

Using PEPA for Epidemiology

Carron Shankland Chris McCaig Rachel Norman Kevin
O'Reilly
`ces@cs.stir.ac.uk`

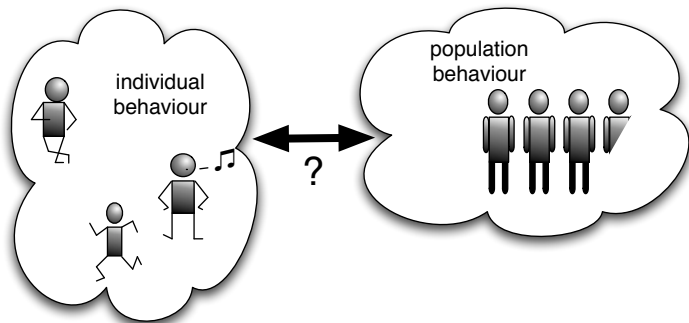
University of Stirling,
Department of Computing Science & Mathematics

PASTA workshop

Disease

- Disease can be viewed as a threat (epidemics) or as a tool (eg pest control)
- Modelling can help us understand the progress of an epidemic (prediction and control)
- Typical questions asked:
 - How much of the population will be infected?
 - Does the behaviour of individuals change the spread of the disease?
 - How long will it take before the disease dies out?
 - What is the most effective way to control the disease?

Information Available



- LHS = process algebra, cellular automata
- RHS = ODEs (traditionally)
- Changing scale - individual based to population based models

Why PEPA?

- Previously used WSCCS
 - Discrete time process algebra
 - Behavioural and Topological models
 - Agents described in terms of actions, sequencing, choice, parallelism (with or without interaction)
 - Actions happen with weights

Why PEPA?

- Previously used WSCCS
 - Discrete time process algebra
 - Behavioural and Topological models
 - Agents described in terms of actions, sequencing, choice, parallelism (with or without interaction)
 - Actions happen with weights
- PEPA
 - Continuous time process algebra
 - Cooperation rather than two-way synchronisation
 - Used to model biochemistry
 - Ability to extract ODEs from syntax

Example: SIR in PEPA

$(S[900] \leftrightarrow I[100]) \langle \text{transmit}, \text{contact} \rangle (\text{Med}[500])$

Example: SIR in PEPA

```
(S[900]<>I[100]) <transmit, contact> (Med[500])
```

```
S = (contact, c).S2;
```

```
S2 = (infect,p_i).I + (not_infect,1-p_i).S;
```

```
I = (transmit, t).I + (recover, p_r).R  
    + (contact,c).I;
```

```
R = (lose_immunity, s).S + (contact,c).R;
```

Example: SIR in PEPA

```
(S[900]<>I[100]) <transmit, contact> (Med[500])  
S = (contact, c).S2;  
S2 = (infect,p_i).I + (not_infect,1-p_i).S;  
I = (transmit, t).I + (recover, p_r).R  
  + (contact,c).I;  
R = (lose_immunity, s).S + (contact,c).R;  
Med = (transmit, infty).Med2;  
Med2 = (contact, infty).Med + (decay, d).Med;
```

Example: SIR in PEPA

```
(S[900]<>I[100]) <transmit, contact> (Med[500])  
S = (contact, c).S2;  
S2 = (infect,p_i).I + (not_infect,1-p_i).S;  
I = (transmit, t).I + (recover, p_r).R  
  + (contact,c).I;  
R = (lose_immunity, s).S + (contact,c).R;  
Med = (transmit, infty).Med2;  
Med2 = (contact, infty).Med + (decay, d).Med;
```

Variations:

- Switching passive and active for contact (so SIR are passive).
Problem for I?
- Importing disease to the Medium to sustain infection.
- No S2 stage; choice in S to be infected or not.

You've got to have a graph

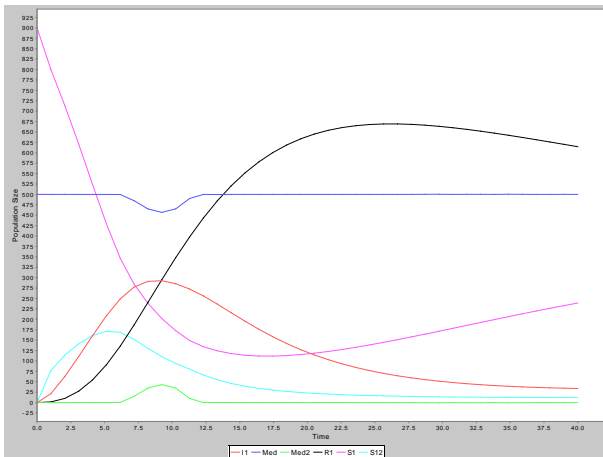


Figure: Output from the PEPA/Eclipse tool.

ODEs - Traditional model

$$dS/dt = -c.S.Med2 + (1 - p_i)S2 + p_s R ,$$

$$dS2/dt = c.S.Med2 - S2 ,$$

$$dI/dt = p_i S2 - p_r I_t ,$$

$$dR/dt = p_r I - p_s R ,$$

$$dMed/dt = c.N.Med2 - t.I.Med + p_d Med2 ,$$

$$dMed2/dt = -c.N.Med2 + t.I.Med - p_d Med2 .$$

where $N = S + I + R$.

ODEs - Fluid Flow version

$$dS/dt = -c.\min(S, Med2) + (1 - p_i)S2 + p_s R ,$$

$$dS2/dt = c.\min(S, Med2) - S2 ,$$

$$dI/dt = p_i S2 - p_r I ,$$

$$dR/dt = p_r I - p_s R ,$$

$$dMed/dt = c.\min(S, Med2) - t.\min(I, Med) + d.Med2 ,$$

$$dMed2/dt = -c.\min(S, Med2) + t.\min(I, Med) - d.Med2 .$$

ODEs - TCS version

$$\begin{aligned}dS/dt &= -cS\theta(Med2) + (1 - p_i)S2 + p_sR , \\dS2/dt &= cS\theta(Med2) - S2 , \\dI/dt &= p_iS2 - p_rI , \\dR/dt &= p_rI - p_sR , \\dMed/dt &= cN\theta(Med2) - tI\theta(Med) + d.Med2 , \\dMed2/dt &= -cN\theta(Med2) + tI\theta(Med) - d.Med2 .\end{aligned}$$

where $N = S + I + R$.

Equations based on the output of the Eclipse Plugin cmdl file are the same in this case.

WSCCS model

```
bs S1 1@1.contact:SI2 + 1.t:S2
bs I1 1@1.contact:I2 + 1.t:I2
bs R1 1@1.contact:R2 + 1.t:R2
bs Med_1 1.t:Med_2
bs Med2_1 1@1.contact^-1:Med_2 + 1.t:Med_2
bs S2 1.t:S3
bs SI2 1.t:SI3
bs I2 1.transmit^-1:I3 + 1.t:I3
bs R2 1.t:R3
bs Med_2 1.transmit:Med2_3 + 1.t:Med_3
bs S3 1.t:S1
bs I3 pr.t:R1 + (1-pr).t:I1
bs R3 ps.t:S1 + (1-ps).t:R1
bs Med2_3 1.t:Med2_1
bs Med_3 1.t:Med_1
bs SI3 pi.t:I1 + (1-pi).t:S1
basi L t
btr Population S1{s}|I1{i}|R1{r}|Med_1{e}/L
```

ODEs - WSCCS model

$$dS/dt = -\frac{p_i Med2_t S_t}{S_t + I_t + R_t} + p_s R_t ,$$

$$dI/dt = -p_r I_t + \frac{p_i Med2_t S_t}{S_t + I_t + R_t} ,$$

$$dR/dt = p_r I_t - p_s R_t ,$$

$$dMed/dt = p_d Med2_t - \frac{Med_t I_t}{Med_t + Med2_t} ,$$

$$dMed2/dt = \frac{Med_t I_t}{Med_t + Med2_t} - p_d Med2_t .$$

Conclusions

- PEPA and WSCCS bring different styles to modelling disease

Conclusions

- PEPA and WSCCS bring different styles to modelling disease
- Choice of methods to derive PEPA ODEs but which one matches the system dynamics?

Conclusions

- PEPA and WSCCS bring different styles to modelling disease
- Choice of methods to derive PEPA ODEs but which one matches the system dynamics?
- More investigation required!

System Dynamics project

- To develop useful process algebra based models of disease spread using the contrasting formalisms WSCCS and PEPA.
- To extend current methods of extracting system dynamics from process algebra.
- To classify the ways individuals relate, extracting population level interaction functions directly.
- To establish features of modelling languages required to describe disease spread and other biological interactions.
- To provide complementary versions of WSCCS and PEPA with extensions to capture those features.
- To encourage wider take-up of process algebra for Systems Biology.