# Parameter Engineering vs. Parameter Tuning: the Case of Biochemical Coordination in $\mathcal{M}o\mathcal{K}$

Stefano Mariani
DISI, ALMA MATER STUDIORUM–Università di Bologna
via Sacchi 3, 47521 Cesena, Italy
Email: s.mariani@unibo.it

***Abstract*—To cope with nowadays MAS complexity, nature-inspired coordination models and languages gained increasing attention: in particular, biochemical coordination models. Being intrinsically stochastic and self-organising, the effectiveness of their outcome likely depends on a correct parameter tuning stage. In this paper, we focus on chemical reactions rates, showing that simply imitating chemistry "as it is" may be not enough for the purpose of effectively engineer complex, self-organising coordinated systems such as $\mathcal{M}o\mathcal{K}$.**

## I. INTRODUCTION

Nowadays MAS are demanding new paradigms and abstractions to deal with their increasing complexity [1]. Such complexity is mostly due to the number and nature of interactions happening within and between MAS [2], [3]. Coordination models and languages – whose main goal is to govern such interactions [4] – have historically drawn inspiration from *self-organising coordination* in natural phenomena—e.g., pheromone-based [5] and chemical [6] coordination. Among the many, *biochemical coordination* has been shown to be particularly effective [7], [8]. Here, there is no central authority ruling the interaction space. Instead, a number of *local*, *stochastic* coordination rules, to which all the interacting agents "implicitly" obey – as they are the "laws of nature" – drive MAS coordination. Thus, it happens *by emergence* as a consequence of the self-organisation between MAS coordinated entities. Being a self-organising process, coordination effectiveness likely depends on a correct *parameter tuning* stage, often performed in loop with a *simulation* stage [9].

In the case of biochemical coordination, being the "laws of nature" the (artificial) chemical reactions installed in the coordination medium, such parameters are, e.g., the *rate* of application of a chemical reaction, the *concentration* of the chemicals participating the reaction and their *stoichiometry*—the "extent" to which chemicals participate. In this paper, we focus on rates, aiming at a twofold goal:

- on one hand, showing that the *law of mass action* for rate expressions may be not enough to effectively engineer a biochemical coordination middleware
- on the other hand, highlighting that designing arbitrary *functional rates* demands for a disciplined and principled approach different from "parameter tuning", which we call *parameter engineering*.

In particular, such goals are defined w.r.t. the $\mathcal{M}o\mathcal{K}$ model and the BioPEPA tool, used as the *subject* and the *means* of investigation, respectively. Nevertheless, a generalisation of such goals suitable for any kind of nature-inspired MAS is possible. First of all, the fact that a given natural system works properly relying on a given set of parameters, each of which has a given set of functional dependencies with others, doesn't necessarily mean that the same sets of parameters and functional dependencies will work for an artificial system drawing inspiration from the natural one. Then, to proficiently identify the relevant parameters and engineer their (possibly reciprocal) functional dependencies, a proper methodology is needed—which will likely rely on simulations.

Accordingly, the remainder of the paper is organized as follows: Section II explains what biochemical coordination is (Subsection II-A) and reminds the importance of simulation tools for self-organising systems development (Subsection II-B), also describing the $\mathcal{M}o\mathcal{K}$ model (Subsection II-A1) as well as the BioPEPA tool (Subsection II-B1); Section III conveys the main contribution of the paper, introducing and motivating the notion of parameter engineering through a number of functional rates engineering examples; finally, Section IV concludes also giving some hints about further works.

## II. BACKGROUND

### A. Biochemical Coordination

The chemical metaphor appears particularly appealing for MAS coordination due to the simplicity of its foundation [6]. The idea is to coordinate any MAS entity (agents as well as information) as "molecules" floating in a chemical "solution", whose evolution is driven by chemical "reactions" continuously and spontaneously consuming and producing molecules. As many chemical reactions can occur at a given time, chemical solution evolution is driven by race conditions among their *rates*, which means certain reactions are *stochastically* executing over others—as in chemistry actually is [10].

Biochemical tuple spaces [7] enhance such metaphor by adding a spatial abstraction: the *compartment*. A compartment is a tuple space equipped with biochemical reactions, driving the evolution of the molecules floating in it. Compartments may be networked in "neighbourhoods" as in chemistry happens through membranes, so as to shape more complex spatial structures—such as tissues and organs. Computationally, biochemical tuple spaces are a stochastic extension of the LINDA model [11]: the idea is to equip each tuple with a "concentration" value, representing a measure of the *pertinency/activity* of the tuple (molecule) within the space (compartment)—the higher it is, the more likely and frequently the tuple will influence system coordination [7]. Such concentration is evolved by biochemical rules installed into the compartment, affecting concentration values over time *exactly* in the same way chemical substances evolve into chemical solutions [10]—that is, according to the law of mass action [12], [10].

The *law of mass action* is[1] a mathematical model that *explains* and *predicts* the behaviour of solutions in dynamic equilibrium. It can be described with respect to two aspects: *(i)* the equilibrium aspect, concerning the composition of a reaction mixture at equilibrium and *(ii)* the kinetic aspect, concerning the *rate equations* for elementary reactions. The law states that the rate of an elementary reaction ($r_f$) – a reaction that proceeds through only one transition state, that is one mechanistic step – is proportional ($k_f$) to the product of the concentrations of the participating molecules ($R^1, R^2$):

$$r_f = k_f[R^1][R^2]$$

$k_f$ is called *rate constant* and, in chemistry, is a function of participating molecules affinity—to learn more, please refer to [12] and therein cited bibliography.

The $\mathcal{M}o\mathcal{K}$ model, briefly described in next section, models MAS coordinated entities as well as coordination processes by *(i)* adopting the chemical metaphor abstractions and *(ii)* borrowing (to some extent) from biochemical tuple spaces the computational model.

*1) The $\mathcal{M}o\mathcal{K}$ Model:* $\mathcal{M}$olecules *o*f $\mathcal{K}$nowledge [13] ($\mathcal{M}o\mathcal{K}$ for short) is a model for knowledge self-organisation in MAS. The main goals of $\mathcal{M}o\mathcal{K}$ are:

- to let information chunks autonomously aggregate into heaps of knowledge
- to let knowledge autonomously flow toward the interested agents—rather than be searched

Here follows a brief summary of $\mathcal{M}o\mathcal{K}$ model components—consider reading [13] and [14] for $\mathcal{M}o\mathcal{K}$ formalisation and early application respectively:

- $\mathcal{M}o\mathcal{K}$ atoms — produced by a given source to convey an "atomic piece of information", atoms should also store some metadata to ease semantic characterisation
- $\mathcal{M}o\mathcal{K}$ molecules — "heaps" for information aggregation, they cluster together semantically related atoms
- $\mathcal{M}o\mathcal{K}$ enzymes — enzymes reify knowledge-oriented (inter-)actions made by agents and are meant to influence molecules' concentration[2]
- $\mathcal{F}_{\mathcal{M}o\mathcal{K}}$ function — as a knowledge-driven model, $\mathcal{M}o\mathcal{K}$ must have a way to determine the semantic correlation between information, therefore, the $\mathcal{M}o\mathcal{K}$ function $\mathcal{F}_{\mathcal{M}o\mathcal{K}}$ should be defined, taking two molecules and returning a value $m \in [0, 1]$.
- $\mathcal{M}o\mathcal{K}$ reactions — the behaviour of a $\mathcal{M}o\mathcal{K}$ system is determined by biochemical reactions, which stochastically – according to their rate – drive molecules aggregation, reinforcement, decay, and diffusion:
  - ○ Aggregation[3] — bounds together semantically related molecules
  - ○ Reinforcement — consumes an enzyme to reinforce the related molecule

    $$\texttt{enzyme}(Molecule^1) + Molecule^1_c \longmapsto^{r_{reinf}} Molecule^1_{c+1}$$
  - ○ Decay — enforcing time situatedness, molecules should fade away as time passes

    $$Molecule_c \longmapsto^{r_{decay}} Molecule_{c-1}$$
  - ○ Diffusion — space situatedness is inspired by biology, therefore based upon diffusion to neighbouring compartments (tuple spaces)

$$\{Molecule^1 \bigcup Molecules^1\}_{\sigma_i} + \{Molecules^2\}_{\sigma_{ii}} \longmapsto^{r_{diffusion}} \{Molecules^1\}_{\sigma_i} + \{Molecules^2 \bigcup Molecule^1\}_{\sigma_{ii}}$$

These four biochemical reactions are the *minimum set* of coordination mechanisms believed (at the moment) to be *necessary* and *sufficient* to properly drive a $\mathcal{M}o\mathcal{K}$-coordinated MAS toward the desired behaviour regarding knowledge self-organisation. Nevertheless, this set may be refined and extended if its lack of expressiveness w.r.t. $\mathcal{M}o\mathcal{K}$ desiderata becomes evident. Anyway, having a well-defined set of *primitives* is a necessary step to start distinguishing what sorts of self-organising behaviours can and cannot be achieved with $\mathcal{M}o\mathcal{K}$.

In fact, once such primitives are fixed, we can focus on the issue of properly engineering their rate expressions—$r_{reinf}$, $r_{decay}$, $r_{diffusion}$. In particular: is it sufficient to stick with the law of mass action to achieve $\mathcal{M}o\mathcal{K}$ goals, or should we build our "custom" functional dependencies? If so, which parameters and which kind of dependencies (direct, inverse, etc.) are to be used in each rate expression? And how can MAS designers make such decisions?

Section III answers these questions through a number of examples exploiting the BioPEPA simulation tool – briefly described in next section – to analyse different alternatives regarding $\mathcal{M}o\mathcal{K}$ reactions rate expressions.

### *B. Biochemical Simulation*

Simulation has been widely recognized as a fundamental development stage in the process of designing and implementing both MAS as well as biochemical processes [16], [9]. This is mostly due to the high number of system parameters needed, the huge number of local interactions between components, the influence of randomness and probability on system evolution. A number of different simulation tools capable of modeling biochemical-like processes exist, either born in the biochemistry field (see [17] for a survey) or in the (Multi-)Agent Based Simulation research area (survey in [18]). Among the many, ALCHEMIST [19], PRISM [20], and BioPEPA [12] at least, are worth to be mentioned. Our choice fell on the latter for its appealing features – briefly described in next section – which perfectly suit the purpose of the paper.

[1] From http://en.wikipedia.org/wiki/Law_of_mass_action.

[2] Please, notice that an atom is a "singleton molecule", hence the term "molecule" will be used also for "atom" from now on.

[3] Aggregation reaction formalisation is not shown here because it has been left out from BioPEPA simulations for the lack of expressiveness of the tool. To learn more, please refer to the technical report [15].

*1) The Bio-PEPA Tool:* BioPEPA [12] is a language for modeling and analysis of biochemical processes. It is based on PEPA [21], a process algebra originally aimed at performance analysis of software systems, extending it to deal with some features of biochemical networks, such as stoichiometry and different kinds of kinetic laws—including the law of mass action. The most appealing features of BioPEPA are:

- custom kinetic laws represented by means of *functional rates*
- definition of stoichiometry ("how many" molecules of a given kind participate) and role played by the species (reactant, product, enzyme, ...) in a given reaction
- theoretical roots in CTMC semantics—behind any BioPEPA specification lies a stochastic labelled transition system modeling a CTMC

In BioPEPA, rate expressions are defined as mathematical equations involving reactants' concentrations (denoted with the reactant name and dynamically computed at run-time) and supporting mathematical operators (e.g. `exp` and `log` functions) as well as built-in kinetic laws (e.g. the law of mass action, denoted with the keyword `fMA`) and time dependency (through the variable `time`, changing value dynamically according to the current simulation time step)[4]. The BioPEPA Eclipse plugin[5] is the tool used in next section to investigate $\mathcal{M}o\mathcal{K}$ reactions' rates influence on system behaviour.

## III. Parameter Engineering in Rate Expressions

As far as nature-inspired MAS are concerned, simulation tools are usually exploited to study how *those parameters inherited from the natural metaphor* influence the overall MAS behaviour. This is done with the aim to fine-tune such parameters value so as to get the better run-time "performances"—whatever this means (often, a behaviour closer to that exhibited in nature).

But, what about the question of wether the natural system's parameters are well suited also for the artificial one? In particular, w.r.t. biochemical coordination (thus, $\mathcal{M}o\mathcal{K}$ also): what about shaping our own rate expressions for biochemical reactions rather than blindly relying on the law of mass action to define their functional dependencies? Do we gain any improvement w.r.t. the overall coordinated MAS behaviour? Furthermore: can the same improvement be achieved by simply fine-tuning the natural system's parameters *as they are* in nature (e.g. the law of mass action *constant rate*)?

Through the following experiments, we aim at answering this kind of questions, hopefully achieving our twofold goal:

- showing that the law of mass action is too weak to effectively express a number of self-organising behaviours—such as $\mathcal{M}o\mathcal{K}$'s
- highlighting that shaping custom functional dependencies for rate expressions is a complex task demanding a well-engineered approach—indeed, *parameter engineering* prior to parameter tuning

By generalisation, our first goal aims at showing there is the need to consider re-engineering natural system's parameters, as well as their functional dependencies, so as to better cope with the problem at hand—as done with other natural metaphors: most notably, the ACO approach to distributed optimisation, in which the original "ant" metaphor is indeed just a metaphor, not the actual implementation [22].

Therefore, for each of the following experiments, we *(i)* identify which are the desiderata for the MAS run-time behaviour, *(ii) engineer* rates by designing functional dependencies which are likely to pursue the chosen goal, *(iii)* include a pure parameter tuning stage to fine-tune the MAS behaviour (if needed). All of this is done one reaction (coordination policy) at a time, thus one functional rate at a time, incrementally accumulated until composing the whole MAS behaviour. This approach is what we call *parameter engineering*.

Furthermore, a principle we believe to be extremely important for engineering self-organsing systems will be kept in mind: keeping the number of *external* parameters as small as possible. For "external" we mean parameters which are *ad hoc* added to the coordination model – $\mathcal{M}o\mathcal{K}$ in our case – to better design functional rate expressions—e.g., the law of mass action constant rate. On the contrary, *internal* parameters are those already present in the coordinated MAS—e.g., in the case of $\mathcal{M}o\mathcal{K}$, the concentration of the reactants or the time flowing. The advantage of using internal parameters as opposed to external ones, lies in the fact that a system using more internal parameters than external ones is much more adaptive and self-regulating, since it only relies on "within-system" information rather than on "outside-system" data to dynamically adjust its behaviour—in the case of $\mathcal{M}o\mathcal{K}$, reactions' rates.

*Technical Notes on Experiments:* Each of the following experiments has been performed by using Gillespie's stochastic simulation algorithm in 30 independent replications. Each of the following plots has been directly generated from BioPEPA as a result of the correspondent experiment—hence, of the 30 Gillespie runs. In each chart, the $x$-axis plots the time steps of the simulation, whereas the $y$-axis the concentration level of the reactants expressed in units of molecules.

### A. Injection Rate

Althought injection of atoms into a $\mathcal{M}o\mathcal{K}$ compartment is not yet part of $\mathcal{M}o\mathcal{K}$'s core set of formalised reactions, its influence on the system is so important to deserve its own analysis. Basically, injection can be described as follows:

Injection — Produces atoms out of *sources* without consuming them

$$\texttt{source}(Molecule^1) \ + \ Molecule^1_c \ \longmapsto^{r_{inj}} \ \texttt{source}(Molecule^1) \ + \ Molecule^1_{c+1}$$

Two contrasting needs have to be addressed: on one hand, atoms should be *perpetually* injected into the MAS, since there is no way to know a-priori *when* some information will be useful; on the other hand, we would likely avoid flooding the system without any control on how many atoms are in play. Thus, three options are viable:

[4] To learn more about BioPEPA syntax, please refer to [12].

[5] Instructions on how to install at http://homepages.inf.ed.ac.uk/s9552712/bio-pepa/download.html, manual at http://homepages.inf.ed.ac.uk/stg/research/biopepa/eclipse/manual/manual.pdf

1) make injection rates decreasing as time passes
2) enforce some kind of "saturation" to stop injection
3) a combination of the two

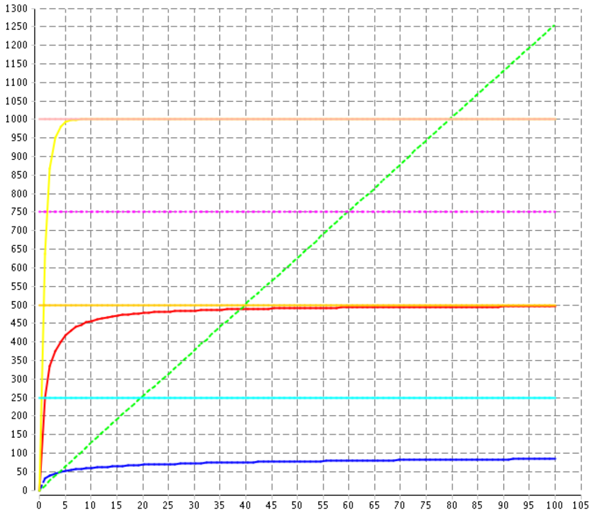

Fig. 1. Comparison of functional rates for atoms injection. Horizontal lines represent correspondent sources' concentration: purple dashed for option (1), pink for option (2), orange for option (3), light-blue for option (4).

Fig. 1 shows option (1) in blue, option (2) in yellow and option (3) in red. The green dashed line plots the law of mass action rate, whereas horizontal lines are the sources. Fig. 2 shows the BioPEPA functional rates specification used.

```
// option (1)
injE = [source_economics/atom_economics * (1 / (1 + time))];
// option (2)
injS = [source_sports - atom_sports];
// option (3)
injC = [(1 / (1 + time)) * (source_crime - atom_crime)];
// option (4)
injP = [fMA(0.05)];
```

Fig. 2. The `fMA` keyword calls a built-in function to compute the law of mass action. Its only parameter is the rate constant. The fMA implicitly consider reactants involved in the reaction exploiting its correspondent functional rate—for the full BioPEPA specification, please refer to [15].

Clearly, using rate expressions based on the law of mass action is out of question: its behaviour follows none of $\mathcal{M}o\mathcal{K}$ injection reaction desiderata. Once discarded also option (1), whose trend is clearly too slow in reaching saturation, options (2) and (3) may seem almost identical. Actually they are not:

- option (2) is "saturation-driven" only, thus if at some point in time `atom_sports` will suddenly decrease in concentration – e.g. due to agents consuming them – they will go back to saturation-level as fast as possible, no matter how long their sources are within the system
- option (3) instead, makes the saturation process time-dependant. In particular, the longer `source_sports` are within the system, the slower saturation will be

Choosing among the two depends on the application-specific context in which the $\mathcal{M}o\mathcal{K}$ model is used. In $\mathcal{M}o\mathcal{K}$-`News` [14], e.g., option (3) is better, since in the news management scenario information (on average) loses relevance as time passes.

### B. Decay Rate

$\mathcal{M}o\mathcal{K}$ decay reaction is an effective way to resemble the relationship between information relevance and time flow. Furthermore, decay enforces a kind of *negative feedback* which, together with the *positive feedback* provided by $\mathcal{M}o\mathcal{K}$ enzymes, enables the *feedback loop* peculiar of natural systems.

Time dependency alone is not enough for a meaningful decay behaviour: by using, e.g., a fixed rate we end-up simply slowing down the saturation process provided by injection reaction. Hence, Fig. 3 shows three different combinations of time dependency and concentration dependency for $\mathcal{M}o\mathcal{K}$ decay reaction—a fourth one (yellow line), based on the law of mass action, is given for comparison purpose:

1) linear time dependency + relative concentration dependency (blue dashed line)
2) logarithmic time dependency + relative concentration dependency (red line)
3) linear time dependency + built-in law of mass action (green dashed line)

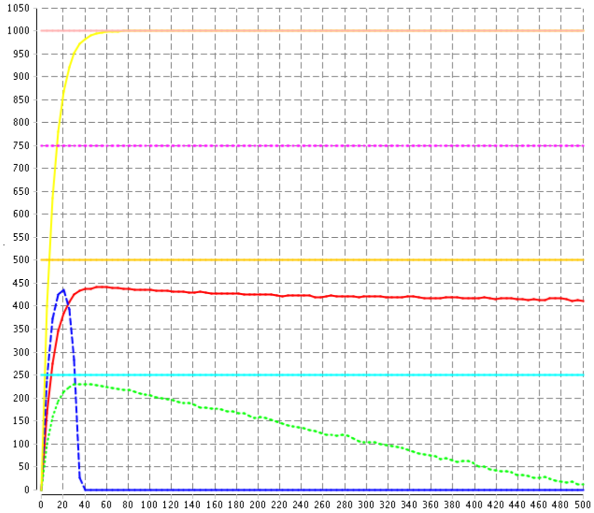

Fig. 3. Comparison of functional rates for atoms decay. Again, horizontal lines represent correspondent sources' concentration: purple dashed for option (1), orange for option (2), light-blue for option (3), pink for option (4).

Fig. 4 shows the BioPEPA functional rates specification used[6]. Again, the law of mass action is unsatisfactory, as well as option (1). Options (2) and (3) are both viable solutions instead. The choice is mostly driven by how fast are the dynamics of the scenario in which $\mathcal{M}o\mathcal{K}$ has to be deployed, thus how fast information should lose relevance—e.g., in $\mathcal{M}o\mathcal{K}$-`News`, choice (2) has been preferred. Nevertheless, please notice that option (3) has an additional parameter w.r.t. option (2): the law of mass action "rate constant". Furthermore, even if such parameter is made dynamic – e.g. the ratio between sources and atoms concentrations as done in options (1), (2) – the

[6] Actually, the Heaviside function has been also used to counter BioPEPA setting which allows rates to become negative—see [12].

```
// option (1)
decayE = [source_economics / atom_economics *
            time];
// option (2)
decayC = [source_crime / atom_crime *
            log(1+time)];
// option (3)
decayP = [fMA(0.05) * time];
// option (4)
decayS = [fMA(0.05)];
```

Fig. 4. BioPEPA specification of rate expressions for MoK decay reaction.

trend still would not match our desiderata for MoK decay reaction—compare with yellow line of Figure 4 in [15].

### C. Reinforcement Rate

To properly engineer MoK reinforcement reaction rate, we have to keep in mind what enzymes are meant for, that is, *(i)* representing a *situated interest* manifested by an agent w.r.t. a piece of knowledge – an atom or a molecule – *(ii)* to be exploited to reinforce such knowledge "relevance" within the MAS. With the word "situated" we mean that reinforcement should take into account the *situatedness* of agents (inter-)actions along a number of dimensions: time, space, type—a "search" action, a "read" action, etc. For these reasons, MoK reinforcement reaction rate should:

- be prompt, that is rapidly increase molecules concentration—despite decay
- limited both in time and space, to resemble relevance relationship with situatedness of (inter-)actions
- depend on the (inter-)action type—e.g. a "read" action could inject more enzymes and/or reinforce atoms with greater stoichiometry w.r.t. a "search" action

Fig. 6 clearly shows that our desiderata are fulfilled only by a reinforcement reaction having a functional dependency on the ratio between the reinforced molecule's concentration and its source own—option (1) in Fig. 5. Once again, sticking with the law of mass action alone is out of question: option (2) – dashed blue line –, even if adopting a dynamic rate constant, exhibits an exceedingly high and fast peak, option (3) – red line –, using a fixed rate constant (as in the law of mass action typically is), almost completely ignores the feedback—enzymes are too slowly consumed (orange line, plotting enzymes concentration).

```
// option (1)
feedS = [(source_sports / atom_sports)];
// option (2)
feedE = [fMA(source_economics / atom_economics)];
// option (3)
feedC = [fMA(0.05)];
```

Fig. 5. BioPEPA specification of rate expressions for MoK reinforcement reaction.

Furthermore, Fig. 7 and Fig. 8 show, respectively, how *concentration* and *stoichiometry* can influence MoK reinforcement reaction behaviour, effectively modeling situatedness—in particular, what we called the "type" of (inter-)actions. In fact, *(i)* in Fig. 7 the initial concentration of "red" enzymes (red line) is doubled w.r.t. "yellow" enzymes (yellow line) in Fig. 6: as a result, the "duration" of the feedback is doubled as well; *(ii)* in Fig. 8 the stoichiometry of "red" atoms (red line) in reinforcement reaction is doubled w.r.t. "yellow" atoms (yellow line) in Fig. 6: as a result, the "intensity" of the feedback is more than doubled.

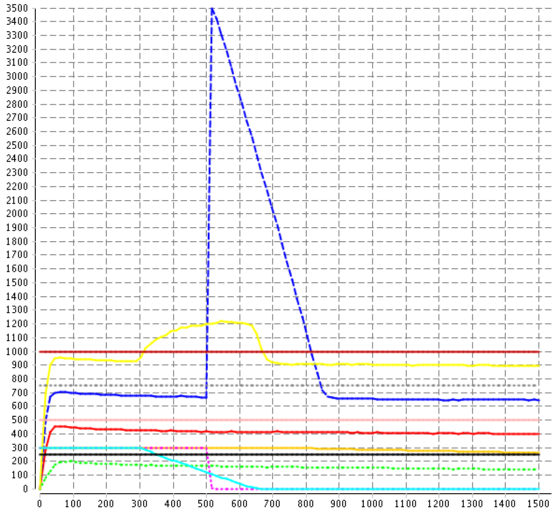

Fig. 6. Comparison of functional rates for atoms reinforcement. Lines worth to be considered are: the yellow one, plotting option (1), the dashed blue one, plotting option (2), the red one, plotting option (3).

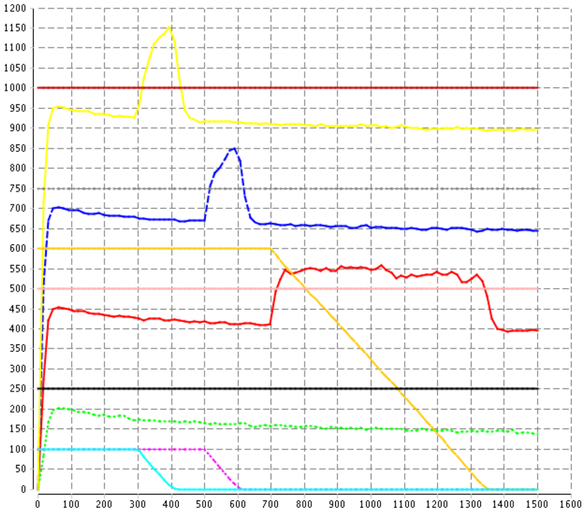

Fig. 7. Enzymes concentration increment effect on reinforcement.

Notice also: *(i)* Fig. 7 shows the opposite holds too, that is, halving the initial concentration halves the duration of the feedback (yellow and blue lines); *(ii)* Fig. 8 shows that no interference happens between concentration and stoichiometry parameters, in fact, reinforcement lasts as long as in Fig. 7.

### D. Diffusion Rate

As regards MoK diffusion reaction, the topology depicted in Fig. 9 has been taken as a reference. Namely, four MoK compartments are imagined to be connected one to each other, allowing in principle any molecule to move anywhere.

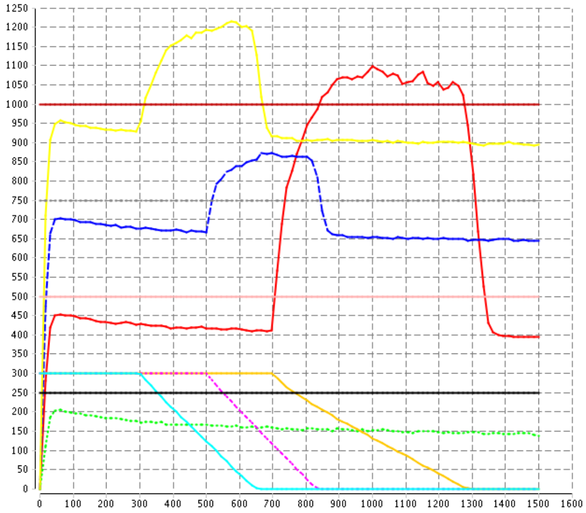

Fig. 8. Atoms stoichiometry increment effect on reinforcement.

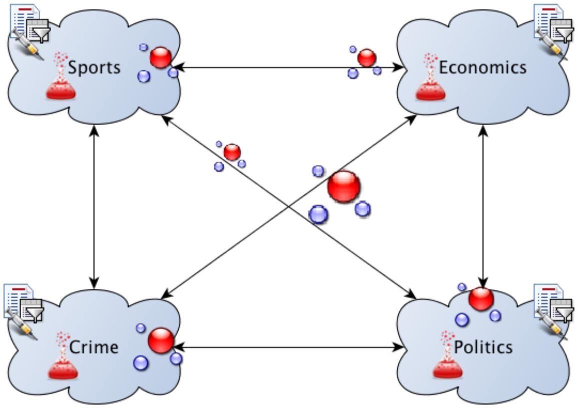

Fig. 9. $\mathcal{M}o\mathcal{K}$ topology to experiment with diffusion reaction.

Our main desiderata regarding $\mathcal{M}o\mathcal{K}$ diffusion reaction are similar to those of $\mathcal{M}o\mathcal{K}$ injection reaction: on one hand, we would like to perpetually spread information around, because agents working in other compartments may be interested in it; on the other hand, we would also like to keep some degree of control about "how much" information is moved around. Such "degree of control" can be achieved by reusing the concept of "saturation", as shown by Fig. 11: in particular, it seems reasonable to allow only a fraction of molecules to move from their "origin" compartment—see Fig. 10. In practice, we can

```
// diffusion weight
DW = 0.75;
// diffusion functional rates (a@x => a@y)
diffSE = [DW * as@sports - as@economics]; // blue line
diffSC = [DW/2 * as@sports - as@crime]; // red line
diffSP = [DW/3 * as@sports - as@politics]; // green line
```

Fig. 10. Notation $r@c$ refers to the concentration of reactant $r$ in compartment $c$. Previous listings did not follow such notation because there was only a single compartment—$\mathcal{M}o\mathcal{K}$ diffusion was not considered.

arbitrarily decrease/increase the saturation-level of the origin compartment in the destination compartment. Furthermore, they are functionally related. As a side note, notice a diffusion reaction featuring the law of mass action is not depicted. The motivation is that it exhibits an unexpected "malfunctioning" affecting also other reactions. More on this "interference problem" in next section.

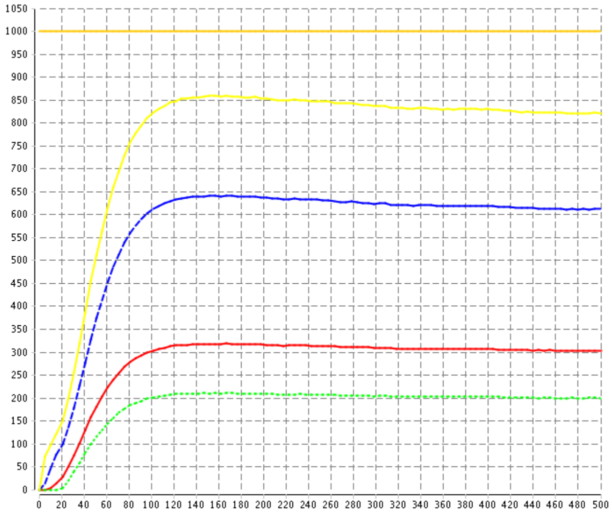

Fig. 11. $\mathcal{M}o\mathcal{K}$ diffusion reaction trend. The yellow line plots the concentration level of the atoms in their "origin" compartment (the orange horizontal line represents their source).

### E. *On the Problem of Interference Between Reactions*

All the experiments in the paper have been conducted incrementally, that is, each $\mathcal{M}o\mathcal{K}$ reaction has been added to the BioPEPA specification one at a time. As reported in [15], when adding diffusion to other $\mathcal{M}o\mathcal{K}$ behaviours, BioPEPA plots highlighted some *interference* between reactions. E.g., Fig. 12 depicts what happened when reinforcement has been added to injection, decay and diffusion.

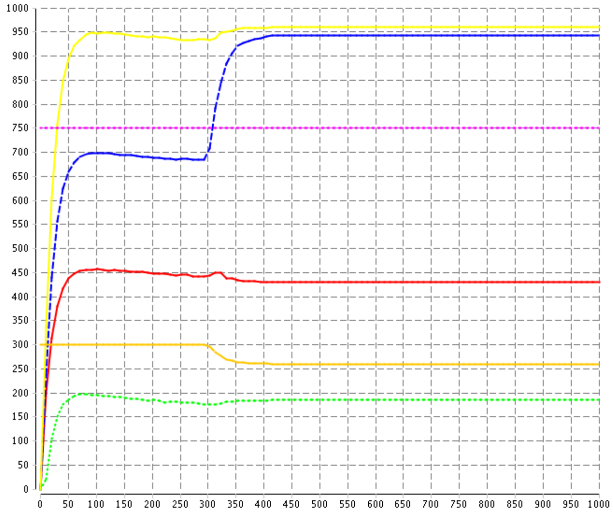

Fig. 12. $\mathcal{M}o\mathcal{K}$ reinforcement reaction addition to injection, decay and diffusion. Not only enzymes are not fully depleted, but also undesirable and unexpected interferences with other reactions are clearly highlighted.

A number of unexpected behaviours can be seen:

- first of all, our desiderata for $\mathcal{M}o\mathcal{K}$ reinforcement reaction are not met (dashed blue line). In particular, it seems atoms cannot go beyond their original compartment concentration level (yellow line)
- second, enzymes are not fully depleted (orange line)
- last but not least, other atoms are affected by a successful application of $\mathcal{M}o\mathcal{K}$ reinforcement reaction (yellow, red and green lines): in particular, in the time interval during which enzymes are consumed *all* other trends experiment some fluctuations

The reason at the root of all these issues is still unknown: being chemical-like reactions scheduling essentially based on race conditions between the correspondent functional rates – evaluated at a given point in time –, understanding what exactly happens within the system at a given time step is not trivial at all—or even impossible, depending on the debugging services the simulation tool adopted provides. Nevertheless, the satisfactory BioPEPA specification shown in Fig. 13 has been found. In particular, $\mathcal{M}o\mathcal{K}$ reinforcement reaction rate has been added a "feed factor" parameter, used to weight the influence of the atoms to be reinforced w.r.t. the concentration of the corresponding source in the compartment the latter belongs to. Fig. 14 shows that our desiderata are now met successfully. Although not shown here for the lack of space, also the functional dependencies on enzymes concentration and atoms stoichiometry shown in Fig. 7 and Fig. 8 are preserved.

```
// feed factor > 1
FF = 2;
// option (1)-revised
feedEC = [se@economics / (ae@crime * FF)];
```

Fig. 13. Adjusted BioPEPA specification of rate expressions for $\mathcal{M}o\mathcal{K}$ reinforcement reaction used together with $\mathcal{M}o\mathcal{K}$ diffusion reaction.

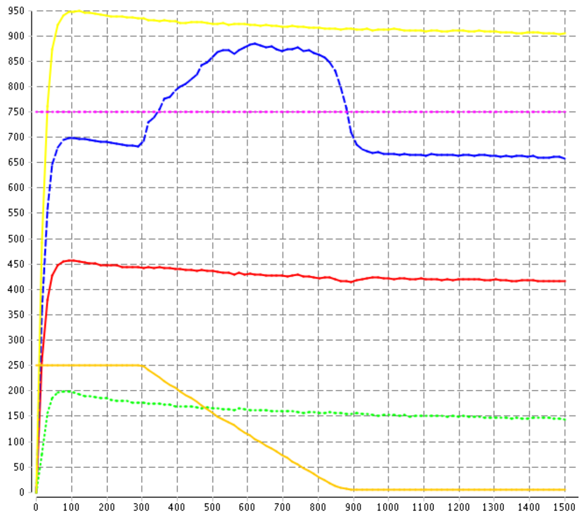

Fig. 14. Adjusted $\mathcal{M}o\mathcal{K}$ reinforcement reaction: enzymes are now completely depleted and other reactions no longer affected.

This clearly demonstrates the intricacies behind rates design in biochemical coordination, therefore motivating the principled and disciplined – namely, *engineered* – approach to parameter tuning we called parameter engineering.

## IV. Conclusion & Further Works Roadmap

In this paper, we showed that simply imitating nature *as is* may be not the optimal approach while engineering nature-inspired MAS. Indeed, once a suitable natural metaphor has been found, MAS designers should ask themselves if the natural system's parameters are the optimal ones also for the artificial system they aim to build. If it is not the case, they should clearly state which goals their MAS is pursuing then detects, preferably within the MAS itself, which parameters better suits their needs as well as which (if any) functional dependencies between such parameters better cope with the problem their MAS aims to solve.

In particular, we focussed on the case of biochemical coordination in $\mathcal{M}o\mathcal{K}$, showing that sticking with the law of mass action for rate expressions is not enough to model interesting behaviours. Furthermore, designing more complex rate expressions demands for a principled approach going beyond parameter tuning, which we call parameter engineering, likely to be supported by incremental simulation of each single basic "law of nature" in play.

To the best of our knowledge, no closely related works exists to date except, to some extent, [9]. Nevertheless, we believe our work to be complementary to that in [23] about self-organising design patterns as well as to [9]: in fact, once a design pattern has been recognized as a potential solution to a given problem, a simulation stage is out of doubts useful, therefore a parameter engineering phase necessary.

As a last note, further works will be devoted to analyze the tradeoff between designing more complex expressions and sticking with the law of mass action at the cost employing more (dual, complementary and/or opposite) reactions to reach the same "complex trend" by composition.

## Acknowledgments

This work has been supported by the EU-FP7-FET Proactive project SAPERE – Self-aware Pervasive Service Ecosystems, under contract no. 256874.

## References

[1] A. Omicini and P. Contucci, "Complexity & interaction: Blurring borders between physical, computational, and social systems. Preliminary notes," in *Computational Collective Intelligence. Technologies and Applications*, ser. LNCS, C. Bădică, N. T. Nguyen, and M. Brezovan, Eds., vol. 8083. Springer Berlin Heidelberg, 2013, pp. 1–10, 5th International Conference (ICCCI 2013). Craiova, Romania, 11–13 Sep. 2013, Proceedings. Invited Paper. [Online]. Available: http://dx.doi.org/10.1007/978-3-642-40495-5_1

[2] P. Wegner, "Why interaction is more powerful than algorithms," *Communications of the ACM*, vol. 40, no. 5, pp. 80–91, May 1997. [Online]. Available: http://dx.doi.org/10.1145/253769.253801

[3] A. Omicini, A. Ricci, and M. Viroli, "The multidisciplinary patterns of interaction from sciences to Computer Science," in *Interactive Computation: The New Paradigm*, D. Q. Goldin, S. A. Smolka, and P. Wegner, Eds. Springer, Sep. 2006, pp. 395–414. [Online]. Available: http://dx.doi.org/10.1007/3-540-34874-3_15

[4] D. Gelernter and N. Carriero, "Coordination languages and their significance," *Communications of the ACM*, vol. 35, no. 2, pp. 97–107, 1992. [Online]. Available: http://dx.doi.org/10.1145/129630.129635

[5] P.-P. Grassé, “La reconstruction du nid et les coordinations interindividuelles chez Bellicositermes natalensis et Cubitermes sp. la théorie de la stigmergie: Essai d’interprétation du comportement des termites constructeurs,” *Insectes Sociaux*, vol. 6, no. 1, pp. 41–80, Mar. 1959. [Online]. Available: http://dx.doi.org/10.1007/BF02223791

[6] J.-P. Banâtre, P. Fradet, and D. Le Métayer, “Gamma and the chemical reaction model: Fifteen years after,” in *Multiset Processing. Mathematical, Computer Science, and Molecular Computing Points of View*, ser. LNCS, C. S. Calude, G. Păun, G. Rozenberg, and A. Salomaa, Eds. Springer, 2001, vol. 2235, pp. 17–44. [Online]. Available: http://dx.doi.org/10.1007/3-540-45523-X_2

[7] M. Viroli and M. Casadei, “Biochemical tuple spaces for self-organising coordination,” in *Coordination Languages and Models*, ser. LNCS, J. Field and V. T. Vasconcelos, Eds. Lisbon, Portugal: Springer, Jun. 2009, vol. 5521, pp. 143–162, 11th International Conference (COORDINATION 2009), Lisbon, Portugal, Jun. 2009. Proceedings. [Online]. Available: http://dx.doi.org/10.1007/978-3-642-02053-7_8

[8] F. Zambonelli, G. Castelli, L. Ferrari, M. Mamei, A. Rosi, G. Di Marzo, M. Risoldi, A.-E. Tchao, S. Dobson, G. Stevenson, Y. Ye, E. Nardini, A. Omicini, S. Montagna, M. Viroli, A. Ferscha, S. Maschek, and B. Wally, “Self-aware pervasive service ecosystems,” *Procedia Computer Science*, vol. 7, pp. 197–199, Dec. 2011, proceedings of the 2nd European Future Technologies Conference and Exhibition 2011 (FET 11). [Online]. Available: http://dx.doi.org/10.1016/j.procs.2011.09.006

[9] L. Gardelli, M. Viroli, and A. Omicini, “On the role of simulations in engineering self-organising MAS: The case of an intrusion detection system in TuCSoN,” in *Engineering Self-Organising Systems*, ser. LNAI, S. A. Brueckner, G. Di Marzo Serugendo, D. Hales, and F. Zambonelli, Eds. Springer, 2006, vol. 3910, pp. 153–168, 3rd International Workshop (ESOA 2005), Utrecht, The Netherlands, 26 Jul. 2005. Revised Selected Papers. [Online]. Available: http://dx.doi.org/10.1007/11734697_12

[10] D. T. Gillespie, “Exact stochastic simulation of coupled chemical reactions,” *The Journal of Physical Chemistry*, vol. 81, no. 25, pp. 2340–2361, Dec. 1977. [Online]. Available: http://dx.doi.org/10.1021/j100540a008

[11] D. Gelernter, “Generative communication in Linda,” *ACM Transactions on Programming Languages and Systems*, vol. 7, no. 1, pp. 80–112, Jan. 1985. [Online]. Available: http://dx.doi.org/10.1145/2363.2433

[12] F. Ciocchetta and J. Hillston, “Bio-PEPA: A framework for the modelling and analysis of biological systems,” *Theoretical Computer Science*, vol. 410, no. 33–34, pp. 3065 – 3084, 2009, concurrent Systems Biology: To Nadia Busi (1968–2007). [Online]. Available: http://dx.doi.org/10.1016/j.tcs.2009.02.037

[13] S. Mariani and A. Omicini, “Molecules of Knowledge: Self-organisation in knowledge-intensive environments,” in *Intelligent Distributed Computing VI*, ser. Studies in Computational Intelligence, G. Fortino, C. Bădică, M. Malgeri, and R. Unland, Eds., vol. 446. Springer, 2013, pp. 17–22, 6th International Symposium on Intelligent Distributed Computing (IDC 2012), Calabria, Italy, 24-26 Sep. 2012. Proceedings. [Online]. Available: http://dx.doi.org/10.1007/978-3-642-32524-3_4

[14] ——, “Self-organising news management: The *Molecules of Knowledge* approach,” in *1st International Workshop on Adaptive Service Ecosystems: Natural and Socially Inspired Solutions (ASENSIS 2012)*, J. L. Fernandez-Marquez, S. Montagna, A. Omicini, and F. Zambonelli, Eds., SASO 2012, Lyon, France, 10 Sep. 2012, pp. 11–16, pre-proceedings. [Online]. Available: http://dx.doi.org/10.1109/SASOW.2012.48

[15] S. Mariani, “Analysis of the Molecules of Knowledge model with the Bio-PEPA Eclipse plugin,” ALMA MATER STUDIORUM–Università di Bologna, Bologna, Italy, AMS Acta Technical Report 3783, 20 Sep. 2013. [Online]. Available: http://amsacta.unibo.it/3783/

[16] E. Merelli, G. Armano, N. Cannata, F. Corradini, M. d’Inverno, A. Doms, P. Lord, A. Martin, L. Milanesi, S. Möller, M. Schroeder, and M. Luck, “Agents in bioinformatics, computational and systems biology,” *Briefings in Bioinformatics*, vol. 8, no. 1, pp. 45–59, 2007. [Online]. Available: http://dx.doi.org/10.1093/bib/bbl014

[17] R. Alves, F. Antunes, and A. Salvador, “Tools for kinetic modeling of biochemical networks,” *Nature biotechnology*, vol. 24, no. 6, pp. 667–672, 2006. [Online]. Available: http://dx.doi.org/10.1038/nbt0606-667

[18] C. Nikolai and G. Madey, “Tools of the trade: A survey of various agent based modeling platforms,” *Journal of Artificial Societies and Social Simulation*, vol. 12, no. 2, p. 2, 2009. [Online]. Available: http://jasss.soc.surrey.ac.uk/12/2/2.html

[19] D. Pianini, S. Montagna, and M. Viroli, “Chemical-oriented simulation of computational systems with Alchemist,” *Journal of Simulation*, 2013. [Online]. Available: http://dx.doi.org/10.1057/jos.2012.27

[20] M. Kwiatkowska, G. Norman, and D. Parker, “PRISM 4.0: Verification of probabilistic real-time systems,” in *Proc. 23rd International Conference on Computer Aided Verification (CAV’11)*, ser. LNCS, G. Gopalakrishnan and S. Qadeer, Eds., vol. 6806. Springer, 2011, pp. 585–591.

[21] S. Gilmore and J. Hillston, “The PEPA workbench: A tool to support a process algebra-based approach to performance modelling,” in *Computer Performance Evaluation Modelling Techniques and Tools*, ser. Lecture Notes in Computer Science, G. Haring and G. Kotsis, Eds. Springer Berlin Heidelberg, 1994, vol. 794, pp. 353–368. [Online]. Available: http://dx.doi.org/10.1007/3-540-58021-2_20

[22] M. Dorigo and M. Birattari, “Ant colony optimization,” in *Encyclopedia of Machine Learning*, C. Sammut and G. Webb, Eds. Springer US, 2010, pp. 36–39. [Online]. Available: http://dx.doi.org/10.1007/978-0-387-30164-8_22

[23] J. Fernandez-Marquez, G. Marzo Serugendo, S. Montagna, M. Viroli, and J. Arcos, “Description and composition of bio-inspired design patterns: a complete overview,” *Natural Computing*, pp. 1–25, 2012. [Online]. Available: http://dx.doi.org/10.1007/s11047-012-9324-y