

# Advanced Topics in Software Engineering: Population Models

**Prof. Michele Loreti**

**Advanced Topics in Software Engineering**

*Corso di Laurea in Informatica (L31)*

*Scuola di Scienze e Tecnologie*

## Example: Infection disease...

We want to study and predict the effect of an **infection disease** in a city/area.

## Example: Infection disease...

We want to study and predict the effect of an **infection disease** in a city/area.

A classical model of this problem considers three kinds of individuals:

- **S**uscettible;
- **E**xposed;
- **I**nfected;
- **R**ecovered.

## Example: Infection disease...

We want to study and predict the effect of an **infection disease** in a city/area.

A classical model of this problem considers three kinds of individuals:

- **S**uscettible;
- **E**xposed;
- **I**nfected;
- **R**ecovered.

Dynamics in *SEIR* model can be described via a CTMC.

## Example: Infection disease...

SEIR via CTMC...

Each state of the CTMC has the following form:

$$(x_S, x_E, x_I, x_R)$$

where

- $x_S$  is the number of *suscettibles*;
- $x_E$  is the number of *exposed*;
- $x_I$  is the number of *infected*;
- $x_R$  is the number of *recovered*.

## Example: Infection disease...

SEIR via CTMC...

Each state of the CTMC has the following form:

$$(x_S, x_E, x_I, x_R)$$

where

- $x_S$  is the number of *suscettibles*;
- $x_E$  is the number of *exposed*;
- $x_I$  is the number of *infected*;
- $x_R$  is the number of *recovered*.

If we let  $N \in \mathbb{N}$  be the number of citizens in the area, the state space of our CTMC is a subset of  $[0, N]^4$ .

# Example: Infection disease...

SEIR via CTMC...

In the SEIR system three kinds of events can occur:

- One **S**uscettible becomes **E**xposed;
- One **E**xposed becomes **I**nfected;
- One **I**nfected becomes **R**ecovered,

## Example: Infection disease...

SEIR via CTMC...

In the SEIR system three kinds of events can occur:

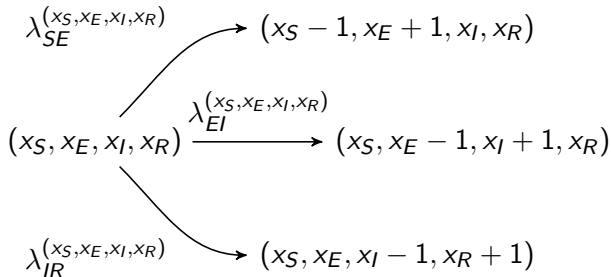
- One **S**uscettible becomes **E**xposed;
- One **E**xposed becomes **I**nfected;
- One **I**nfected becomes **R**ecovered,

Rates of the above events depends on the number/fraction of citizens of the different kinds!



# Example: Infection disease...

SEIR via CTMC...



## Population models...

A Population Continuous Time Markov Chain (PCTMC) model is a tuple  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$  where:

- $\mathbf{X} = (X_1, \dots, X_n)$  is a vector of variables;
- each  $X_i$  takes values in a *finite or countable* domain  $\mathcal{D}_i \subset \mathbb{R}$ ;
- $\mathcal{D} = \mathcal{D}_0 \times \dots \times \mathcal{D}_n = \prod_i \mathcal{D}_i$ ;
- $\mathbf{d}_0 \in \mathcal{D}$  is the *initial state* of the model;
- $\mathcal{T} = \{\tau_1, \dots, \tau_m\}$  is the set of *transitions*  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r)$  where:
  - $\ell$  is the *label* of the transition;
  - $\mathbf{s} \in \mathbb{R}_{\geq 0}^n$ , is the *pre-vector*;
  - $\mathbf{t} \in \mathbb{R}_{\geq 0}^n$ , is the *post-vector*;
  - $r : \mathcal{D} \rightarrow \mathbb{R}_{\geq 0}$  is a *rate function* such that for any  $\mathbf{d} \in \mathcal{D}$ , if  $\mathbf{d} - \mathbf{s} + \mathbf{t} \notin \mathcal{D}$  then  $r(\mathbf{d}) = \mathbf{0}$ .

## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r) \in \mathcal{D}$ .

## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r) \in \mathcal{D}$ .

We let  $\rightarrow_{\tau_i} \subseteq \mathcal{D} \times \mathbb{R}_{>0} \times \mathcal{D}$  denote the transition relation induced by transition  $\tau_i$ :

$$\frac{r(\mathbf{d}_1) = \lambda \neq 0 \quad \mathbf{d}_2 = \mathbf{d}_1 - \mathbf{s} + \mathbf{t}}{\mathbf{d}_1 \xrightarrow{\lambda}_{\tau_i} \mathbf{d}_2}$$

## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r) \in \mathcal{D}$ .

We let  $\rightarrow_{\tau_i} \subseteq \mathcal{D} \times \mathbb{R}_{>0} \times \mathcal{D}$  denote the transition relation induced by transition  $\tau_i$ :

$$\frac{r(\mathbf{d}_1) = \lambda \neq 0 \quad \mathbf{d}_2 = \mathbf{d}_1 - \mathbf{s} + \mathbf{t}}{\mathbf{d}_1 \xrightarrow{\lambda}_{\tau_i} \mathbf{d}_2}$$

We say that  $\tau_i$  is *enabled* in  $\mathbf{d}_1$  if and only if  $r(\mathbf{d}_1) > 0$ .

## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r) \in \mathcal{D}$ .

We let  $\rightarrow_{\tau_i} \subseteq \mathcal{D} \times \mathbb{R}_{>0} \times \mathcal{D}$  denote the transition relation induced by transition  $\tau_i$ :

$$\frac{r(\mathbf{d}_1) = \lambda \neq 0 \quad \mathbf{d}_2 = \mathbf{d}_1 - \mathbf{s} + \mathbf{t}}{\mathbf{d}_1 \xrightarrow{\lambda}_{\tau_i} \mathbf{d}_2}$$

We say that  $\tau_i$  is *enabled* in  $\mathbf{d}_1$  if and only if  $r(\mathbf{d}_1) > 0$ .

Finally, function  $\rho_{\tau_i} : \mathcal{D} \times \mathcal{D} \rightarrow \mathbb{R}_{\geq 0}$  is used to denote the rate of a transition  $\tau_i$  from  $\mathbf{d}_1$  to  $\mathbf{d}_2$ :

$$\rho_{\tau_i}(\mathbf{d}_1, \mathbf{d}_2) = \begin{cases} r(\mathbf{d}_1) & \mathbf{d}_2 = \mathbf{d}_1 - \mathbf{s} + \mathbf{t} \\ 0 & \text{otherwise} \end{cases}$$

## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (l, \mathbf{s}, \mathbf{t}, r) \in \mathcal{D}$ .

## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r) \in \mathcal{T}$ .

Function  $\rho_{\mathcal{T}} : \mathcal{D} \times \mathcal{D} \rightarrow \mathbb{R}_{\geq 0}$  is used to denote the rate of a transition in  $M$  from  $\mathbf{d}_1$  to  $\mathbf{d}_2$ :

$$\rho_{\mathcal{T}}(\mathbf{d}_1, \mathbf{d}_2) = \sum_{\tau_i \in \mathcal{T}} \rho_{\tau_i}(\mathbf{d}_1, \mathbf{d}_2)$$



## Population models...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  and  $\tau_i = (\ell, \mathbf{s}, \mathbf{t}, r) \in \mathcal{D}$ .

Function  $\rho_{\mathcal{T}} : \mathcal{D} \times \mathcal{D} \rightarrow \mathbb{R}_{\geq 0}$  is used to denote the rate of a transition in  $M$  from  $\mathbf{d}_1$  to  $\mathbf{d}_2$ :

$$\rho_{\mathcal{T}}(\mathbf{d}_1, \mathbf{d}_2) = \sum_{\tau_i \in \mathcal{T}} \rho_{\tau_i}(\mathbf{d}_1, \mathbf{d}_2)$$

We let  $\rightarrow_{\mathcal{T}} \subseteq \mathcal{D} \times \mathbb{R}_{>0} \times \mathcal{D}$  denote the transition relation induced by transitions  $\mathcal{T}$ :

$$\frac{\rho_{\mathcal{T}}(\mathbf{d}_1, \mathbf{d}_2) = \lambda \neq 0}{\mathbf{d}_1 \xrightarrow{\lambda}_{\tau_i} \mathbf{d}_2}$$

# Example: Infection disease...

SEIR via Population Model...

**Vector Variables:** (S, E, I, R)

## Example: Infection disease...

SEIR via Population Model...

**Vector Variables:**  $(S, E, I, R)$

**Counting Domain:**  $[0, N] \times [0, N] \times [0, N] \times [0, N]$

## Example: Infection disease...

SEIR via Population Model...

**Vector Variables:**  $(S, E, I, R)$

**Counting Domain:**  $[0, N] \times [0, N] \times [0, N] \times [0, N]$

**Initial state:**  $(N - N_I, 0, N_I, 0)$

# Example: Infection disease...

SEIR via Population Model...

**Vector Variables:**  $(S, E, I, R)$

**Counting Domain:**  $[0, N] \times [0, N] \times [0, N] \times [0, N]$

**Initial state:**  $(N - N_I, 0, N_I, 0)$

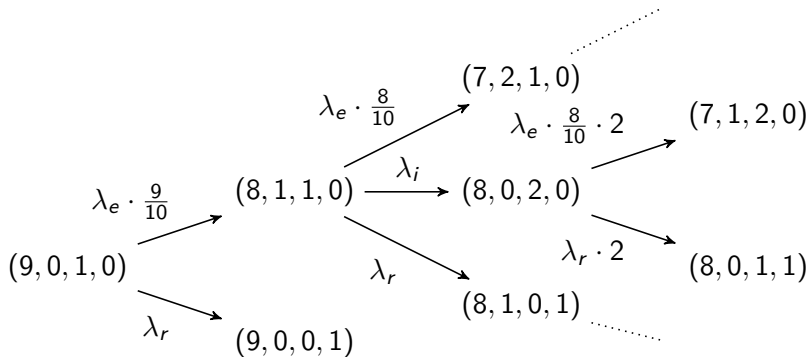
**Transitions:**

- $(S\_E, \mathbf{1}_S, \mathbf{1}_E, \lambda_e \cdot \frac{X_S}{N} \cdot X_I)$
- $(E\_I, \mathbf{1}_E, \mathbf{1}_I, \lambda_i \cdot X_I)$
- $(I\_R, \mathbf{1}_I, \mathbf{1}_R, \lambda_r \cdot X_I)$

# Example: Infection disease...

Trajectories...

$$\left( S_E, \mathbf{1}_S, \mathbf{1}_E, \lambda_e \cdot \frac{X_S}{N} \cdot X_I \right) \quad \left( E_I, \mathbf{1}_E, \mathbf{1}_E, \lambda_i \cdot X_I \right) \quad \left( I_R, \mathbf{1}_I, \mathbf{1}_R, \lambda_r \cdot X_I \right)$$



# From Population Models to CTMC...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  be a population model, we can easily define the associated CTMC.

## From Population Models to CTMC...

Let  $M = (\mathbf{X}, \mathcal{D}, \mathcal{T}, \mathbf{d}_0)$ ,  $\mathbf{d}_1, \mathbf{d}_2 \in \mathcal{D}$  be a population model, we can easily define the associated CTMC.

This is obtained as  $(\mathcal{D}, \mathbf{R}_M)$  where the rate transition matrix  $\mathbf{R}_M$  is defined as follows:

$$\mathbf{R}_M(\mathbf{d}_1, \mathbf{d}_2) = \rho_{\mathcal{T}}(\mathbf{d}_1, \mathbf{d}_2)$$



**To be continued...**