

Constructing a Knowledge Base for Gene Regulatory Dynamics by Formal Concept Analysis Methods

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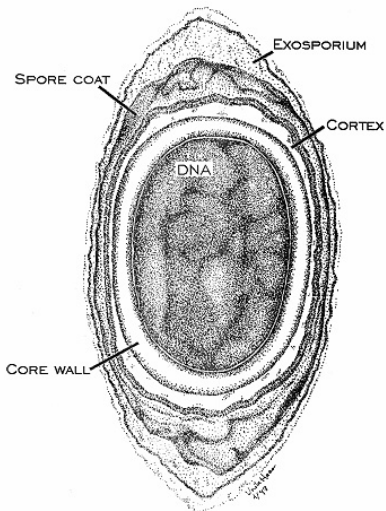
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Outline

- 1 The Example: Sporulation in *Bacillus subtilis*
- 2 Introduction of 4 Formal Contexts
- 3 Attribute Exploration of the Transitive Context Representing a Complete Simulation
- 4 Outlook

Bacillus subtilis



- Gram positive soil bacterium.
- Produces single endospores under environmental stress, which can survive ultraviolet or gamma radiation, acid, hours of boiling, or starvation.
- Switch between two completely different genetic programs.
- Model organism.

Boolean Network for the Sporulation Decision [Ste07]

AbrB	=	SigA $\overline{\text{AbrB}}$ $\overline{\text{Spo0AP}}$
SigF	=	(SigH Spo0AP $\overline{\text{SinR}}$) + (SigH Spo0AP SinI)
KinA	=	SigH $\overline{\text{Spo0AP}}$
Spo0A	=	(SigH $\overline{\text{Spo0AP}}$) + (SigA $\overline{\text{Spo0AP}}$)
$\overline{\text{Spo0A}}$	=	($\overline{\text{SigA}}$ SinR $\overline{\text{SinI}}$) + ($\overline{\text{SigH}}$ $\overline{\text{SigA}}$) + Spo0AP
Spo0AP	=	Signal Spo0A $\overline{\text{Spo0E}}$ KinA
Spo0E	=	SigA $\overline{\text{AbrB}}$
SigH	=	SigA $\overline{\text{AbrB}}$
Hpr	=	SigA AbrB $\overline{\text{Spo0AP}}$
SinR	=	(SigA $\overline{\text{AbrB}}$ $\overline{\text{Hpr}}$ $\overline{\text{SinR}}$ $\overline{\text{SinI}}$ Spo0AP) + (SigA $\overline{\text{AbrB}}$ $\overline{\text{Hpr}}$ SinR SinI Spo0AP)
SinI	=	SinR
SigA	=	TRUE (input to the model)
Signal	=	TRUE or FALSE (constant, depending on the input state)

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Formal Contexts and Concepts

Definition

A **formal context** (G, M, I) defines a relation $I \subseteq G \times M$ between objects G and attributes M . For $A \subseteq G$ and $B \subseteq M$, derivation operators $'$ are defined by:

$$A' := \{m \in M \mid glm \text{ for all } g \in A\}$$

$$B' := \{g \in G \mid glm \text{ for all } m \in B\}$$

Definition

A **formal concept** of the context (G, M, I) is a pair (A, B) with $A \subseteq G$, $B \subseteq M$, $A' = B$ and $B' = A$. A is the **extent**, B the **intent** of the concept (A, B) .

" defines closure operators on G and M .

(A'', A') and (B', B'') are concepts, for all $A \in G$, $B \in M$.

A State Context Representing a Simulation without Stress

Given: sets E (entities) and F (fluents),
states $\varphi \in F_1 \times \dots \times F_n$, $n = |E|$, $F_1 = \dots = F_n = F$.

Definition

A **state context** is a formal context (G, M, I) with
 $G \subseteq F^E := \{\varphi : E \rightarrow F\}$ and $M \subseteq E \times F$; its relation I is given as
 $\varphi I(e, f) :\Leftrightarrow \varphi(e) = f$, for all $\varphi \in G$, $e \in E$ and $f \in F$.

State	KinA	Spo0A	Spo0AP	AbrB	Spo0E	SigH	Hpr	...
φ_0	-	+	-	-	-	-	+	
φ_1	-	+	-	+	+	+	-	
φ_2	+	+	-	-	-	-	+	

A state context in the form of a many-valued context.

A State Context Representing a Simulation without Stress

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State	KinA.off	KinA.on	Spo0A.off	Spo0A.on	Spo0AP.off	Spo0AP.on	AbrB.off	AbrB.on	Spo0E.off	Spo0E.on	SigH.off	SigH.on	Hpr.off	Hpr.on	...
φ_0	x			x	x		x		x		x			x	
φ_1	x			x	x			x		x		x	x		
φ_2		x		x	x		x		x		x			x	

The state context scaled to a one-valued context (corresponding to Def.)

A State Context Representing a Simulation without Stress

Given: sets E (entities) and F (fluents),

states $\varphi \in F_1 \times \dots \times F_n$, $n = |E|$, $F_1 = \dots = F_n = F$.

Definition

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State	KinA.off	KinA.on	Spo0A.off	Spo0A.on	Spo0AP.off	AbrB.off	Spo0E.off	SigH.off	Hpr.on	Spo0AP.on	AbrB.on	Spo0E.on	SigH.on	Hpr.off	...
φ_0	x			x	x	x	x	x	x						
φ_2		x		x	x	x	x	x	x						
φ_1	x			x	x						x	x	x	x	

Concept = maximal rectangle, after permutation of rows and columns.

Transition Context

Definition

Given a state context (G, M, I) and a relation $R \subseteq G \times G$, a **transition context** \mathbb{K} is the context $(R, M \times \{in, out\}, \tilde{I})$ with the property

$$(\varphi_1, \varphi_2)\tilde{I}(e, f, i) \Leftrightarrow \begin{cases} \varphi_1(e) = f & \text{for } i = in \\ \varphi_2(e) = f & \text{for } i = out. \end{cases}$$

Transition	KinA.in.off	KinA.in.on	AbrB.in.off	AbrB.in.on	Spo0E.in.off	Spo0E.in.on	SigH.in.off	SigH.in.on	Hpr.in.off	Hpr.in.on	...	KinA.out.off	KinA.out.on	AbrB.out.off	AbrB.out.on	Sp0E.out.off	Sp0E.out.on	SigH.out.off	SigH.out.on	Hpr.out.off	Hpr.in.on	...
(φ_0, φ_1)	x	x	x	x	x	x	x	x	x	x		x		x	x	x	x	x	x	x	x	
(φ_1, φ_2)	x		x	x	x	x	x	x	x				x	x	x	x	x					x
(φ_2, φ_1)		x	x	x	x	x	x			x		x		x	x	x	x	x	x	x		

Transitive context \mathbb{K}_t : transitively closed relation $t(R) := \bigcup_{n \in \mathbb{N} \setminus \{0\}} R^n$.

The Concept Lattice of the Transitive Context

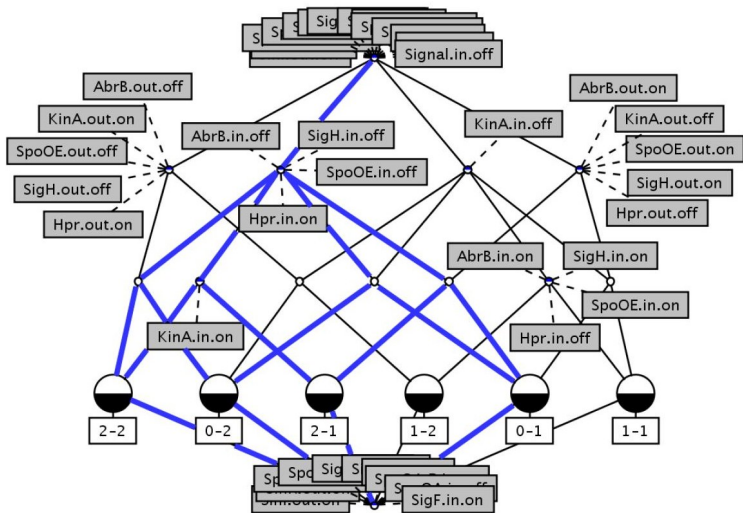


Figure: *Signal*: starvation; *AbrB*, *Hpr*, *SigA*, *SigF*, *SigH*, *SinR*, *Spo0A* (phosphorylated form *Spo0AP*): transcription factors; *KinA*: kinase; *Spo0E*: phosphatase; *SinI* inactivates *SinR* by binding to it.

Boolean Network for the Sporulation Decision [Ste07]

AbrB	=	SigA $\overline{\text{AbrB}}$ $\overline{\text{Spo0AP}}$
SigF	=	(SigH Spo0AP $\overline{\text{SinR}}$) + (SigH Spo0AP SinI)
KinA	=	SigH $\overline{\text{Spo0AP}}$
Spo0A	=	(SigH $\overline{\text{Spo0AP}}$) + (SigA $\overline{\text{Spo0AP}}$)
$\overline{\text{Spo0A}}$	=	($\overline{\text{SigA}}$ SinR $\overline{\text{SinI}}$) + ($\overline{\text{SigH}}$ $\overline{\text{SigA}}$) + Spo0AP
Spo0AP	=	Signal Spo0A $\overline{\text{Spo0E}}$ KinA
Spo0E	=	SigA $\overline{\text{AbrB}}$
SigH	=	SigA $\overline{\text{AbrB}}$
Hpr	=	SigA AbrB $\overline{\text{Spo0AP}}$
SinR	=	(SigA $\overline{\text{AbrB}}$ $\overline{\text{Hpr}}$ $\overline{\text{SinR}}$ $\overline{\text{SinI}}$ Spo0AP) + (SigA $\overline{\text{AbrB}}$ $\overline{\text{Hpr}}$ SinR SinI Spo0AP)
SinI	=	SinR
SigA	=	TRUE (input to the model)
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Extended State Context

Supplementary temporal attributes $\text{always}(m)$, $\text{never}(m)$, $\text{eventually}(m)$...

State	KinA	Spo0A	Spo0AP	AbrB	Spo0E	SigH	Hpr	$\text{ev}(\text{KinA})$	$\text{alw}(\text{KinA})$	$\text{nev}(\text{Spo0AP})$	$\text{ev}(\text{AbrB})$	$\text{alw}(\text{AbrB})$	$\text{ev}(\text{Hpr})$...
φ_0	-	+	-	-	-	-	+	x		x	x		x	
φ_1	-	+	-	+	+	+	-	x		x	x		x	
φ_2	+	+	-	-	-	-	+	x		x	x		x	

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The Attribute Exploration Algorithm

- Interactive algorithm.
- Generates implications $A \rightarrow B$ between attribute sets of a given formal context.
- An expert or a computer program decides about the general validity of the rule, e.g. by comparison of a simulation with observed time series.
- No \curvearrowright counterexample = new object.
- Yes \curvearrowright add $A \rightarrow B$ to the stem base of the context.
- Sound, complete, non redundant - each valid implication is derivable by the Armstrong rules in linear time ($W, X, Y, Z \subseteq M$):

$$\frac{\top}{X \rightarrow X}$$

$$\frac{X \rightarrow Y}{X \cup Z \rightarrow Y}$$

$$\frac{X \rightarrow Y, Y \cup Z \rightarrow W}{X \cup Z \rightarrow W}$$

- Mathematical foundation: Pseudo-closed sets, Theorem of Duquenne-Guigues [GW99, Theorem 8]

Some Interesting Implications of the Stem Base

- 4224 transitions from all possible $2^{12} = 4096$ initial states.
- 11.700 transitions in the transitive context.
- Stem base: 524 implications with support > 0 (computing time $< 12\text{h}$).
- $11.023.494 \approx 2^{24}$ concepts in the lattice.

SigH.out.off \rightarrow AbrB.out.off, SpoOE.out.off, SinR.out.off, SinI.out.off

All these genes are coregulated: $\overline{gene.out} = \overline{SigA.in} + AbrB.in (+ \dots)$.

SigF.out.on \rightarrow KinA.out.off, Spo0A.out.off, Hpr.out.off, AbrB.out.off

Spo0AP is reported to activate the production of SigF but also to repress its own expression (mutual exclusion). [De 04]

Implications Specific for the Transitive Context

< 4500 > Spo0AP.in.on, KinA.out.off \rightarrow Hpr.out.off

< 4212 > SigH.in.on, KinA.out.off \rightarrow Hpr.out.off

< 3972 > AbrB.in.off, KinA.out.off \rightarrow Hpr.out.off

$\overline{\text{Hpr}}$ and $\overline{\text{KinA}}$ are determined by different Boolean functions, but they are coregulated in all states emerging from any input state characterized by the single attributes Spo0AP.on, SigH.on or AbrB.on.

< 3904 > AbrB.out.on

\rightarrow SigA.in.on, SigA.out.on, SigF.out.off, Spo0A.out.on,
Spo0E.out.on, SigH.out.on, Hpr.out.off, SinR.out.off, SinI.out.off

AbrB is an important "marker" for the regulation of many genes, which is understandable from the Boolean rules with hindsight. By a PubMed query, a direct confirmation was found for the downregulation of SigF together with upregulation of AbrB [C. A. Tomas et al. 2003].

Querying the Stem Base

"For example, we know that in the absence of nutritional stress, sporulation should never be initiated [De 04]. We can use model checking to show this holds in our model by proving that no reachable state exists with $SigF = 1$ starting from any initial state in which $Signal = 0$, $SigF = 0$ and $Spo0AP = 0$." [Ste07, 341]

This is equivalent to the implication following from the stem base:

$$Signal.in.off, SigF.in.off, Spo0AP.in.off \rightarrow SigF.out.off$$

A Query to the PROLOG Knowledge Base

```
:- table off/1.           on(signal.in)   :- on(signal.out).
:- table on/1.           on(signal.out) :- on(signal.in).
off(sigF.in).           on(sigA.in)    :- on(sigA.out).
off(spo0AP.in).        on(sigA.out)   :- on(sigA.in).
on(sigF.out).           off(abrB.out)  :- on(sigF.out).
                        off(kinA.out)   :- on(sigF.out).
                        off(spo0AP.out) :- off(spo0A.in), on(sigF.out).
on(signal)              :- off(sigH.in), on(sigF.out).
```

SigF.in.off Spo0AP.in.off SigF.out.on

→ Signal.in.on Signal.out.on SigA.in.on SigA.out.on Spo0AP.out.off
Spo0A.out.off AbrB.out.off KinA.out.off Hpr.out.off

The initial presence of the signal and the ubiquitous transcription factor SigA only are necessary for the initiation of sporulation.

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Towards Realistic Computability

- Attribute exploration is an exponential algorithm.
- Querying the stem base is possible in linear time.
- Background knowledge: state \rightarrow transition \rightarrow transitive context.
- Automatic decision of implications by model checking or automatic text mining.
- Structural and functional analysis of Boolean networks [S. Klamt 2006].
- Conclude dynamical properties of Boolean networks by regarding them as polynomial dynamical systems over finite fields and by exploiting theoretical work in the context of cellular automata [Laubenbacher 2005].

Further Research

- Comparison to observed time series: current work related to the construction and deconstruction of the extracellular matrix in the case of human rheumatoid arthritis. (See also Wollbold 2007.)
- Validation of the simulated transitions: thresholds of support and confidence for the observed transitions.
- Expert based exploration.
- Split attribute exploration into partial problems - decomposition theory of concept lattices.

Literature



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