Population models from PEPA descriptions

Jane Hillston. LFCS, University of Edinburgh

19th April 2006

Joint work with Jeremy Bradley, Muffy Calder and Stephen Gilmore

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Population models from PEPA descriptions

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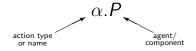
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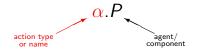
Models consist of agents which engage in actions.



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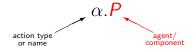
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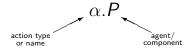
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Models consist of agents which engage in actions.



The structured operational (interleaving) semantics of the language is used to generate a labelled transition system.

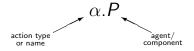
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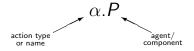
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Process algebra model

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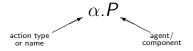
Process algebra model

SOS rules

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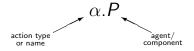
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Process algebra model SOS rules Labelled transition system

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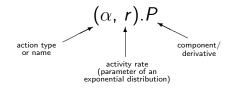
Process algebra model SOS rules Labelled transition system

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Stochastic Process Algebra

 Models are constructed from components which engage in activities.



The language may be used to generate a Markov Process (CTMC).

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Population models from PEPA descriptions

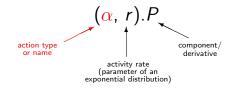
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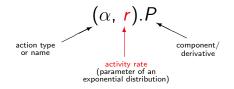
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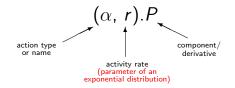
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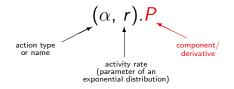
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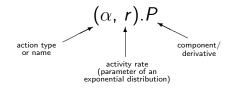
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SPA MODEL

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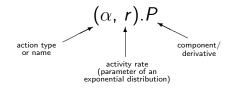
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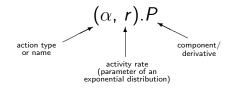
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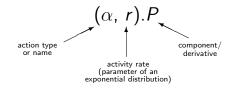
SPA SOS rules LABELLED MODEL SYSTEM

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Stochastic Process Algebra

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The language may be used to generate a Markov Process (CTMC).

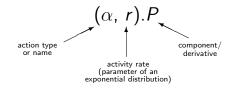
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 Models are constructed from components which engage in activities.



The language may be used to generate a Markov Process (CTMC).

SPA SOS rules LABELLED TRANSITION SYSTEM diagram CTMC Q

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PEPA

$$S ::= (\alpha, r).S | S + S | A$$
$$P ::= S | P \bowtie_{L} P | P/L$$

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PEPA

$$S ::= (\alpha, r).S | S + S | A$$

$$P ::= S | P \bowtie_{L} P | P/L$$

PREFIX: $(\alpha, r).S$ designated first action

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PEPA			
	\mathbf{C}	$C \mid C \mid C \mid A$	

$$S ::= (\alpha, r).S | S + S | A$$
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PREFIX:

CHOICE:

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PEPA			
	<i>S</i> ::=	$(\alpha, r).S \mid S + S \mid A$	
	P ::=	$S \mid P \bowtie_{L} P \mid P/L$	
PREFIX:	$(\alpha, r).S$	designated first action	
CHOICE:	S + S	competing components	
		(race policy)	
CONSTA	NT: $A \stackrel{def}{=} S$	assigning names	

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PEPA			
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COOPEF	RATION: $P \bowtie_{L} P$	$\alpha \notin L$ concurrent activity (<i>individual actions</i>) $\alpha \in L$ cooperative activity (<i>shared actions</i>)	

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PEPA			
		$(\alpha, r).S \mid S + S \mid A$ $S \mid P \bowtie_{L} P \mid P/L$	
PREFIX:	$(\alpha, r).S$	designated first action	
CHOICE:	S + S	competing components (race policy)	
CONSTA	NT: $A \stackrel{\text{\tiny def}}{=} S$	assigning names	
COOPER	ATION: $P \bowtie_{L} P$	$\alpha \notin L$ concurrent activity (<i>individual actions</i>) $\alpha \in L$ cooperative activity (<i>shared actions</i>)	
HIDING:	P/L	abstraction $\alpha \in L \Rightarrow \alpha \to \tau$	

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The CTMC semantics of PEPA and other SPA incurs problems of state space explosion.

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 The CTMC semantics of PEPA and other SPA incurs problems of state space explosion. (A problem shared by all discrete state modelling formalisms.)

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- The CTMC semantics of PEPA and other SPA incurs problems of state space explosion. (A problem shared by all discrete state modelling formalisms.)
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State Space Explosion			

- The CTMC semantics of PEPA and other SPA incurs problems of state space explosion. (A problem shared by all discrete state modelling formalisms.)
- Numerical solution of the underlying CTMC and model checking become intractable when the state space becomes too large.
- Symmetries, or repeated copies of the same components, offer ways to tackle this problem.

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Individuals vs. Populations

Whenever we have a system consisting of a large number of individuals we can consider treating them instead as a population.

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Individuals vs. Populations

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These alternative styles of model are already available in the systems biology arena:

ace Models

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Individuals vs. Populations

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These alternative styles of model are already available in the systems biology arena:

Stochastic Simulations (Gillespie *et al.*) are individual-based models in which each molecule is treated separately.

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Continuous State Space Models

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- Ordinary Differential Equations are population-based models in which populations of molecules are represented abstractly as concentrations.

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- Ordinary Differential Equations are population-based models in which populations of molecules are represented abstractly as concentrations.

These are alternative analysis techniques and we would like access to both and be able to carry out process algebra-based analyses.

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State Space Explosion		

PEPA models can be analysed for quantified dynamic behaviour in a number of different ways.

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Deriving quantitative data

PEPA models can be analysed for quantified dynamic behaviour in a number of different ways.

e Models

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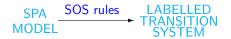
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Deriving quantitative data

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syntactic SPA MODEL analysis

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SPA syntactic RATE MODEL analysis EQUATIONS

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State Space Explosion		

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The language may be used to generate a system of ordinary differential equations (ODEs).

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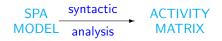
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Each of these has tool support so that the underlying model is derived automatically according to the predefined rules.

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Analysis based on Continuous-time Markov Chains

Modelling with quantified process algebras

Tiny example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2$

$$P_{2} \stackrel{\text{\tiny def}}{=} (run, r).P_{3} \qquad P_{3} \stackrel{\text{\tiny def}}{=} (stop, r).P_{1}$$

System $\stackrel{\text{\tiny def}}{=} (P_{1} \parallel P_{1})$

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This example defines a system with nine reachable states:

 1. $P_1 \parallel P_1$ 4. $P_2 \parallel P_1$ 7. $P_3 \parallel P_1$

 2. $P_1 \parallel P_2$ 5. $P_2 \parallel P_2$ 8. $P_3 \parallel P_2$

 3. $P_1 \parallel P_3$ 6. $P_2 \parallel P_3$ 9. $P_3 \parallel P_3$

The transitions between states have quantified duration r which can be evaluated against a CTMC or ODE interpretation.

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Analysis based on Continuous-time Markov Chains

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Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 0:

1. 1.0000	4. 0.0000	7. 0.0000
2. 0.0000	5. 0.0000	8. 0.0000
3. 0.0000	6. 0.0000	9. 0.0000

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Conclusions

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Using transient analysis we can evaluate the probability of each state with respect to time. For t = 1:

1. 0.1642	4. 0.1567	7. 0.0842	
2. 0.1567	5. 0.1496	8. 0.0804	
3. 0.0842	6. 0.0804	9. 0.0432	

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Analysis based on Continuous-time Markov Chains

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Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 2:

1. 0.1056	4. 0.1159	7. 0.1034	
2. 0.1159	5. 0.1272	8. 0.1135	
3. 0.1034	6 . 0.1135	9. 0.1012	

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Analysis based on Continuous-time Markov Chains

Analysis based on Continuous-time Markov Chains

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 3:

1. 0.1082	4. 0.1106	7. 0.1100
2. 0.1106	5. 0.1132	8. 0.1125
3. 0.1100	6 . 0.1125	9 . 0.1119

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Continuous-time Markov Chains

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Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 4:

1. 0.1106	4. 0.1108	7. 0.1111
2. 0.1108	5. 0.1110	8. 0.1113
3. 0.1111	6 . 0.1113	9 . 0.1116

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Continuous-time Markov Chains

Analysis based on Continuous-time Markov Chains

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 5:

1. 0.1111	4. 0.1110	7. 0.1111	
2. 0.1110	5. 0.1110	8. 0.1111	
3. 0.1111	6 . 0.1111	9. 0.1111	

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

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Analysis based on Continuous-time Markov Chains

Analysis based on Continuous-time Markov Chains

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 6:

1 . 0.1111	4. 0.1111	7. 0.1111	
2. 0.1111	5. 0.1110	8. 0.1111	
3. 0.1111	6 . 0.1111	9. 0.1111	

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Continuous-time Markov Chains

Analysis based on Continuous-time Markov Chains

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using transient analysis we can evaluate the probability of each state with respect to time. For t = 7:

1 . 0.1111	4. 0.1111	7. 0.1111	
2. 0.1111	5. 0.1111	8. 0.1111	
3. 0.1111	6 . 0.1111	9. 0.1111	

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

Case Study in Internet Worms

Conclusions

Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 0$$
: P_1 2.0000
 P_2 0.0000
 P_3 0.0000

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 1$$
: P_1 0.8121
 P_2 0.7734
 P_3 0.4144

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

Case Study in Internet Worms

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 2$$
: P_1 0.6490
 P_2 0.7051
 P_3 0.6457

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

Case Study in Internet Worms

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 3$$
: P_1 0.6587
 P_2 0.6719
 P_3 0.6692

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

Case Study in Internet Worms

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 4$$
: P_1 0.6648
 P_2 0.6665
 P_3 0.6685

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Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 5$$
: P_1 0.6666
 P_2 0.6663
 P_3 0.6669

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 6$$
: P_1 0.6666
 P_2 0.6666
 P_3 0.6666

Jane Hillston. LFCS, University of Edinburgh.

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Analysis based on Ordinary Differential Equations

Tiny example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ System $\stackrel{\text{def}}{=} (P_1 \parallel P_1)$

Using the ordinary differential equation semantics we can compute the expected number of each type of component.

For
$$t = 7$$
: P_1 0.6666
 P_2 0.6666
 P_3 0.6666

Jane Hillston. LFCS, University of Edinburgh.

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 0$$
: P_1 3.0000
 P_2 0.0000
 P_3 0.0000

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Ordinary Differential Equations

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Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 1$$
: P_1 1.1782
 P_2 1.1628
 P_3 0.6590

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

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Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 2$$
: P_1 0.9766
 P_2 1.0754
 P_3 0.9479

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

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Analysis based on Ordinary Differential Equations

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Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 3$$
: P_1 0.9838
 P_2 1.0142
 P_3 1.0020

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Slightly larger example $P_1 \stackrel{\text{def}}{=} (start, r).P_2$ $P_2 \stackrel{\text{def}}{=} (run, r).P_3$ $P_3 \stackrel{\text{def}}{=} (stop, r).P_1$ $System \stackrel{\text{def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 4$$
: P_1 0.9981
 P_2 0.9995
 P_3 1.0023

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Ordinary Differential Equations

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Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 5$$
: P_1 1.0001
 P_2 0.9996
 P_3 1.0003

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Ordinary Differential Equations

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Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 6$$
: P_1 1.0001
 P_2 0.9999
 P_3 1.0000

Jane Hillston. LFCS, University of Edinburgh.

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A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 7$$
: P_1 1.0000
 P_2 0.9999
 P_3 0.9999

Jane Hillston. LFCS, University of Edinburgh.

Case Study in Internet Worms

Conclusions

Analysis based on Ordinary Differential Equations

Analysis based on Ordinary Differential Equations

Slightly larger example $P_1 \stackrel{\text{\tiny def}}{=} (start, r).P_2 \quad P_2 \stackrel{\text{\tiny def}}{=} (run, r).P_3 \quad P_3 \stackrel{\text{\tiny def}}{=} (stop, r).P_1$ $System \stackrel{\text{\tiny def}}{=} (P_1 \parallel P_1 \parallel P_1)$

A slightly larger example with a third copy of the process also initiated in state P_1 .

For
$$t = 8$$
: P_1 1.0000
 P_2 1.0000
 P_3 1.0000

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

Conclusions

Analysis based on Ordinary Differential Equations

Isn't this just the Chapman-Kolmogorov equations?

It is possible to perform transient analysis of a continuous-time Markov chain by solving the Chapman-Kolmogorov differential equations:

$$\frac{d\pi(t)}{dt} = \pi(t)Q$$

[Stewart, 1994]

Jane Hillston. LFCS, University of Edinburgh.

Continuous State Space Models

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Analysis based on Ordinary Differential Equations

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It is possible to perform transient analysis of a continuous-time Markov chain by solving the Chapman-Kolmogorov differential equations:

$$\frac{d\pi(t)}{dt} = \pi(t)Q$$

[Stewart, 1994]

That's not what we're doing. We go directly to ODEs.

Jane Hillston. LFCS, University of Edinburgh.

Introduction	

Deriving Differential Equations

Use a more abstract state representation rather than the CTMC complete state space.

Jane Hillston. LFCS, University of Edinburgh.

Deriving Differential Equations

- Use a more abstract state representation rather than the CTMC complete state space.
- Assume that these state variables are subject to continuous rather than discrete change.

Jane Hillston. LFCS, University of Edinburgh.

Deriving Differential Equations

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- No longer aim to calculate the probability distribution over the entire state space of the model.

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- Assume that these state variables are subject to continuous rather than discrete change.
- No longer aim to calculate the probability distribution over the entire state space of the model.

Appropriate for models in which there are large numbers of components of the same type.

Conclusions

Introduction

Deriving Differential Equations

- In a PEPA model the state at any current time is the local derivative or state of each component of the model.
- We can represent the state of the system as the count of the current number of each possible local derivative or component type.
- We can approximate the behaviour of the model by treating each count as a continuous variable, and the state of the model as a whole as the set of such variables.
- The evolution of each count variable can then be described by an ordinary differential equation

Differential equations from PEPA models

Continuous State Space Models

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Differential equations from PEPA models

Continuous State Space Models

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Conclusions

Introduction

Deriving Differential Equations

- In a PEPA model the state at any current time is the local derivative or state of each component of the model.
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- We can represent the state of the system as the count of the current number of each possible local derivative or component type.
- We can approximate the behaviour of the model by treating each count as a continuous variable, and the state of the model as a whole as the set of such variables.
- The evolution of each count variable can then be described by an ordinary differential equation (assuming rates are deterministic).

Conclusions

Deriving Differential Equations

- The PEPA definitions of the component specify the activities which can increase or decrease the number of components exhibited in the current state.
- The cooperations show when the number of instances of another component will have an influence on the evolution of this component.

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Deriving Differential Equations

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- The cooperations show when the number of instances of another component will have an influence on the evolution of this component.

Differential equations from PEPA models

Let $N(C_{i_i}, t)$ denote the number of C_{i_i} type components at time t.

Jane Hillston. LFCS, University of Edinburgh.



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Conclusions

Differential equations from PEPA models

Let $N(C_{i_j}, t)$ denote the number of C_{i_j} type components at time t. Consider the change in a small time δt :

$$N(C_{i_j}, t + \delta t) - N(C_{i_j}, t) = -\sum_{\substack{(\alpha, r) \in E \times (C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E \times (\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

exit activities
$$+ \sum_{\substack{(\alpha, r) \in En(C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E \times (\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

entry activities

Population models from PEPA descriptions

Differential equations from PEPA models

Let $N(C_{i_j}, t)$ denote the number of C_{i_j} type components at time t. Consider the change in a small time δt :

$$N(C_{i_j}, t + \delta t) - N(C_{i_j}, t) = -\sum_{\substack{(\alpha, r) \in E_x(C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E_x(\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

exit activities
$$+ \sum_{\substack{(\alpha, r) \in E_n(C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E_x(\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

entry activities

Population models from PEPA descriptions

Conclusions

Differential equations from PEPA models

Let $N(C_{i_j}, t)$ denote the number of C_{i_j} type components at time t. Consider the change in a small time δt :

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exit activities
$$+ \sum_{\substack{(\alpha, r) \in En(C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E \times (\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

entry activities

Population models from PEPA descriptions

Jane

Differential equations from PEPA models

Let $N(C_{i_i}, t)$ denote the number of C_{i_i} type components at time t. Consider the change in a small time δt :

$$N(C_{i_{j}}, t + \delta t) - N(C_{i_{j}}, t) = -\sum_{(\alpha, r) \in E_{X}(C_{i_{j}})} r \times \min_{C_{k_{l}} \in E_{X}(\alpha, r)} (N(C_{k_{l}}, t)) \, \delta t$$

exit activities
$$+ \sum_{(\alpha, r) \in E_{R}(C_{i_{j}})} r \times \min_{C_{k_{l}} \in E_{X}(\alpha, r)} (N(C_{k_{l}}, t)) \, \delta t$$

entry activities
Jane Hillston. LFCS, University of Edinburgh.

Conclusions

Differential equations from PEPA models

Let $N(C_{i_j}, t)$ denote the number of C_{i_j} type components at time t. Consider the change in a small time δt :

$$N(C_{i_j}, t + \delta t) - N(C_{i_j}, t) = -\sum_{\substack{(\alpha, r) \in E_X(C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E_X(\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

exit activities
$$+ \sum_{\substack{(\alpha, r) \in E_I(C_{i_j})}} r \times \min_{\substack{C_{k_l} \in E_X(\alpha, r)}} (N(C_{k_l}, t)) \, \delta t$$

entry activities

Population models from PEPA descriptions

Conclusions

Differential equations from PEPA models

Let $N(C_{i_j}, t)$ denote the number of C_{i_j} type components at time t. Dividing by δt and taking the limit, $\delta t \longrightarrow 0$:

$$\frac{dN(C_{i_j}, t)}{dt} = -\sum_{(\alpha, r) \in E_X(C_{i_j})} r \times \min_{\substack{C_{k_l} \in E_X(\alpha, r)}} (N(C_{k_l}, t)) + \sum_{(\alpha, r) \in E_I(C_{i_j})} r \times \min_{\substack{C_{k_l} \in E_X(\alpha, r)}} (N(C_{k_l}, t))$$

Jane Hillston. LFCS, University of Edinburgh.

Derivation of the system of ODEs representing the PEPA model then proceeds via an activity matrix which records the influence of each activity on each component type/derivative.

The matrix has one row for each component type and one column for each activity type.

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Population models from PEPA descriptions

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Introduction	

Background

Internet worms (e.g. Nimbda, Slammer, Code Red, Sasser and Code Red 2) are malicious programs that exploit operating system security weaknesses to propagate themselves.

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Introducti	on

Background

- Internet worms (e.g. Nimbda, Slammer, Code Red, Sasser and Code Red 2) are malicious programs that exploit operating system security weaknesses to propagate themselves.
- While the security flaws go unpatched, the worm spreads epidemic-like and uses large amounts of available bandwidth.

Jane Hillston. LFCS, University of Edinburgh.

Background

- Internet worms (e.g. Nimbda, Slammer, Code Red, Sasser and Code Red 2) are malicious programs that exploit operating system security weaknesses to propagate themselves.
- While the security flaws go unpatched, the worm spreads epidemic-like and uses large amounts of available bandwidth.
- Far more destructive is the worms' effect on the Internet routing infrastructure [Nicol 2003], due to overload from nonexistent IP lookups.

Introduction

Background

- Internet worms (e.g. Nimbda, Slammer, Code Red, Sasser and Code Red 2) are malicious programs that exploit operating system security weaknesses to propagate themselves.
- While the security flaws go unpatched, the worm spreads epidemic-like and uses large amounts of available bandwidth.
- Far more destructive is the worms' effect on the Internet routing infrastructure [Nicol 2003], due to overload from nonexistent IP lookups.
- The estimated cost of computer worms and related activities is about \$50 billion a year [Slate 2004].

An Internet-scale Problem

We wish to study the emergent behaviour of Internet worms as they spread to thousands and then hundreds-of-thousands of hosts.

Jane Hillston. LFCS, University of Edinburgh.

An Internet-scale Problem

- We wish to study the emergent behaviour of Internet worms as they spread to thousands and then hundreds-of-thousands of hosts.
- Markovian process algebras are founded on an interleaving semantics. Existing explicit state-based methods for calculating steady-state, transient or passage-time measures are limited to state-spaces of the order of 10⁹.

An Internet-scale Problem

- We wish to study the emergent behaviour of Internet worms as they spread to thousands and then hundreds-of-thousands of hosts.
- Markovian process algebras are founded on an interleaving semantics. Existing explicit state-based methods for calculating steady-state, transient or passage-time measures are limited to state-spaces of the order of 10⁹.
- By transforming our stochastic process algebra model into a set of ODEs, we can obtain a plot of model behaviour against time for models with global state spaces in excess of 10¹⁰⁰⁰⁰ states.

Derived forms and additional syntax

 $P_1 \parallel P_2$ is a derived form for $P_1 \bowtie_{0} P_2$.

Jane Hillston. LFCS, University of Edinburgh.

Population models from PEPA descriptions

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Derived forms and additional syntax

 $P_1 \parallel P_2$ is a derived form for $P_1 \bowtie P_2$.

Because we are interested in transient behaviour we use the deadlocked process *Stop*.

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Derived forms and additional syntax

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When working with large numbers of hosts which transmit worm infections, we write P[n] to denote an array of n copies of P executing in parallel.

$$P[5] \equiv (P \parallel P \parallel P \parallel P \parallel P)$$

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Suceptible-Infective-Removed (SIR) model

 We apply a version of an SIR model of infection to various computer worm attack models.

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Suceptible-Infective-Removed (SIR) model

- We apply a version of an SIR model of infection to various computer worm attack models.
- An SIR model explicitly represents the total number of susceptible, infective and removed hosts in a system and is more commonly used to model disease epidemics.

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Population models from PEPA descriptions

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Introduction

Suceptible-Infective-Removed (SIR) model

$$\frac{\mathrm{d}s(t)}{\mathrm{d}t} = -\beta \, s(t) \, i(t)$$

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Introduction

Conclusions

Suceptible-Infective-Removed (SIR) model

$$\frac{\mathrm{d}s(t)}{\mathrm{d}t} = -\beta \, s(t) \, i(t)$$

$$\frac{\mathrm{d}i(t)}{\mathrm{d}t} = \beta \, s(t) \, i(t) - \gamma \, i(t)$$

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Introduction

Suceptible-Infective-Removed (SIR) model

$$\begin{array}{ll} \displaystyle \frac{\mathrm{d}s(t)}{\mathrm{d}t} &=& -\beta\,s(t)\,i(t) \\ \displaystyle \frac{\mathrm{d}i(t)}{\mathrm{d}t} &=& \beta\,s(t)\,i(t) - \gamma\,i(t) \\ \displaystyle \frac{\mathrm{d}r(t)}{\mathrm{d}t} &=& \gamma\,i(t) \end{array}$$

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This is our most basic infection model and is used to verify that we get recognisable qualitative results.

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- This is our most basic infection model and is used to verify that we get recognisable qualitative results.
- ► Initially, there are *N* susceptible computers and one infected computer.
- As the system evolves more susceptible computers become infected from the growing infective population.
- An infected computer can be patched so that it is no longer infected or susceptible to infection.
- This state is termed removed and is an absorbing state for that component in the system.

Suceptible-Infective-Removed over a network

► The parameter *M* denotes the number of concurrent, independent connections that the network can sustain.

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Suceptible-Infective-Removed over a network

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- ► The parameter *M* denotes the number of concurrent, independent connections that the network can sustain.
- An attempted network connection can fail or timeout, indicated by the *fail* action.
- This might be due to network contention or the lack of availability of a susceptible machine to infect.
- A certain number of infections will attempt to reinfect hosts; in this instance, the host is unaffected.

$$S \stackrel{\text{def}}{=} (infectS, \top).I$$

$$I \stackrel{\text{def}}{=} (infectI, \beta).I + (infectS, \top).I + (patch, \gamma).R$$

$$R \stackrel{\text{def}}{=} Stop$$

$$Net \stackrel{\text{def}}{=} (infectI, \top).Net'$$

$$Net' \stackrel{\text{def}}{=} (infectS, \beta).Net + (fail, \delta).Net$$

$$Sys \stackrel{\text{def}}{=} (S[N] \parallel I) \bowtie Net[M]$$

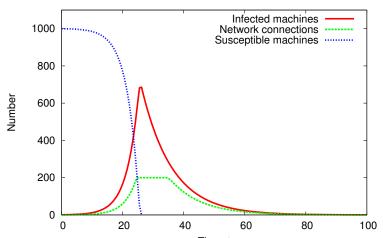
where $L = \{ infectI, infectS \}$

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Introduction

Patch rate $\gamma = 0.1$. Connection failure rate $\delta = 0.5$

Worm infection dynamics for gamma=0.1, delta=0.5



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Patch rate $\gamma = 0.3$. Connection failure rate $\delta = 0.5$

Infected machines 1000 Network connections Susceptible machines 800 Number 600 400 200 0 20 40 60 80 100 0

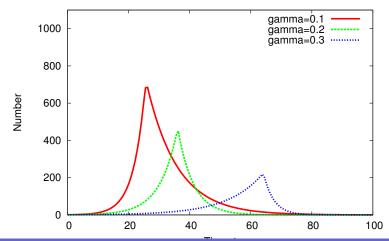
Worm infection dynamics for gamma=0.3

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Increasing machine patch rate γ from 0.1 to 0.3

Infected machines for different values of gamma



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Susceptible-Infective-Removed-Reinfection (SIRR) model

Here a small modification in the process model of infection allows for removed computers to become susceptible again after a delay.

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Susceptible-Infective-Removed-Reinfection (SIRR) model

- Here a small modification in the process model of infection allows for removed computers to become susceptible again after a delay.
- We use this to model a faulty or incomplete security upgrade or the mistaken removal of security patches which had previously defended the machine against attack.

Susceptible-Infective-Removed-Reinfection (SIRR) model

$$S \stackrel{\scriptscriptstyle def}{=} (infectS, \top).I$$

$$I \stackrel{\text{\tiny def}}{=} (infectI, \beta).I + (infectS, \top).I + (patch, \gamma).R$$

$$R \stackrel{\text{\tiny def}}{=} (unsecure, \mu).S$$

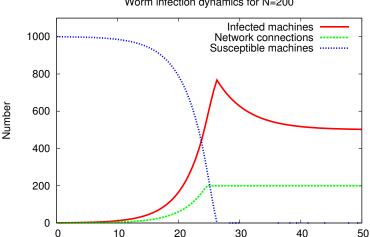
Net
$$\stackrel{\text{\tiny def}}{=}$$
 (*infectI*, \top).*Net*'

$$\mathsf{Net}' \stackrel{\scriptscriptstyle{\mathsf{def}}}{=} (\mathsf{infectS}, \beta).\mathsf{Net} + (\mathsf{fail}, \delta).\mathsf{Net}$$

Sys
$$\stackrel{\text{\tiny def}}{=}$$
 (S[1000] || I) \bowtie_{l} Net[M]

where $L = \{infectI, infectS\}$.

Unsecured SIR model (M = 200 network channels)



Worm infection dynamics for N=200

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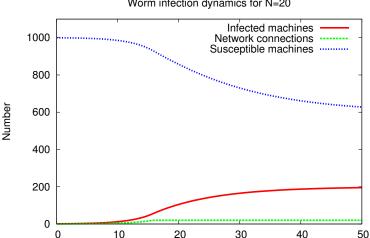
Introduction

Unsecured SIR model (M = 50 network channels)

Worm infection dynamics for N=50 Infected machines 1000 Network connections Susceptible machines 800 Number 600 400 200 0 10 30 40 20 50 0



Unsecured SIR model (M = 20 network channels)



Worm infection dynamics for N=20

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Susceptible-Infective-Removed-Attack (SIR-Attack) model

This example describes a modified SIR-Attack model. This simulates a possible distributed denial-of-service (DDOS) attack mode of an Internet worm.

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Susceptible-Infective-Removed-Attack (SIR-Attack) model

- This example describes a modified SIR-Attack model. This simulates a possible *distributed denial-of-service* (DDOS) attack mode of an Internet worm.
- Some worms have bimodal behaviour either a worm can infect another computer or it can start an attack on a victim computer.

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Introduction

Susceptible-Infective-Removed-Attack (SIR-Attack) model

- This example describes a modified SIR-Attack model. This simulates a possible *distributed denial-of-service* (DDOS) attack mode of an Internet worm.
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- The attack may be as simple as requesting a specific web page, or issuing a *ping* request.

Introduction

Susceptible-Infective-Removed-Attack (SIR-Attack) model

- This example describes a modified SIR-Attack model. This simulates a possible *distributed denial-of-service* (DDOS) attack mode of an Internet worm.
- Some worms have bimodal behaviour either a worm can infect another computer or it can start an attack on a victim computer.
- The attack may be as simple as requesting a specific web page, or issuing a *ping* request.
- The combination of perhaps millions of machines making such requests quickly overwhelms the target computer, which either crashes under the huge load, or becomes unusably slow.

Continuous State Space Models

Susceptible-Infective-Removed-Attack (SIR-Attack) model

$$S \stackrel{\text{def}}{=} (infectS, \top).I$$

$$I \stackrel{\text{def}}{=} (infectI, \beta).I + (infectS, \top).I + (patch, \gamma).R + (attack, \chi).A$$

$$A \stackrel{\text{def}}{=} (attackA, \lambda).A + (patch, \gamma).R$$

$$R \stackrel{\text{def}}{=} Stop$$

$$Net \stackrel{\text{def}}{=} (infectI, \top).Net' + (attackA, \top).Net''$$

$$Net' \stackrel{\text{def}}{=} (infectS, \beta).Net + (fail, \delta).Net$$

$$Net'' \stackrel{\text{def}}{=} (attackV, \rho).Net + (fail, \delta).Net$$

$$V \stackrel{\text{def}}{=} (attackV, \top).V'$$

$$V' \stackrel{\text{def}}{=} (release, \sigma).V$$

$$Sys \stackrel{\text{def}}{=} (S[100] \parallel I \parallel V) \bowtie Net[M]$$

where $L = \{infectI, infectS, attackA, attackV\}$.

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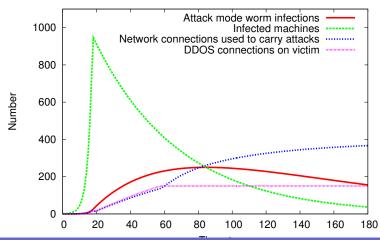
Population models from PEPA descriptions

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Introduction

DDOS attack that overwhelms a victim machine

DDOS attack with victim saturation at 150 connections



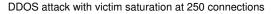
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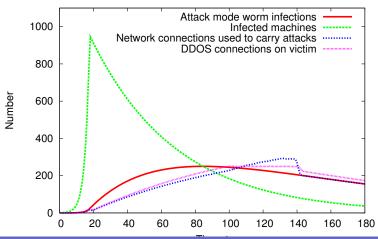
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Introduction

DDOS attack that briefly incapacitates a victim machine

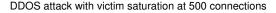


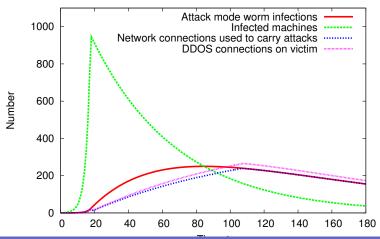


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DDOS attack that does not saturate the victim's capacity





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Case Study Conclusions

The scale of the effects of Internet worms defeats attempts to model their behaviour in very close detail, and thus impedes the analysis which has the potential to bring understanding of their function and distribution.

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Case Study Conclusions

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- Large-scale modelling can be effective here, because it abstracts away from modelling of individual behaviour and considers population-based representations.

Introduction

Case Study Conclusions

- The scale of the effects of Internet worms defeats attempts to model their behaviour in very close detail, and thus impedes the analysis which has the potential to bring understanding of their function and distribution.
- Large-scale modelling can be effective here, because it abstracts away from modelling of individual behaviour and considers population-based representations.
- The scale of problems which can be modelled in this way vastly exceeds those which are founded on explicit state representations.

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Outline

Introduction

Stochastic Process Algebra State Space Explosion

Continuous State Space Models

Analysis based on Continuous-time Markov Chains Analysis based on Ordinary Differential Equations Deriving Differential Equations

Case Study in Internet Worms

Conclusions

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Population models from PEPA descriptions

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Introduction	

Conclusions

The derivation of differential equations appears to offer an interesting alternative to existing modelling approaches to performance evaluation of large scale models.

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Alternative Representations

ODEs (Continuous Approximation)

Stochastic Simulation

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Case Study in Internet Worms

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Alternative Representations

SPA models with discrete levels of population

ODEs (Continuous Approximation)

SPA models of individuals

Stochastic Simulation

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Population models from PEPA descriptions

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Case Study in Internet Worms

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Alternative Representations

CTMCs with discrete levels of population

ODEs (Continuous Approximation)

CTMCs with individuals

Stochastic Simulation

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Alternative Representations

CTMCs with discrete levels of population

ODEs (Continuous Approximation) Agreement for large numbers of individuals

Stochastic Simulation

CTMCs with individuals

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Alternative Representations

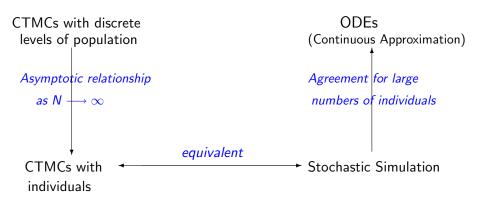
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CTMCs with discrete
levels of population
Asymptotic relationship
as N \rightarrow \infty
CTMCs with
individuals
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ODEs (Continuous Approximation) Agreement for large numbers of individuals

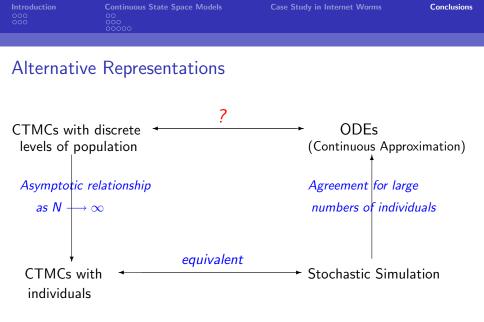
Stochastic Simulation

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Alternative Representations



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Introduction	
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 Establish the relationship between the ODE model and the population model CTMC

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Introduction

- Establish the relationship between the ODE model and the population model CTMC
 - When can we use verification (ie model checking) on a CTMC population model and expect the results to hold with respect to the ODE population model?

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Introduction	

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- Reintroduce a stochastic element:

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 - Use of random or stochastic differential equations;

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 - When can we use verification (ie model checking) on a CTMC population model and expect the results to hold with respect to the ODE population model?
- Reintroduce a stochastic element:
 - Use of random or stochastic differential equations;
 - Limit the continuous element to a few continuous component types, with others having usual CTMC semantics (c.f. fluid stochastic Petri models)

Introduction	

Thank You!

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