  - Which types of treatments to use
- Interventions can distribute other interventions

```
1 ▼ {
2   "Campaign_Name": "Initial Seeding",
3   "Events": [
4     {
5       "Event_Coordinator_Config": {
6         "Demographic_Coverage": 0.05,
7         "Intervention_Config": {
8           "Antigen": 0,
9           "Genome": 0,
10          "Outbreak_Source": "PrevalenceIncrease",
11          "class": "OutbreakIndividual"
12        },
13        "Target_Demographic": "Everyone",
14        "class": "StandardInterventionDistributionEventCoordinator"
15      },
16      "Event_Name": "Outbreak",
17      "Nodeset_Config": {
18        "class": "NodeSetAll"
19      },
20      "Start_Day": 30,
21      "class": "CampaignEvent"
22    }
23  ],
24  "Use_Defaults": 1
25
26
27 }
```

[www.idmod.org/docs/general/software-campaign.html](http://www.idmod.org/docs/general/software-campaign.html)

# EMOD campaign file structure

```
{  
    "Events": [{  
        "class": "CampaignEvent",  
        "Event_Name": "High-risk vaccination",  
        "Start_Day": 1,  
        "Nodeset_Config": {  
            "class": "NodeSetAll"  
        },  
        "Event_Coordinator_Config": {  
            "class": "CalendarEventCoordinator",  
            "Demographic_Coverage": 1,  
            "Property_Restrictions": [  
                "Risk:High"  
            ],  
            "Number_Repetitions": 1,  
            "Timesteps_Between_Repetitions": 0,  
            "Target_Demographic": "Everyone",  
            "Target_Residents_Only": 1,  
            "Distribution_Times": [100, 200, 400, 800, 1200],  
            "Distribution_Coverages": [0.01, 0.05, 0.1, 0.2, 1.0],  
            "Intervention_Config": {  
                "Cost_To_Consumer": 0,  
                "Vaccine_Take": 1,  
                "Vaccine_Type": "AcquisitionBlocking",  
                "class": "SimpleVaccine",  
                "Waning_Config": {  
                    "Initial_Effect": 1,  
                    "Box_Duration": 1825,  
                    "class": "WaningEffectBox"  
                }  
            }  
        }  
    }]  
}
```



**CAMPAIGN EVENT:**  
“Where/when” things will be distributed



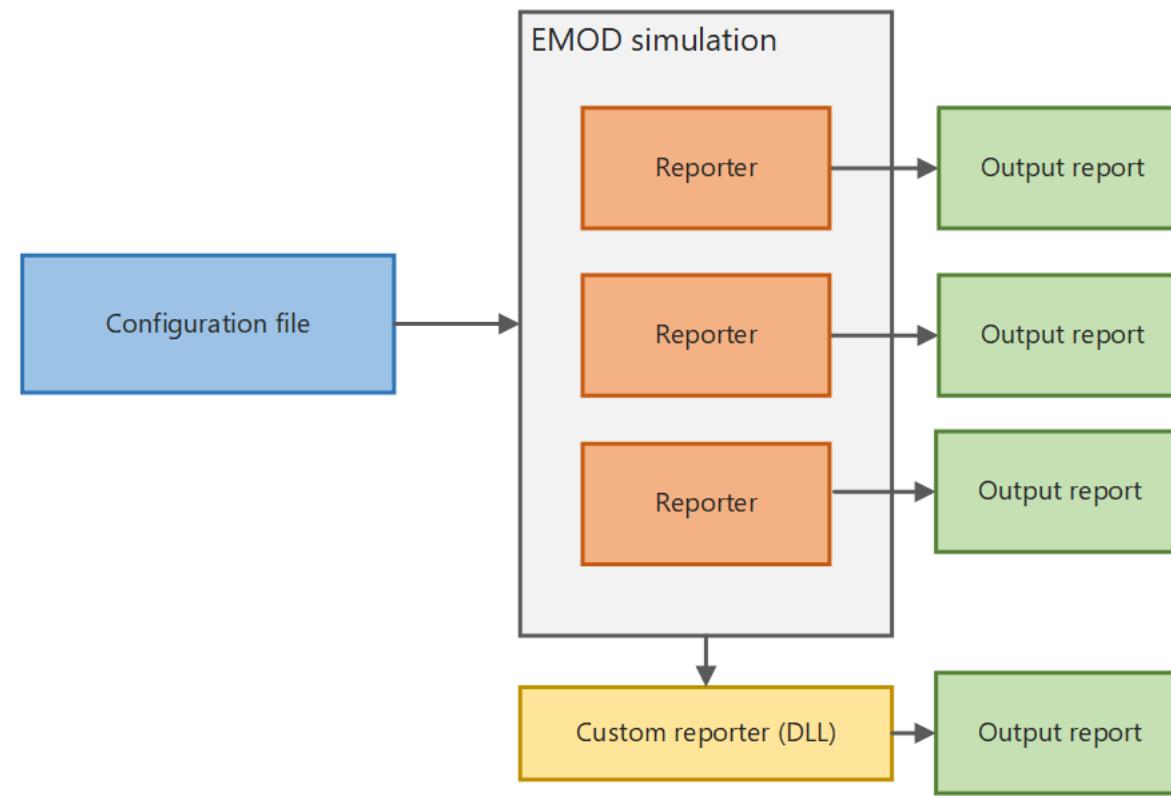
**EVENT COORDINATOR:**  
“Who” will be targeted  
“When” distributions are repeated



**INTERVENTION:**  
“What” will be distributed

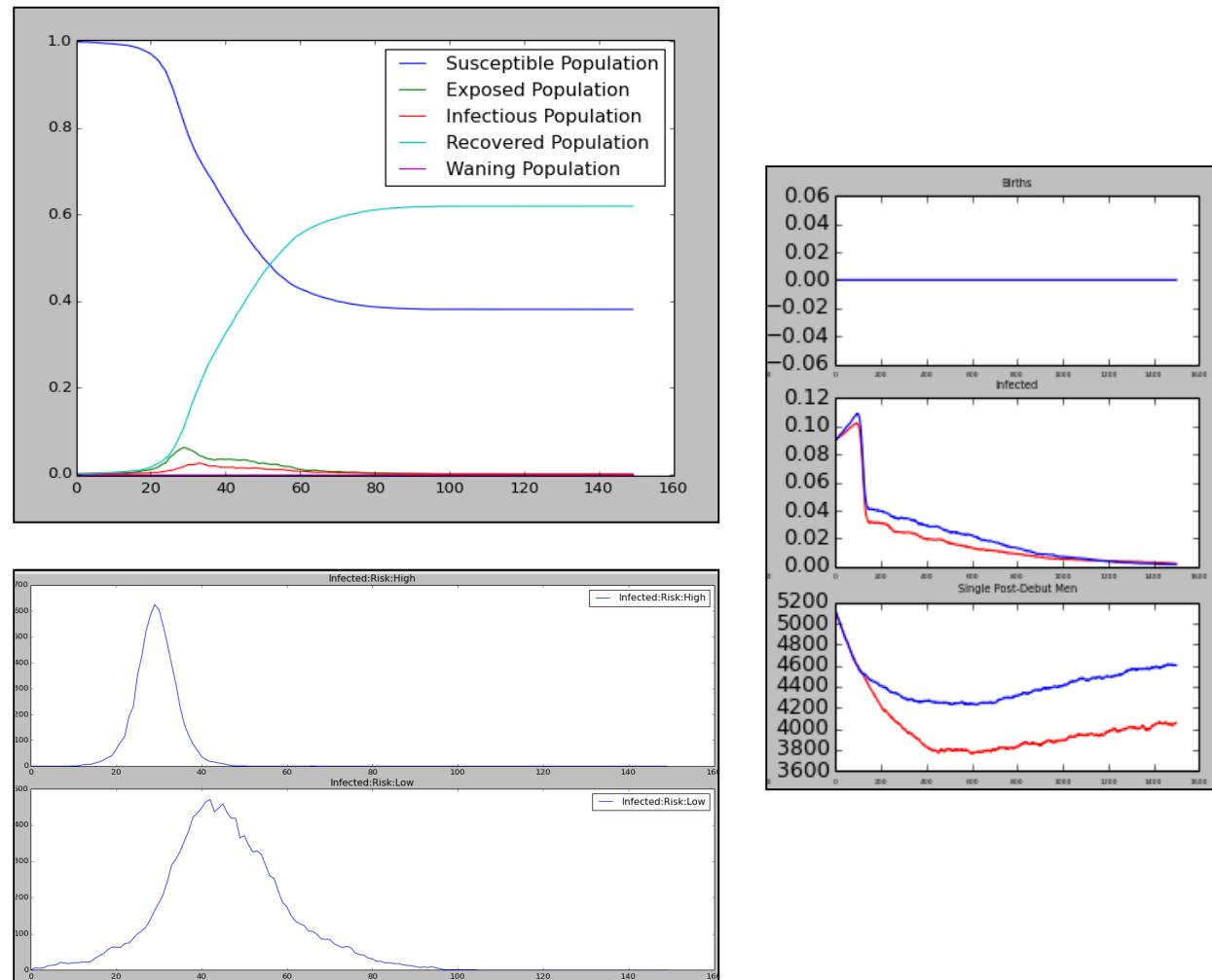
# EMOD output reports

Reports are simply output files that contained grouped, extracted data that's ready for analysis. EMOD contains pre-made Built-in reports (that can be modified), but also allows the user to create custom reports.



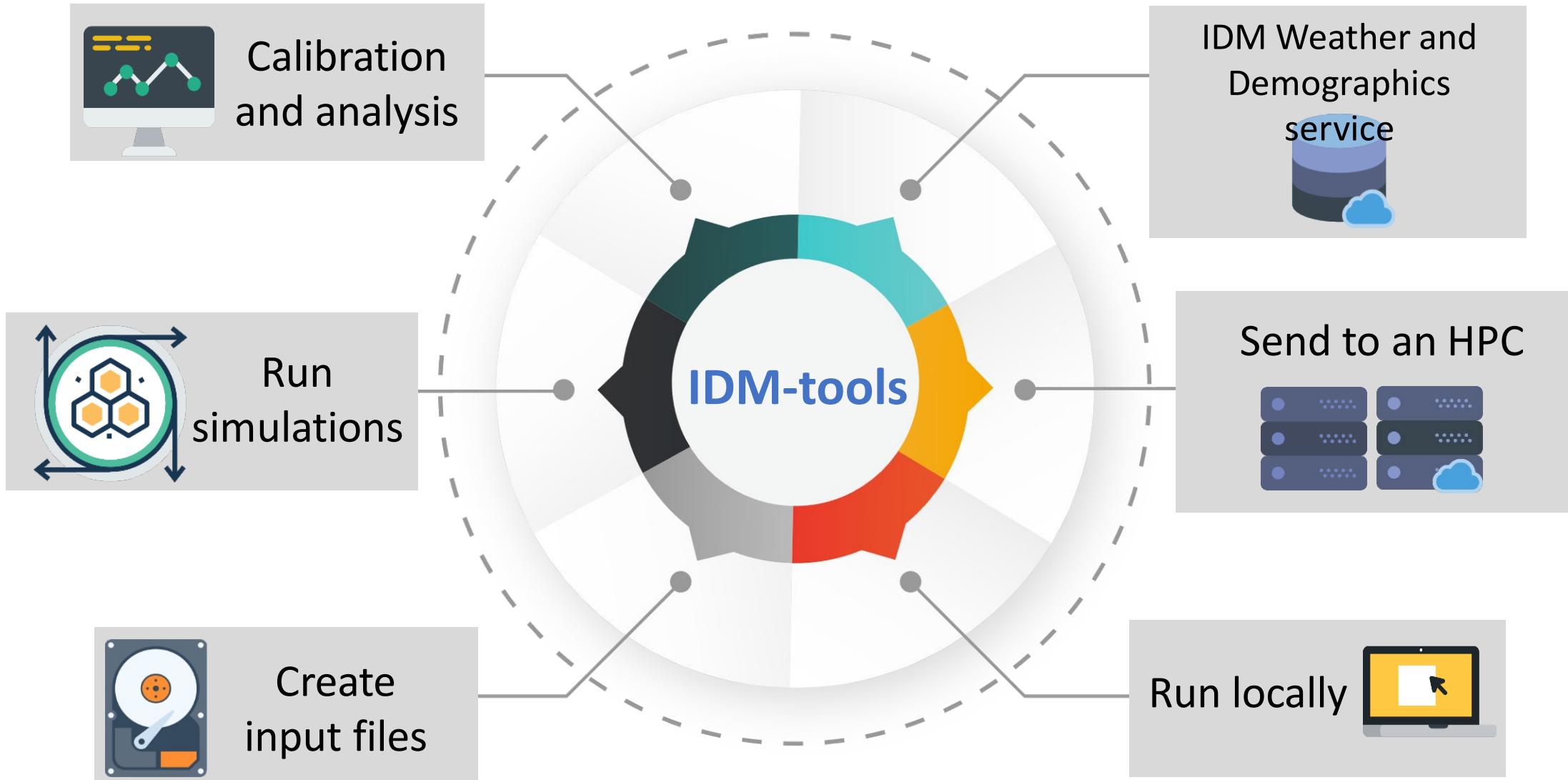
# EMOD built-in output reports

- Channel reports (InsetChart.json)
  - Birth, non-disease death, susceptible, infectious, recovered, etc.
  - Data for each time step
- Binned reports
  - Channel data put into age bins instead of time steps
- Property reports
  - Data organized by individual or node property values
- Python scripts provided to view data

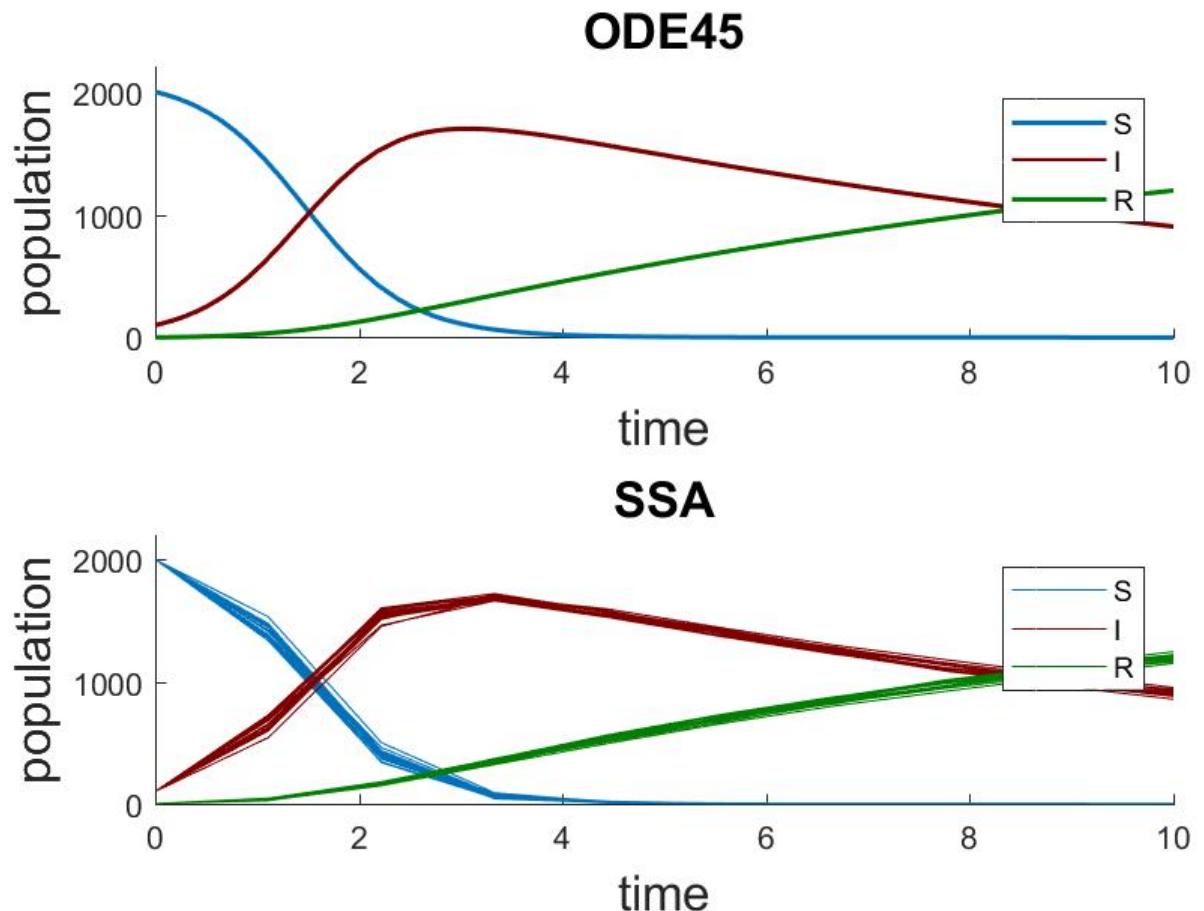
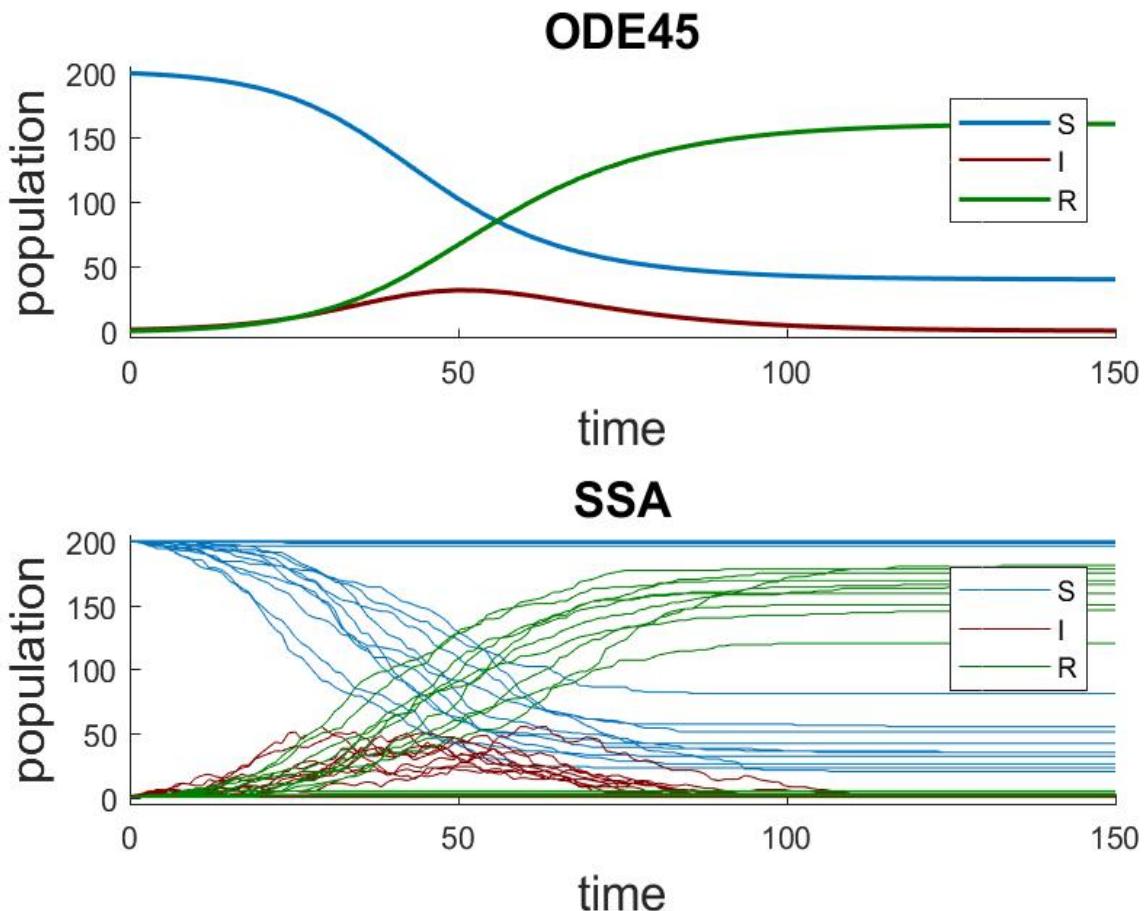


## Additional IDM software

# IDM-Tools



# Compartmental Modeling Software (CMS)



<https://github.com/InstituteforDiseaseModeling/IDM-CMS>

Documentation: <http://idmod.org/documentation>

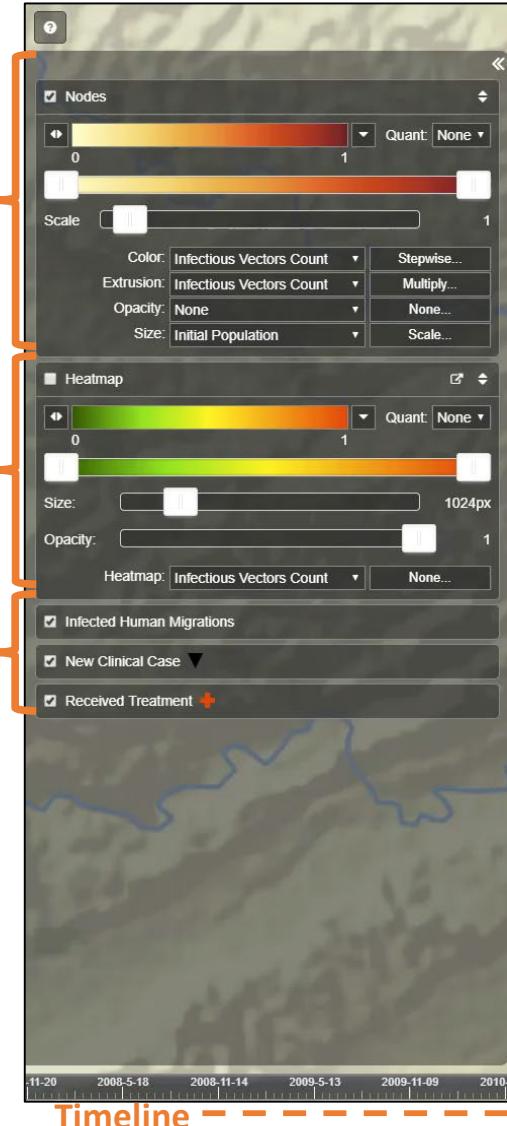
# Vis-Tools

Nodes layer controls

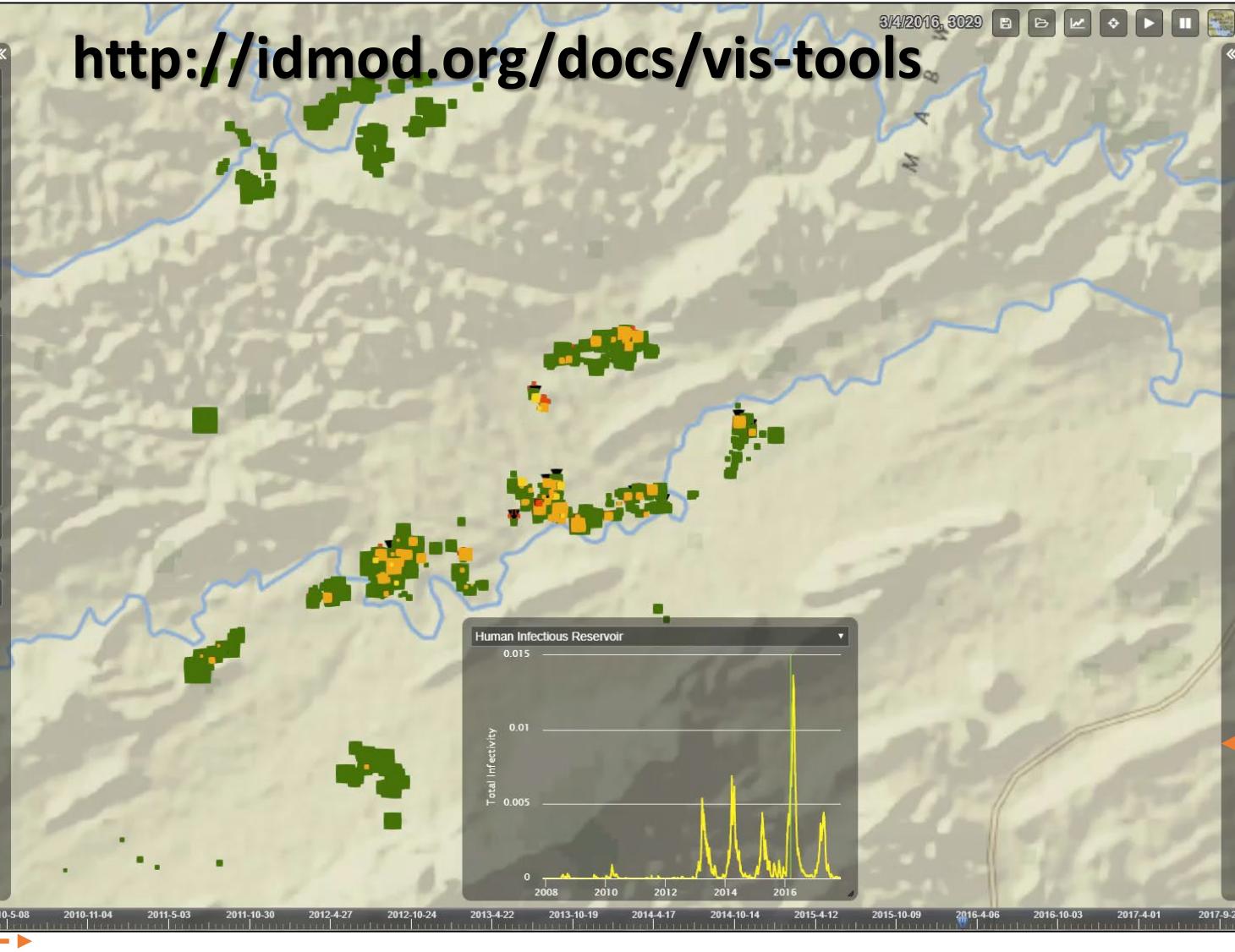
Bindings

Heatmap layer controls

Other layers



<http://idmod.org/docs/vis-tools>



Transport controls  
Node info (when selected)

Per-node inset charts (when selected)

Data summary graphs