Overview of the Tutorial

- 1. Introduction
 - Transposing programming concepts to the analysis of living processes
- 2. Rule-based modeling of biochemical systems
 - " Syntax: molecules, reactions, regulations, SBML/SBGN Biocham notations
 - " Semantics: Boolean, Differential and Stochastic interpretations of reactions
 - " Static analyses: consistency, influence graph circuits, protein functions,&
 - " Examples in cell signaling, gene expression, virus infection, cell cycle
- 3. Temporal Logic based formalization of biological properties
 - " *Qualitative model-checking* in propositional Computation Tree Logic CTL
 - " Quantitative model-checking in Linear Time Logic LTL(R)
 - " Parameter search in high dimension w.r.t. LTL(R) specifications
 - " Robustness and sensitivity analyses w.r.t. LTL(R) specifications
- 4. Conclusion



Cell Cycle Control by Cyclins: $G1 \rightarrow S \rightarrow G2 \rightarrow M$





Cdk1-cyclin B Cdk1-cyclin A G2 M G1 Cdk4-cy Di Cdk4-cy Di Cdk6-cy D Cdk2-cyclin A Cdk2-cyclin E

G1: CdK4-CycD Cdk6-CycD Cdk2-CycE S: Cdk2-CycA G2,M: Cdk1-CycA Cdk1-CycB (MPF)









Mammalian Cell Cycle Control Map [Kohn 99]





Kohn s map detail for Cdk2

Complexation with CycA and CycE

Biocham Rule Patterns:

cdk2~\$P + cycA-\$C => cdk2~\$P-cycA-\$C
 where \$C in {_,cks1} .
cdk2~\$P + cycE~\$Q-\$C => cdk2~\$P-cycE~\$Q-\$C
 where \$C in {_,cks1} .
p57 + cdk2~\$P-cycA-\$C => p57-cdk2~\$P-cycA-\$C
 where \$C in {_, cks1}.
cycE-\$C =[cdk2~{p2}-cycE-\$S]=> cycE~{T380}-\$C
 where \$S in {_, cks1} and \$C in {_, cdk2~?, cdk2~?-cks1}
Total: 147 rule patterns 2733 expanded rules [Chiaverini Danos 03]



PT380

C25

CVCE

C19

C4

cdk2

Q - C13

Computation Tree Logic CTL

Temporal logics extend classical logic with modal operators for time & non-det. Introduced for program verification by [Pnueli 77]





About *reachability*:

- " Can the cell produce some protein P? reachable (P) ==EF (P)
- " Can the cell produce P, Q and not R?



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Can the cell reach a set s of (partially described) states while passing by another set of states s_2 ?



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- " Is state s_2 a necessary checkpoint for reaching state s?

checkpoint $(s_2, s) = \neg E (\neg s_2 U s)$



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" Is s_2 always a checkpoint for s? AG ($\neg s \rightarrow checkpoint(s_2, s)$)

About <u>stability</u>.

" Is state s a stable state? stable(s) == AG(s)



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- " Must the cell reach a stable state s? AG(stable(s))
- What are the stable states? Not expressible in CTL.
 needs to combine CTL with search [Chan 00, Calzone-Chabrier-Fages-Soliman 05, Fages-Rizk 07 09].



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- " How long does it take for a molecule to become activated?
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About oscillations:

Can the system exhibit a cyclic behavior w.r.t. the presence of P? oscil(P) == EG((F $\neg P$) ^ (F P))

temporal operators not preceded by a path operator: CTL* formula

approximation in CTL: $oscil(P) == EG((EF \neg P) \land (EF P))$



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" Add ϕ to the states satisfying ϕ



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Model-checking algorithm in O($|K|^*|\phi|$).

Complexity: CTL model-checking is Ptime-complete,



Symbolic CTL Model-Checking Algorithm

Represent *finite* Kripke structures using Boolean constraints for

- " sets of states as a boolean constraint c(V)
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Ordered Binary Decision Diagrams OBDD [Bryant 85] provide *canonical forms* for Boolean formulas (decides SAT in NP, and equivalence TAUT in co-NP)

 $(x \vee \neg y) \land (y \vee \neg z) \land (z \vee \neg x)$ and $(x \vee \neg z) \land (z \vee \neg y) \land (y \vee \neg x)$ are equivalent, they have the same BDD(x,y,z)





Mammalian Cell Cycle Control Map [Kohn 99]





Mammalian Cell Cycle Control Benchmark

147-2733 rules, 165 proteins and genes, 500 variables, 2⁵⁰⁰ states. BIOCHAM NuSMV model-checker time in seconds: [Chabrier Fages 03 CMSB]

Initial state G2	Query:	Time:
	compiling	29s
Reachability G1	EF CycE	2s
Reachability G1	EF CycD	1.9s
Reachability G1	EF PCNA-CycD	1.7s
Checkpoint		2.2s
for mitosis complex	U Cdk1~{Thr161}-CycB)	
Oscillations CycA	EG ((EF – CycA) & (EF CycA))	31.8s
Osciallations CycB	EG ((EF – CycB) & (EF CycB)) false !	6s



Linear Time Logic with Constraints LTL(R)

Constraints over *concentrations* and *derivatives* as formulae over the reals:

[M] > 0.2 [M]+[P] > [Q] d([M])/dt < 0

LTL(R) formulae

minimum threshold value reached: F([M]>0.2)minimum threshold value reached and maintained: FG([M]>0.2)local maximum V: F([M]<V & F([M]=V & F([M]<V))F([M]>2 & F(d([M])/dt<0 & F([M]<2 & d([M])/dt>0 & F(d([M])/dt<0))))oscil(M,n) defined as at least n alternances of the sign of the derivative



LTL(R) Constraints with Real-time Variable

LTL(R) formulae with real-time variable

Threshold value with a minimum delay $F([M]>0.2) \& G(Time<5 \Rightarrow [M]<0.2)$

Numerical data time series (for curve fitting) **F**(Time=1 & [M]=0.05 & **F**(Time=2 & [M]=0.12& **F**(Time=3 & [M]=0.25)))

Period constraint

 $\begin{aligned} \text{Period}(A,75) &= \exists \ t \ \exists v \ \textbf{F}(\text{Time} = t \ \& \ [A] = v \ \& \ d([A])/dt > 0 \ \& \ \textbf{X}(d([A])/dt < 0) \\ & \& \ \textbf{F}(\text{Time} = t + 75 \ \& \ [A] = v \ \& \ d([A])/dt > 0 \ \& \ \textbf{X}(d([A])/dt < 0))) \end{aligned}$



Numerical Integration of ODE Models

dX/dt = f(X). Initial conditions X_0

Idea: discretize time t_0 , $t_1 = t_0 + \Delta t_0$, $t_2 = t_1 + \Delta t_1$, & and compute a numerical trace $(t_0, X_0, dX_0/dt)$, $(t_1, X_1, dX_1/dt)$, & , $(t_n, X_n, dX_n/dt)$

Euler s method $t_{i+1} = t_i + \Delta t$ $X_{i+1} = X_i + f(X_i)^* \Delta t$ error estimation $E(X_{i+1}) = |f(X_i) - f(X_{i+1})|^* \Delta t$

Runge-Kutta s method intermediate computations at $\Delta t/2$ adaptive step method: $\Delta t_{i+1} = \Delta t_i/2$ while E>Emax, otherwise $\Delta t_{i+1} = 2^*\Delta t_i$

Rosenbrock s implicit method for stiff systems: $_{34}$ solve $X_{i+1} = X_i + f(X_{i+1})^* \Delta t$ by formal differentiation $_{534}$ by formal differentiation Hutorial ICSB TO Edinburgh



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 Label each state of the trace with the formula sconstraints that are true,



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 Add X φ₁ to the immediate predecessors of states labeled by φ₁,



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 - Add $\phi_1 \mathbf{W} \phi_2$ to the states labelled by $\phi_1 \wedge \phi_2$, to the last state if it is labelled by ϕ_1 , and to the predecessors of states labelled by $\phi_1 \mathbf{W} \phi_2$ while they satisfy ϕ_1 ,



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 Beture true if the initial state is labelled by φ₁ and folce otherwise.
 - Return true if the initial state is labelled by φ, and false otherwise41François Fages Tutorial ICSB'10 Edinburgh



Input: an ODE model M(p) with n parameters p in range [pmin,pmax], an LTL(R) specification φ
 Output: parameter values v such that M(v) |= φ or fail if no such values



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Exponential complexity in O(s^n) where s is the maximum number of tried values in the range of n parameters

Gradient-based methods need a satisfaction degree for LTL(R) formulae&



Cell Cycle Control Model [Tyson 91]

k1 for _=>Cyclin.

k2*[Cyclin] for Cyclin=>_.

 $\label{eq:k3*[Cyclin]*[Cdc2~{p1}] for Cyclin+Cdc2~{p1}=>Cdc2~{p1}-Cyclin~{p1}. \\ k4p*[Cdc2~{p1}-Cyclin~{p1}] for Cdc2~{p1}-Cyclin~{p1}=>Cdc2-Cyclin~{p1}. \\ k4*[Cdc2-Cyclin~{p1}]^2*[Cdc2~{p1}-Cyclin~{p1}] for \\ k4*[Cdc2-Cyclin~{p1}]^2*[Cdc2~{p1}-Cyclin~{p1}] for \\ k4*[Cdc2-Cyclin~{p1}]^2*[Cdc2-{p1}-Cyclin~{p1}] for \\ k4*[Cdc2-Cyclin~{p1}-Cyclin~{p1}] for \\ k4*[Cdc2-Cyclin~{p1}-Cyclin~{p1}-Cyclin~{p1}] for \\ k4*[Cdc2-Cyclin~{p1}$

 $Cdc2 \sim \{p1\}-Cyclin \sim \{p1\}=[Cdc2-Cyclin \sim \{p1\}]=>Cdc2-Cyclin \sim \{p1\}.$

 $k5^{Cdc2-Cyclin}{p1} for Cdc2-Cyclin}{p1}=>Cdc2{p1}-Cyclin}{p1}.$

 $k6^{t}[Cdc2-Cyclin \{p1\}]$ for Cdc2-Cyclin $\{p1\}=>Cdc2+Cyclin \{p1\}$.

```
k7^{*}[Cyclin~{p1}] for Cyclin~{p1}=>_.
```

 $k8^{*}[Cdc2]$ for Cdc2=>Cdc2~{p1}.

 $k9^{(Cdc2^{p1})} for Cdc2^{p1} =>Cdc2.$

parameter(k1,0.015). parameter(k2,0.015). parameter(k3,200).

parameter(k4p,0.018). parameter(k4,180). parameter(k5,0).

parameter(k6,1). parameter(k7,0.6). parameter(k8,100).parameter(k9,100).

present(Cdc2,1).



biocham: learn_parameter([k3,k4],[(0,200),(0,200)],20, oscil(Cdc2-Cyclin~{p1},3),150).



biocham: learn_parameter([k3,k4],[(0,200),(0,200)],20,



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First values found :

parameter(k3,10).

parameter(k4,70).

biocham: learn_parameter([k3,k4],[(0,200),(0,200)],20, oscil(Cdc2-Cyclin~{p1},3) & F([Cdc2-Cyclin~{p1}]>0.15), 150).

First values found : parameter(k3,10). parameter(k4,120).





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biocham: learn_parameter([k3,k4],[(0,200),(0,200)],20,

period(Cdc2-Cyclin~{p1},35), 150).

First values found: parameter(k3,10). parameter(k4,280).





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Coupling Cell and Circadian Cycles through Wee1



[L. Calzone, S. Soliman 2006]





Entrainment in period constraint expressed in LTL with the period formula

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