The perspective we take on a system determines the features and properties of the system that we focus on. It determines where we search for causes to explain the effects on the system that we observe. It determines the terms in which we expect the information about the system to be expressed. And it can also influence the choice of formalism that will be used to convey the information. This paper proposes to start making these considerations concrete in order to draw a practical benefit out of them.

1 Networks

In the context of this paper, a network – a.k.a. an interaction system – is any set of entities/parameters that we consider as a whole for the following reason: we presume that the changes underwent by the entities in the set are causally related to one another and account for the global system changes that we are interested in.

Remark: An interaction system can be comprised of just one entity (the human body for instance, as it might been seen in the light of a different culture). In this case, to explain the system’s global state changes, the only thing we have is, precisely, the system’s global state changes – and also the system’s environment, i.e. everything that is not the system. So to explain the system’s global state changes by something else than themselves, we must turn to the environment and find an external cause. In other terms, we must add to the system a second entity (or more) that interacts with the original. Under different circumstances, the same object might also be regarded as an interaction system comprised of several interacting entities (e.g. the human body as seen by modern medicine). In this case, the environment is not the only place where explanations can be sought. Finer explanations might also come from considering alternative interactions between the different entities of the system. Gladly, since our present representations of objects can be questioned, in neither case are we condemned to uncovering the same sorts of explanations in the same sorts of ways.

In this paper, we will illustrate the five following observations about interaction systems.

Observation 1:
Some properties that we regard as properties of systems – properties that the systems may have or not have – are actually properties of the way we look at the systems.

Observation 2:
A statement like “There exists no interaction between entity X and entity Y.” has no essential meaning in itself. Its truth value is dependent on the specific level of
abstraction from which the system – its entities, the interactions between them – is being looked at and defined.

**Observation 3:**
Incomplete data is not the only reason for the model of a real interaction system to fail to account for existing interactions between entities of the system. Despite the modeller’s flawless observation and formalisation of the system, some causal relationships between entities might still be intrinsically imperceptible to him/her under his/her current perspective.

**Observation 4:**
What information a formal object can provide about the real system it is meant to model, and what uninterpretable, non-modelling information it provides on top of that, does not just depend on the semantics associated to the formalism describing the formal object, it also essentially depends on the relative consistency of those semantics.

**Observation 5:**
The semantics associated to a formal object can be decisively affected by the history of the object and how our scientific community came to inherit it. And thus, so can the precise definition of the object that we choose among different customary variations of the definition, and the properties it has that we take interest in, and those we don’t.

## 2 Prototypes of networks

To illustrate those five observations, we are going to use a minimalist mathematical prototype of interaction systems named *Boolean Automata Networks* (BANs).

I will introduce the formalism of BANs using the BAN $\mathcal{N}$ represented below in Fig.1.

![Fig. 1: The BAN $\mathcal{N}$. LEFT: The interaction digraph $G = (V, A)$ of $\mathcal{N}$. RIGHT: $\mathcal{N}$’s defining local update functions.](image)

$\mathcal{N}$ is comprised of $n = 6$ entities, namely $\{1, 2, 3, 4, 5, 6\}$, a.k.a. automata 1, 2, 3, 4, 5 and 6. Each automaton $i \in V = [1, n]$ has a variable state in $\mathbb{B} = \{0, 1\}$. If
∀i ∈ V, x_i denotes the current state of i, then x = (x_1, x_2, ..., x_n) ∈ B^n denotes the current state of N. On the right of Fig.1 are listed six functions f_i : B^n → B. One for each automaton Ω. Function f_i defines the possible variations of Ω’s state depending on N’s. In state x ∈ B^n of N, Ω’s state can change if and only if Ω belongs to the set $U(x) = \{i \in V : f_i(x) \neq x_i\}$ of automata that are unstable in x. The state of Ω actually does change if: (i) it can and (ii) Ω is updated. For instance, in state $x = (1, 1, 0, 0, 1)$ of N, if Ω, Ω, and Ω are updated, and Ω, Ω, and Ω aren’t, then N transitions to state $x' = (f_1(x), f_2(x), x_3, f_4(x), x_5, x_6) = (0, 1, 1, 1, 0, 1)$.

Formally, a BAN is defined as a set of Boolean functions $\mathcal{N} = \{f_i : B^n \to B \mid i \in V\}$ with no mention to automata updates. A BAN is therefore not a dynamical system. This choice of definition is deliberate although nontraditional. In the literature, Automata Networks (ANs) are usually taken to represent dynamical systems [1–20, 21–28]. Their definitions are made to imply specific updating conditions. The notions of causality and time are thereby fused together and a distinction is implied between (1) process of change and (2) (result of) change – the latter being either an approximation of the former or an observed consequence of it. The object of this paper requires to take a less abstract view on the formalism, and not make this semantical distinction, so:

*Change is anything that has observable consequence, if only the observable consequence of us noticing it. Process of change is change if it has observable consequence in itself; if it hasn’t, then it’s not something there is anything to be said about.*

In agreement with the formalism of BANs, we will assume that in a BAN, all considered changes are represented with the same status. The focus is therefore not so much on automata states, as it is on their changes.

### 3 Illustrations

**Observation 1:**

Some properties that we regard as properties of interaction systems – properties that they can have or not have – are actually properties of the way we look at them.

Observation 1 can be illustrated with the BAN properties of *monotony* and *non-monotony*. A BAN is said to be monotone when the following holds for any two of its automata Ω and Ω. If Ω influences Ω, then it always does so in the same way: either Ω always influences Ω positively, or Ω always influences Ω negatively. In mathematical terms this translates to the following where $x^i ∈ B^n$ is the state defined by $\forall k \neq i : \bar{x}^i_k = x_k$ and $\bar{x}^i = \neg x_i$. By definition, in a monotone BAN, for any $i, j \in V$ such that $(i, j) ∈ A$, i.e. such that the Conjunctive Normal Form of $f_j(x)$ depends on $x_i$: either $\forall x ∈ B^n, x_i = 1 ⇒ f_j(x) ≥ f_j(\bar{x}^i)$, or $\forall x ∈ B^n, x_i = 1 ⇒ f_j(x) ≤ f_j(\bar{x}^i)$.
Traditionally, when BANs model biological (genetic) regulation networks\cite{12,15,29–31}, they are supposed to be monotone, like BAN $\mathcal{N}$ of Fig.1 and unlike BAN $\mathcal{N}'$ of Fig.2.

$$
\begin{align*}
\mathcal{N}_1 & : x \rightarrow x_2 \oplus x_3 = (\neg x_2 \lor \neg x_3) \land (x_2 \lor x_3) \\
\mathcal{N}_2 & : x \rightarrow x_3 \\
\mathcal{N}_3 & : x \rightarrow \neg x_3 \\
\mathcal{N}_5 & : x \rightarrow x_1 \lor x_6 \\
\mathcal{N}_6 & : x \rightarrow x_6 \lor x_5
\end{align*}
$$

Fig. 2: The BAN $\mathcal{N}'$. LEFT: The interaction digraph $\mathcal{G} = (\mathcal{V}, \mathcal{A})$ of $\mathcal{N}'$. RIGHT: $\mathcal{N}'$’s defining local update functions.

Despite BAN $\mathcal{N}'$ being non-monotone, it is the exact representation of what we see of the monotone BAN $\mathcal{N}$ in some circumstances.

Imagine that there exists a real system in nature that works exactly like the monotone BAN $\mathcal{N}$ of Fig.1 does. Call the real system $\mathcal{N}$ too. Imagine that we human observers of reality are observing $\mathcal{N}$ in action, and at the time we are doing that, for some reason, parts of $\mathcal{N}$ are behaving rhythmically: state changes of 1 and 4 are happening at the same frequency with a slight phase offset; everything is exactly as if 4 was systematically updated immediately before 1 is. If we were witnessing each event occurring in $\mathcal{N}$ and knew that we were, then we would have enough information to build the representation of $\mathcal{N}$ given in Fig.1. But assume that deliberately, we are considering $\mathcal{N}$ from a specific level of abstraction (as opposed to considering $\mathcal{N}$ from the godlike perspective of the Laplacian demon that sees Everything because it is interested in Everything). In other terms, assume we have specific interests, and because of that we are focusing on specific attributes of $\mathcal{N}$. Imagine that in the present case, this results in us being unaware of 4’s existence.

NB: This does not imply a default in our observation. What it is we are looking at in the entities 1 $i \neq 4$ of system $\mathcal{N}$ might simply not exist, not make sense, or not be measurable in entity 4. For instance, 4’s state changes might represent rapid decoding of mRNA sequences, while the state changes of the other 1 $i \neq 4$ might represent slower processes such the increase of protein concentrations in the cell during the protein’s synthesis.

Every time we witness 1 change states, 4 just has. While $\mathcal{N}$ is taking trajectory:
\[ \cdots \rightarrow x = (x_1, x_2, x_3, x_4, x_5, x_6) \xrightarrow{f_4} x' = (x_1, x_2, x_3, f_4(x), x_5, x_6) \xrightarrow{f_1} x'' = (f_1(x'), x_2, x_3, f_4(x), x_5, x_6) \rightarrow \cdots \]

we observers are just seeing:

\[ \cdots \rightarrow (x_1, x_2, x_3, x_5, x_6) \xrightarrow{f_1} (f_1(x'), x_2, x_3, x_5, x_6) \rightarrow \cdots . \]

The BAN description of a system that behaves like this is the BAN description given in Fig.2. Under such circumstances – circumstances that constrain the temporality of events in \( \mathcal{N} \) together with the way we observe those events, the level of abstraction from which we do that, and the temporality of our observations of \( \mathcal{N} \)’s changes with respect to the temporality of \( \mathcal{N} \)’s changes – what is given of \( \mathcal{N} \) for us to understand is \( \mathcal{N} \).

In agreement with Observation 1, this shows that monotony and non-monotony are not so much properties qualifying the interactions of a system as they are of how we look at it.

In the literature, wherever BANs are considered as stand-alone mathematical objects, it is customary to restrict the local update functions \( f_i \) to a certain class of functions for convenience. A typical example is the restriction to functions that are expressible in terms of a limited number of logical connectors \([2,7,9,32–36,21,22,37,38]\). And as mentioned above, the \( f_i \)’s are also often restricted to functions that are expressible, on the contrary, without certain connectors such as the \( \oplus \) (XOR) connector which makes the BAN severely non-monotone \([39,40,37,41]\).

If we want the mathematical understanding we develop about mathematical representations of ’real’ interaction systems to apply and to apply rightly, then we need to understand the meaning of the restrictions we make when we derive this mathematical understanding. Observation 1 shows how important it is to consider thoroughly the way our perspective on a system and our interpretation of its representation are involved in the properties that we build our understanding on.

**Observation 2:**
A statement like “There exists no interaction between entity X and entity Y.” has no essential meaning in itself. Its truth value is dependent on the specific level of abstraction from which the system – its entities, the interactions between them – is being looked at.
Observation 3:
Incomplete data is not the only reason for the model of a real interaction system to fail to account for existing interactions between entities of the system. Despite the modeller’s flawless observation and formalisation of the system, some causal relationships between entities might still be intrinsically imperceptible to him/her under his/her current perspective.

To illustrate observations 2 and 3, consider the system represented by BAN $\tilde{\mathcal{N}}$ of Fig. 3.

![Fig. 3: The BAN $\tilde{\mathcal{N}}$. Left: $\tilde{\mathcal{N}}$'s interaction graph $\tilde{G} = (\tilde{V}, \tilde{A})$. Right: $\tilde{\mathcal{N}}$'s local update functions.](image)

This system is actually three independent systems that we have no reasons to consider as a whole. Automaton $\mathcal{A}_1$ in particular, is stuck in state 0. There is no reason for us to consider $\mathcal{A}_1$ as an interacting entity interacting with other entities. Yet in some circumstances, this BAN too is the perfect representation of what is given of system $\mathcal{N}$ (of Fig. 1) for us to understand.

Imagine that entities $\mathcal{A}_3, \mathcal{A}_2, \mathcal{A}_4, \mathcal{A}_4$ of $\mathcal{N}$ happen to be caught in the same rhythm, and for the same sort of reasons as before, we are unaware of entity $\mathcal{A}_4$ (e.g. we are looking at interactions between varying concentrations $\mathcal{A}_i i \neq 4$ in the cell of different proteins, and are thereby unable to perceive changes affecting genes like $\mathcal{A}_4$).

In $\mathcal{N}$, everything is as if updates were being made in the following periodic order:

$$\ldots 3, 2, 4, 1, 3, 2, 4, 1, 3, 2, 4, 1 \ldots$$

Imagine also, that we are observing the system $\mathcal{N}$ with regularity. But still, we are not there absolutely each and every time something in $\mathcal{N}$ changes. More precisely, imagine that in $\mathcal{N}$ the changes of states of entities happen very fast in comparison to the whole duration of a period of updates $(3, 2, 4, 1)$. Because of the that and because of the regularity of our observations with respect to that, while $\mathcal{N}$ takes trajectory:
\[ x = (x_1, x_2, x_3, x_4, x_5, x_6) \]\[ \xrightarrow{2} x' = (x_1, x_2, f_3(x_3), x_4, x_5, x_6) \]
\[ x'' = (x_1, f_2(x'), f_3(x_4), x_5, x_6) \]\[ \xrightarrow{1} x''' = (x_1, f_2(x'), f_3(x), f_4(x'''), x_5, x_6) \]
\[ \xrightarrow{1} (f_1(x'''), f_2(x'), f_3(x), f_4(x'''), x_5, x_6) \xrightarrow{\cdots} \]

we observers of reality just see:

\[ x = (x_1, x_2, x_3, x_5, x_6) \]\[ \xrightarrow{1, 2} (f_1(x'''), f_2(x'), f_3(x), x_5, x_6) \xrightarrow{\cdots} \]

where \( \forall x \in \mathbb{B}^n \):

\[
\begin{align*}
f_1(x''') &= f_4(x''') \land \neg f_2(x') \lor \neg f_3(x) \\
&= (f_2(x') \lor f_3(x)) \land \neg f_2(x') \lor \neg f_3(x) \\
&= (f_3(x) \lor f_3(x)) \land \neg f_3(x) \lor \neg f_3(x) \\
&= 0.
\end{align*}
\]

So under these circumstances, \( \tilde{N} \) accurately represents all the information we get out of our absolutely flawless observation of \( \mathscr{N} \) under those circumstances. And according to this accurate representation of \( \mathscr{N} \), in particular there exists no interaction between entities \( \odot \) and \( \odot \): \( (1, 5) \notin \tilde{A} \).

Traditionally in the Bioinformatics literature\(^{42-45}\), at best only three cases are considered for any two entities \( \odot \) and \( \odot \) of a real system \( \mathscr{N} \):

**Case 1:** Entity \( \odot \) really impacts on entity \( \odot \), possibly indirectly, and the model \( \tilde{N} \) of \( \mathscr{N} \) formalises this through the arc \( (i, j) \in \tilde{A} \).

**Case 2:** Entity \( \odot \) really has no influence on entity \( \odot \) and the model accounts for this through the absence of arc \( (i, j) \notin \tilde{A} \).

**Case 3:** Entity \( \odot \) really impacts on entity \( \odot \) but the experimental data collected upstream by biologists has failed to evidence this fact about reality. As a consequence, the theory is failing to represent it: arc \( (i, j) \in \tilde{A} \) is accidentally missing from \( \tilde{N} \)'s interaction graph \( \tilde{G} = (\tilde{V}, \tilde{A}) \).

In agreement with Observation 2, the example of BAN \( \tilde{N} \) of Fig.3 modelling system \( \mathscr{N} \) of Fig.1 shows that **Case 2** doesn’t make any sense at all beyond the ‘reality’ of a specific level of abstraction (e.g. the one at which concentrations \( \odot \) \( i \neq 4 \) of proteins in the cell are meaningful and visible, and a gene \( \odot \) isn’t).
In agreement with Observation 3, the example also evidences there can be other reasons – different from the “unfortunate data deficit” underpinning Case 3 – for the representation $\hat{N}$ of a system $\mathcal{N}$ to fail to account for interactions between entities.

Now, consider again $\hat{N}$ – the BAN of Fig.3 representing precisely what we see of the system $\mathcal{N}$ of Fig.1 under the conditions described above. Under the conditions described above, if one entity of $\mathcal{N}$ were to change pace, slightly slow down for instance, even if only momentarily, then $\hat{x}$ might at some point take state 1. The oscillations of $\hat{3}$ might even spread to $\hat{5}$. Or, if $\hat{5}$ and $\hat{6}$ had been locked in state 0 until then, $\hat{1}$ might unlock $\hat{5}$ which in turn might generate the irrevocable effect of allowing $\hat{6}$ to take state 1. With our perspective on $\mathcal{N}$, none of this would fit with what we know. Worse, we would be essentially unable to foresee and even understand any of it if it happened.

**Observation 4:**
*What information a formal object can provide about the real system it is meant to model, and what uninterpretable, non-modelling information it provides on top of that, does not just depend on the semantics associated to the formalism describing the formal object, it also essentially depends on the relative consistency of the semantics.*

**Observation 5:**
The semantics associated to a formal object can be decisively affected by the history of the object and how our scientific community came to inherit it. And thus, so can the precise definition of the object that we choose among different customary variations of the definition, and the properties it has that we take interest in, and those we don’t.

The last two observations can be illustrated with the notion of “synchronism”.

A surprisingly great many occidental modellers of biological regulation networks confuse synchronism in BANs with the parallel update schedule (PUS) of BANs\[^{8,46–59}\]. The PUS is the update schedule originally used and made sense of by McCulloch and Pitts in their seminal BANs\[^{60}\]. The PUS forces a BAN to systematically update all its automata so that $\forall x \in \mathbb{B}^n$, the BAN transitions from $x$ to $(f_1(x), \ldots, f_n(x)) \in \mathbb{B}^n$. When this makes some automata react more quickly than we would like them to, intermediary automata can simply be added as it was originally done in the McCulloch and Pitts BANs. Asynchronism, to which the PUS is wrongly opposed, is the update constraint that rules out the possibility of updating more than one automaton in $x$. Non-asynchronism, a.k.a synchronism is the possibility of updating more than one in $x$. Formally, it is expressed by: $|U(x)| > 1$ (more than 1 automata can change states in $x$).
Such great tenacity for such a coarse confusion can only be explained by the fact that wherever it is made, it does not matter, or at least, it is not made to matter. A widespread confusion is nonetheless still a confusion. Since it is widespread, in agreement with Observation 5, it is much more likely to be the legacy of a community blind spot induced by inherited semantics, than to be the responsibility of individual err. And indeed, the blind spot around synchronism seems to be a natural effect of the constant diverse historical reprocessing of BANs and of the way sense is made out of them[5,60–64]. Extensive interdisciplinary interest in BANs has been reassigning modelling responsibilities to BANs faster then it has been answering questions about what BANs can, and actually do formalise.

The confusion between the parallel update schedule and the notion of synchronism results in:

(1) The neglect of all intermediary updating possibilities that neither rule out synchronism altogether, nor rule out asynchronism altogether (around $2^{153} \cdot 2^{153}$ in the case of BAN $\mathcal{N}^*$ of Fig.4), and

(2) Research being confined to frameworks in which synchronism is never considered independently of the other very strong characteristic features of the PUS (e.g. determinism, periodicity) for the reason that in those frameworks, it cannot be.

![Fig. 4: The interaction graph $G^*$ of BAN $\mathcal{N}^*$](image)

The disregard synchronism owes in particular to its misguided association with determinism, is aggravated by two assumptions commonly used to motivate an asynchronous updating in some communities that are interested in modelling genetic regulation with (B)ANs[65]:

(1) Simultaneity in nature is highly fortuitous, and

(2) Simultaneity in nature maps bijectively onto synchronism in (B)ANs.

The notion of simultaneity implied in these assumptions requires a notion of “objective time” to make sense. A priori, in BANs, it doesn’t. At least not spontaneously. What synchronism in BANs conveys is the absence of a causal relation:

Synchronously possible events are events that don’t need one another to occur.

So the relation of synchronism relates possible events without specifying anything about how these events are otherwise related – that is, how they are related otherwise
than by the relation created by their synchronous possibility. In particular, knowing only
that events A and B can occur synchronously, means: not knowing what effect the
occurrence of A might have on B and vice versa\(^1\). Forcing asynchronism in BANs –
\emph{i.e.} forcing asynchronism in \(x, \forall x \in \mathbb{B}^n\) despite \(|U(x)| > 1\) possibly being true in some
\(x\) – contradicts the fact mentioned above ("In BANs synchronously possible events
are events that don't need one another to occur"). To rule out the possibility of the
synchronous occurrences of possible events by imposing asynchronous updatings, is
to assume that the occurrence of any event prevents the occurrence of all other that are
also possible – \emph{or else that the model conveys the causality that we expect very poorly}.
In an asynchronous BAN, automata that find themselves synchronously unstable are
therefore necessarily automata that have the ability of influencing each other. For the
BAN \(\mathcal{N}\) of Fig.4, this means that 23256 arcs are missing from \(G^a\). This inconsistency
between what we want the BAN to mean and what we want its constituent updating
schedule to mean squarely dismantles the intrinsically discrete modelling capacity
of the mathematical formalism of BANs and severely stakes the relevance of any
information we might subsequently draw out of it about a real system. In agreement
with Observation 4, this shows that overloading formalism with incompatible semantics
is generally \emph{not} innocuous.

4 Conclusion

The observations and examples given above call for a shift of attention from specifics
and realism to definition and consistency. They show the need for us to systematically
endeavour to refine and update our scientific views so that instead of speaking of
\emph{theory and formalism} as opposed to \emph{reality and nature}, we rather speak of objects
that are abstractions of one another in a sense of the term "abstraction" that we can
actually formally explicit.

A characteristic strength (and beauty) of science is its ability and tradition of tackling
problems and questions through many different angles. Science does not especially
aspire at a one-dimensional history of science-making. Different perspectives currently
upheld by different contemporary scientific communities may co-exist. They don’t
need to mutually invalidate one another since science doesn’t especially need a single
consistent "survivor scientific perspective" to be selected in the end. So if science-
making presently makes sense in itself, then the same way, having different scientific
communities upholding different scientific perspectives on the same objects must

\(^1\)This absence of information conveyed by the relation of synchronism is a typical example of absence
of information traditionally getting outshined by specialised knowledge and the assumptions inspired
by specialised knowledge. If anything, what this absence of information represents is "wiggle room"
(see [66] Section 9). And making sense out of it calls for the careful attention of Computer Science with
its fundamental ability to soundly manipulate representations of information and systems, much more
than it is calls for the other natural sciences’ specialised detailed knowledge about the complexity and
diversity of real life systems in need of modelling.
presently make sense in itself too. We have yet to study and explicit the general coherence there must thereby be in the present coexistence of those perspectives. This paper suggests that the minimalist formalism of BANs may be of value in that.

Science has been concentrating on a certain kind of information, emerging directly from objects, from the explicit statements we make about them. The BAN examples above suggest that if we want to rely on the representations we make for ourselves of the objects we take interest in, then we need to have practical in-depth understanding of how a piece of information’s meaning and formalisation relate to one another. The five observations of this paper undercut the assumption that there are representations that are fundamentally more “objective” – as in more “accurate”, more “complete” or more “realistic” – than others. In that, they undercut the necessity of restricting ourselves to looking for new information where beacons the information we already have precisely as we presently represent it and precisely as we presently interpret it.

Let us assume the following. (1) There is such a thing as changes of perspective that makes sense with respect to science-making. In other terms, there are differences in perspectives that are meaningful in science. (2) A change of perspectives on object O, from perspective A to perspective B, does not systematically result from acquiring new information about O under A and simply increasing the set of features we take into account when we consider O. In other terms, the difference between two perspectives on the same object is not necessarily information explicitly expressed about that object. And if it’s not then it raises the following question about the new information we get on O as a result of seeing O with perspective B instead of perspective A. Other than waiting for a fortuitous change of perspective, concentrating on clearing data deficits in the meantime at the risk of ending up mislead by a series of questions and answers that only are relevant under a perspective that isn’t . . . How do we access this new information on O given that it is not (fully) dependent on what we know of O under A?

This paper suggests that a first step to answer this question is to tame implicit information of the kind that explains how BANs $\tilde{\mathcal{N}}$ and $\tilde{\mathcal{N}}^r$ of Fig.2 and Fig.3 can both

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2Incidentally, this differs significantly from what the academic trend of interdisciplinarity is actually proposing. As far as Computer Science/Biology collaborations around BANs go, interdisciplinary operates as discipline-concatenation, prejudicially opposing a conglomerate notion of “fundamental/-theoretical-ness” to a notion of “applied-ness”. From it ensues an effective separation between specialists’ contributions: the work of one starts where the work of the other ends. The fatalistic view on information lack captured by CASE 3 on Page 7 – information lack assumed to be necessarily unfortunate and accidental – is bound to consolidate under such circumstances: the validity of the models built by computer scientists for biologists is conditional to the quality and completeness of data that computer scientists have no say on. Under such circumstances, making the interests of distinct academic fields coincide rather than punctually relay each other, becomes a matter of educating the affiliates of one discipline to the specialised knowledge of the other, or else inventing a new discipline circumscribed to their intersection. Interdisciplinarity’s proposition therefore draws its sense out of the fact that specialised academic knowledge reinforces interdisciplinary separation. This paper means to emphasise issues that draw their meaning before any differences between disciplines need be considered.
be flawless representations of the BAN $\mathcal{V}$ of Fig.1, and more generally understand the possibilities and the limits of what one given formal representation can actually represent.

Bibliography

[1] C. L. Barrett, H. B. Hunt, M. V. Marathe, S. S. Ravi, D. J. Rosenkrantz, R. E. Stearns, and P. T. Tosic. Gardens of Eden and fixed points in sequential dynamical systems. In DM-CCG, 2001.

[2] O. Colón-Reyes, R. Laubenbacher, and B. Pareigis. Boolean monomial dynamical systems. Ann. Comb., 8:425–439, 2004.

[3] F. Delaplace, H. Klaudel, T. Melliti, and S. Sené. Modular organisation of interaction networks based on asymptotic dynamics. arXiv:1111.2313, 2011.

[4] J. Demongeot, J. Aracena, Ben Lamine S., and et al. Comparative genomics: empirical and analytical approaches to gene order dynamics, map alignment and the evolution of gene families, chapter Hot spots in chromosomal breakage: from description to etiology. Kluwer Academic Publishers, 2000.

[5] E. Goles and S. Martínez. Neural and automata networks: dynamical behaviour and applications. Kluwer Academic Publishers, 1990.

[6] E. Goles, L. Salinas. Comparison between parallel and serial dynamics of Boolean networks. Theor. Comp. Sci., 396:247–253, 2008.

[7] A. J. Jarrah, R. Laubenbacher, and A. Veliz-Cuba. The dynamics of conjunctive and disjunctive Boolean network models. Bulletin of Mathematical Biology, 72:1425–1447, 2010.

[8] D. Bérenguier, C. Chaouiya et al. Dynamical modeling and analysis of large cellular regulatory networks. Chaos, 23(2), 2013.

[9] H.S. Mortveit, C.M. Reidys. Discrete, sequential dynamical systems. Discrete Math., 226:281–295, 2001.

[10] H.S. Mortveit and C.M. Reidys. Towards a calculus of biological networks. Z. Phys. Chem., 216:1–13, 2001.

[11] J. Aracena, E. Goles, A. Moreira, L. Salinas. On the robustness of update schedules in Boolean networks. Biosystems, 97:1–8, 2009.

[12] L. Mendoza and E. R. Alvarez-Buylla. Dynamics of the genetic regulatory network for Arabidopsis thaliana flower morphogenesis. Journal of Theoretical Biology, 193:307–319, 1998.
[13] É. Remy, P. Ruet, and D. Thieffry. Graphic requirement for multistability and attractive cycles in a Boolean dynamical framework. *Advances in Applied Mathematics*, 41:335–350, 2008.

[14] É. Remy, P. Ruet. From minimal signed circuits to the dynamics of Boolean regulatory networks. *Bioinformatics*, 24:i220–i226, 2008.

[15] É. Remy, B. Mossé, C. Chaouiya, and D. Thieffry. A description of dynamical graphs associated to elementary regulatory circuits. *Bioinformatics*, 19:i172–i178, 2003.

[16] A. Richard and J.-P. Comet. Necessary conditions for multistationarity in discrete dynamical systems. *Discrete Applied Mathematics*, 155:2403–2413, 2007.

[17] A. Richard. Positive circuits and maximal number of fixed points in discrete dynamical systems. *Discrete Applied Mathematics*, 157:3281–3288, 2009.

[18] F. Robert. *Discrete iterations: a metric study*. Springer Verlag, 1986.

[19] H. Siebert. Dynamical and structural modularity of discrete regulatory networks. In *COMPMOD*, volume 6 of *Electronic Proceedings in Theoretical Computer Science*, 2009.

[20] L. Tournier and M. Chaves. Uncovering operational interactions in genetic networks using asynchronous Boolean dynamics. *Journal of Theoretical Biology*, 260:196–209, 2009.

[21] J. Demongeot, M. Noual, and S. Sené. Combinatorics of Boolean automata circuits dynamics. *Discrete Applied Mathematics*, 160:398–415, 2010.

[22] E. Goles and M. Noual. Disjunctive networks and update schedules. *Advances in Applied Mathematics*, 48(5):646 – 662, 2012.

[23] J.-P. Comet, M. Noual, A. Richard, J. Aracena, L. Calzone, D. Demongeot, M. Kaufman, A. Naldi, E.H. Snoussi, and D. Thieffry. On circuit functionality in Boolean networks. *Bulletin of Mathematical Biology*, 75(6):906–19, 2013.

[24] J. Aracena, É. Fanchon, M. Montalva, and M. Noual. Combinatorics on update digraphs in Boolean networks. *Discrete Applied Mathematics*, 159:401–409, 2011.

[25] J. Demongeot, E. Goles, M. Morvan, M. Noual, and S. Sené. Attraction basins as gauges of robustness against boundary conditions in biological complex systems. *PLoS One*, 5:e11793, 2010.

[26] J. Demongeot, H. Ben Amor, A. Elena, P. Gillois, M. Noual, and S. Sené. Robustness in regulatory interaction networks. A generic approach with applications at different levels: physiologic, metabolic and genetic. *International Journal of Molecular Sciences*, 10:4437–4473, 2009.

[27] J. Demongeot, A. Elena, M. Noual, S. Sené, and F. Thuderoz. "Immunetworks", intersecting circuits and dynamics. *Journal of Theoretical Biology*, 280:19–33, 2011.
[28] J. Demongeot, M. Morvan, and S. Sené. Robustness of dynamical systems attraction basins against state perturbations: theoretical protocol and application in systems biology. In *CISIS*, 2008.

[29] C. Chaouiya, E. Remy, P. Ruet, and D. Thieffry. *ICATPN*, chapter Qualitative Modelling of Genetic Networks: From Logical Regulatory Graphs to Standard Petri Nets, pages 137–156. Springer Berlin Heidelberg, 2004.

[30] J. Aracena, M. González, A. Zuniga, M. A. Mendez, and V. Cambiazo. Regulatory network for cell shape changes during Drosophila ventral furrow formation. *Journal of Theoretical Biology*, 239(1):49 – 62, 2006.

[31] F. Blanchini, E. Franco, and G. Giordano. A structural classification of candidate oscillators and multistationary systems. *bioRxiv*, 2013.

[32] E. Goles and J. Olivos. The Convergence of Symmetric Threshold Automata. *Information and Control*, 51(2):98–104, 1981.

[33] R. Laubenbacher, A.S. Jarrah, H.S. Mortveit, and S.S. Ravi. *Computational Complexity: Theory, Techniques, and Applications*, chapter Agent Based Modeling, Mathematical Formalism for, pages 88–104. Springer New York, 2012.

[34] C.L. Barrett, H.S. Mortveit, and C.M. Reidys. Elements of a theory of simulation III: equivalence of SDS. *Applied Mathematics and Computation*, 122(3):325–340, 2001.

[35] J. Aracena, J. Demongeot, and E. Goles. Fixed points and maximal independent sets in AND-OR networks. *Discrete Applied Mathematics*, 138:277–288, 2004.

[36] F. Fogelman-Soulie, E. Goles-Chacc, and G. Weisbuch. Specific roles of different Boolean mappings in random networks. *Bulletin of Mathematical Biology*, 44:715–730, 1982.

[37] M. Noual, D. Regnault, and S. Sené. About non-monotony in Boolean automata networks. *Theoretical Computer Science*, 504:12 – 25, 2013.

[38] E. Goles and M. Noual. Block-sequential update schedules and Boolean automata circuits. In *AUTOMATA*, pages 41–50. Discrete Mathematics & Theoretical Computer Science (DMTCS), 2010.

[39] Henning S. Mortveit and Christian M. Reidys. *An Introduction to Sequential Dynamical Systems*. Springer-Verlag New York, Inc., 2007.

[40] A. Alcolei, K. Perrot, and S. Sené. On the flora of asynchronous locally non-monotonic Boolean automata networks. In *Proceedings of SASB*. Springer, 2015. to appear.

[41] M. Noual, D. Regnault, and S. Sené. Boolean networks synchronism sensitivity and XOR circulant networks convergence time. In *AUTOMATA & JAC*, volume 90 of *Electronic Proceedings in Theoretical Computer Science (EPTCS)*, pages 37–52. Open Publishing Association, 2012.
[42] H. Ben Amor, F. Corblin, E. Fanchon, A. Elena, L. Trilling, J. Demongeot, and N. Glade. Formal Methods for Hopfield-Like Networks. *Acta Biotheoretica*, 61(1):21–39, 2013.

[43] I. Shmulevich, E.R. Dougherty, S. Kim, and W. Zhang. Probabilistic boolean networks: a rule-based uncertainty model for gene regulatory networks. *Bioinformatics*, 18(2):261–274, 2002.

[44] R. Dehghannasiri, B.-J. Yoon, and E.R. Dougherty. Efficient experimental design for uncertainty reduction in gene regulatory networks. *BMC Bioinformatics*, 16:410, 2015.

[45] J. Barnat, L. Brim, A. Krejci, A. Streck, D. Safranek, M. Vejnar, and T. Vejpustek. On Parameter Synthesis by Parallel Model Checking. *IEEE/ACM Trans. Comput. Biol. Bioinfo.*, 9(3):693–705, 2012.

[46] G. Bernot, J.-P. Comet, A. Richard, and J. Guespin. Application of formal methods to biological regulatory networks: extending thomas’ asynchronous logical approach with temporal logic. *J. Theor Biol*, 229:339–347, 2004.

[47] N. Vijesh, S. Chakrabarti, and J. Sreekumar. Modeling of gene regulatory networks: A review. *Journal of Biomedical Science and Engineering*, 6:223–231, 2013.

[48] F. Hinkelmann, M. Br, B. Guang, R. Mcneill, G. Blekherman, A. Veliz-cuba, and R. Laubenbacher. ADAM: Analysis of Discrete Models of Biological Systems Using Computer Algebra. BioMed Central, 2011.

[49] A. Garg, A. Di Cara, I. Xenarios, L. Mendoza, and G. De Micheli. Synchronous Versus Asynchronous Modeling of Gene Regulatory Networks. *Bioinformatics*, 24(17):1917–1925, 2008.

[50] H. De Jong. Modeling and simulation of genetic regulatory systems : a literature review. *Med Sci*, 18, 2002.

[51] F. Képès P. Amar and V. Norris, editors. *Probabilistic Gene Network*. EDP Science, 2015.

[52] A. Naldi, P.T. Monteiro, and C. Müssel *et al.* Cooperative development of logical modelling standards and tools with colomoto. *Bioinformatics*, 31:1154–1159, 2015.

[53] F. Delaplace, H. Klaudel, A. Cartier-Michaud. Discrete causal model view of biological networks. In *CMSB*, pages 4–13. ACM Press, 2010.

[54] H. de Jong. Modeling and simulation of genetic regulatory systems : a literature review. Rapport de recherche INRIA, 2000.

[55] C. Chaouiya *et al.* Sbml qualitative models: A model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. *BMC Systems Biology*, 7, 2013.

[56] A. Streck, T. Lorenz, and H. Siebert. Minimization and equivalence in multi-valued logical models of regulatory networks. *Natural Computing*, 14(4):555–566, 2015.
[57] C. Chaouiya, A. Naldi, and D. Thieffry. Logical modelling of gene regulatory networks with GINsim. *Methods in molecular biology*, 804:463–79, 2012.

[58] C.J. Kuhlman, H.S. Mortveit, D. Murrugarra, V.S.A. Kumar. *Bifurcations in Boolean Networks*. In *AUTOMATA*, pages 29–46, 2011.

[59] R. Thomas and R. d’Ari. *Biological feedback*. CRC Press, 1990.

[60] W. S. McCulloch and W. H. Pitts. A logical calculus of the ideas immanent in nervous activity. *Bull Math Biophys*, 5:115–133, 1943.

[61] J.J. Hopfield. Neural networks and physical systems with emergent collective computational abilities. *ONAS USA*, 79(8):2554–2558, 1982.

[62] H.G. Schaap. *Ising models and neural networks*. PhD thesis, Groningen, 2005.

[63] S. A. Kauffman. Metabolic stability and epigenesis in randomly constructed genetic nets. *Journal of Theor. Biol.*, 22:437–467, 1969.

[64] R. Thomas. Boolean formalization of genetic control circuits. *J. Theor. Biol.*, 42:563–585, 1973.

[65] R. Thomas. Regulatory networks seen as asynchronous automata: a logical description. *J. Theoret. Biol.*, 153:1–23, 1991.

[66] M. Noual. Causality and Boolean Automata Networks. Research report, 2016.