

METHODOLOGY

Formal models of biological networks in ANIMO 2

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Abstract

Background: The large amount of data with which an experimental biologist must deal makes it nearly impossible to reason on the dynamics of complex systems without relying on computational support. In order to be fully profitable, computational modelling tools must be both accessible and powerful, providing a means to formalise and analyse experimental outcomes without requiring additional training.

Results: We show that the software tool ANIMO (Analysis of Networks with Interactive MOdelling) can be used in different modelling tasks, and illustrate how this can be an asset for the biological researcher. ANIMO models for *Drosophila melanogaster* circadian clock and signal transduction events downstream of TNF α and EGF in HT-29 human colon carcinoma cells are used as case studies to illustrate the possibilities offered by the tool.

Conclusions: The software tool ANIMO, recently updated to version 2, allows the biologist to develop a formal model through a user friendly interface, achieving useful insight without the need to study any mathematical formalism.

Keywords: modelling; signalling pathway; timed automata; dynamic behaviour

Background

Modelling in cell biology

In living cells, processes are regulated by networks of interacting molecules. Aberrations in these networks underlie a wide range of pathologies. The development of new therapies requires a thorough insight in the functioning of these networks. Obtaining such insight can be a challenging task. Feedback loops and crosstalk between pathways lead to an intricate wiring of the network. Since the human brain is ill-suited to grasp the non-linear dynamics of these complex networks and the entailed emergent properties, the role of computational support is increasing in molecular biology. In this context, we can profit from models in different ways:

- 1 to organize data and store knowledge,
- 2 to structure reasoning and discussion
- 3 to perform *in silico* experiments and derive hypotheses.

As models are a formalization of knowledge or theories, an underlying formalism is needed to express this knowledge. Different formal methods have been successfully applied to construct representations of biological systems. Among these methods are Boolean logic [1, 2, 3], ordinary differential equations (ODEs, reviewed by [4]), interacting state machines [5, 6], process calculi [7, 8, 9], Timed Automata [10, 11, 12] and Petri nets [13, 14, 15]. Most of these formal methods have been implemented into software tools to aid the process of modelling. Due to the lack of such a supporting tool, Timed Automata have remained a less frequently applied method.

Timed Automata for biological models

Timed Automata have been developed to model the dynamic behaviour of systems with processes running in parallel [16]. As such, Timed Automata have been applied in communication protocols and industrial control engineering [17, 18, 19]. The parallels between these application areas and regulatory processes in cells have triggered the step towards their use in biology. In [10], the authors used Timed Automata to extend a classical modelling paradigm [20], allowing to add temporal dynamics to gene network models. In [11], a model of biological oscillators was described and synchronization properties were tested in this dynamic system. A discretization of ODEs to Timed Automata was proposed in [12], applying a translation between the two formalisms to an example gene regulatory network. Two different approaches to transforming a Petri net model into Timed Automata were presented in [21], where the important issue of state space explosion was also addressed. Finally, the authors of [22] proposed an *ad hoc* Timed Automata model of a radiation treatment system, which was then validated through the analysis tool UPPAAL [Larsen et al., 1997].

Each of these approaches has been successfully validated, demonstrating the potential of Timed Automata in biological applications. However, these approaches were all limited to simple or specific examples and none of these modelling methods has led to a tool implementation of the proposed method to encourage a broader use of Timed Automata in molecular biology. We have recently introduced the software tool ANIMO (Analysis of Networks with Interactive MOdelling, [Schivo et al., 2012]), which aims at making available the power of Timed Automata to the experimental biologists without requiring them to be fluent in any mathematical formalism.

In this paper we present ANIMO 2, an updated version of ANIMO which allows for a considerably more efficient analysis of models. ANIMO 2 also introduces new features, such as the possibility to interrogate an ANIMO model with model checking queries represented as human language sentences instead of mathematical formulae. The case studies presented in this paper are centered around possible usage scenarios for ANIMO, and aim at illustrating how a biologist can profit from the tool in its latest iteration. An installation and user manual for ANIMO 2 is available at <http://fmt.cs.utwente.nl/tools/animo/manual.html>.

A short introduction to ANIMO

[[briefly describe ANIMO, its modelling assumptions and its intended use. Refer to Gene paper?]]

Results

Modelling oscillation

Results obtained with ANIMO are comparable to results with other modeling approaches. To demonstrate this, Figure 2 represents an ANIMO model of the circadian clock in *Drosophila Melanogaster*, based on the work by [Fathallah-Shaykh et al., 2009], where ordinary differential equations (ODEs) were used. The cyclic behavior of the circadian clock is based on the alternating formation and destruction of the CYC/CLK protein complex. Concentration levels of this complex are in turn regulated by a series of proteins which are produced as a consequence of CYC/CLK

formation. The CWO protein is central to the functioning of the network, as it degrades the mRNA for most of the involved proteins. As such, CWO acts as an inhibitor that counterbalances the effect of CYC/CLK. The positive influence of the light-regulated cryptochrome CRY on the degradation of TIM is a consequence of the passage between day and night, allowing the circadian clock to synchronize to a time zone (see Suppl. Sect.).

The output of the ANIMO model in Figure 2 closely matches the original ODE model. In particular, the oscillations in both models show the same periods and phases (see Suppl. Fig S5). Due to the compositional nature of Timed Automata ANIMO allows for intuitive *in silico* knock-out experiments, by right-clicking a node in the model and disabling it. Such experiments have been done before [Fathallah-Shaykh et al., 2009] and give similar results in our model.

[[Insert description of K.O. experiments with Drosophila model]]

Using ANIMO to generate hypotheses

We constructed a model of the signaling network downstream of TNF α and EGF, formalizing the crosstalk that takes place between the pathways at different levels of cellular regulation. We first modeled the two pathways in isolation (Suppl. Figs. S6, S7), using information on protein interactions from the KEGG [26] and phosphosite [27] databases. These models were fitted to experimental data from studies by [28] and [Janes et al., 2006]. We then merged the two pathways into a single model and added autocrine crosstalk between the pathways that has been described by [Janes et al., 2006]. Briefly, stimulation with TNF α (TNFa in the model) leads to a rapid release of TGF α (TGFa), which activates the EGF receptor (EGFR). This activation causes secretion of IL-1 α (IL-1a) at later time points. The effect of IL-1 α is down-regulated by the secretion of IL-1 receptor antagonist (IL-1ra) downstream of TNF α . The resulting model (Fig. 3A) was compared to the experimental data for treatments with 100 ng/ml TNF alone and 100 ng/ml EGF alone (data not shown) [28].

At this point, the behavior of the model deviated from the data for some of the nodes. Changing the parameters of the model was not enough to reproduce the behaviour shown by experimental data. This is an interesting situation, as it requires changes in the topology of the model, which can be interpreted as new hypotheses. Below, we give two examples and show how adaptation of the model can be used to generate novel testable hypotheses.

Experimentally, treatment with TGF α alone does not lead to secretion of IL-1 α . Instead, a co-stimulation with TGF α and TNF α is required [Janes et al., 2006]. However, in the first version of the model, treatment with TGF α was sufficient for IL-1 α expression (Fig. 3B). Given the time delay until secretion of IL-1 α , it can be expected that *de novo* synthesis of IL-1 α is required and that both TNF α and TGF α are needed to activate transcription of the IL-1 α gene. JNK1 and ERK signal downstream of TNF α and TGF α , respectively, and are known to affect the activity of multiple transcription factors. We altered the model to make activation of IL-1 α expression dependent on both JNK1 activity and ERK activity (Suppl. Fig. S8, arrows linking JNK1 and ERK to IL-1a gene). After this modification to the model,

IL-1 α was no longer secreted upon stimulation with TGF α alone, which greatly improved the fit between the measured IL-1 α levels and the model (Fig. 4B). This hypothesis could now be used to design a new experiment to validate IL-1 α as a target of combined JNK1 activity and ERK activity in HT-29 cells. For example, kinase inhibitors specific to JNK1 and ERK could be used to confirm that activity of both kinases is required for expression and secretion of IL-1 α . Performing the experiment is beyond the scope of this study, but this hypothesis finds support in literature. Transcription factors c-Jun and c-Fos together form a heterodimer known as AP-1 and are activated by JNK1 and ERK, respectively [30, 31]. AP-1 has been reported to bind to the promoter of IL-1 α , providing evidence for a role in the regulation of IL-1 α expression [32]. Based on these findings in literature we included c-Jun and c-Fos in our model as transcriptional activators of IL-1 α (Fig. 4A).

As a second example, we considered the behaviour of JNK1 and MK2. In the model, both proteins were located downstream of TNF α but not TGF α or EGF. Hence, the model did not show an effect of C225, a pharmacological inhibitor of ligand-EGFR binding, on activation of JNK1 or MK2 after stimulation with TNF α . However, experimental data show that C225 strongly reduces activation of JNK1 and MK2 upon stimulation with TNF α [Janes et al., 2006]. This fact is indicative of a role for EGFR in activation of JNK1 and MK2. Since both JNK1 and MK2 are located downstream of MEKK1, we hypothesized that activation of MEKK1 is dependent on both TNF α -signalling and TGF α -signalling. In the model we added a new hypothetical node Hyp 2 (hypothesis 2) to link EGFR to MEKK1 (Suppl. Fig. S8). This addition led to an improved fit of the model to the data upon treatment with TNF α + C225: activation of both MK2 and JNK1 was strongly suppressed by C225 (Fig. 4C). Stimulation with EGF alone did not lead to activation of JNK1 and MK2. These data support the validity of the modification to the model. Further support for a link between EGFR and MEKK1 was found in literature. Specifically, Ras has been reported as a direct activator of MEKK1 [33]. EGFR is a well-known and potent activator of Ras, which is why it was already in our network [26]. Other studies also report activation of JNK1 and phosphorylation of c-Jun downstream of Ras, which is consistent with an interaction between Ras and MEKK1 [31, 34]. Based on these findings, we adapted our model by removing the Hyp 2 node and creating a direct interaction between Ras and MEKK1 (Fig. 4A). Experimentally, the role of Ras could be confirmed by using a pharmacological inhibitor of Ras activity, and measuring the effect of this inhibitor on the activation of JNK1 and MK2. Together, our model suggests that EGFR activity is required but not sufficient for activation of JNK1 and MK2 in HT-29 cells.

There are other nodes for which the experimental data deviates from the model in one or more of the experimental conditions. A comparison between model and experimental data can be found in Figures S9, S10 and S11. A complete deciphering of the signalling events in this biological system is outside the scope of this paper. Instead, we illustrated how interactive modelling of the dynamic behaviour of a signal transduction network can be used to extend previous pathway topologies and can lead to the generation of novel hypotheses.

Testing the performances of ANIMO 2

The most important development we introduce in ANIMO 2 is a faster analysis process, thanks to the more efficient modelling approach (see Methods section). In order to measure how significant the performance increase is, we applied a number of analysis queries to a case study, comparing the performances of ANIMO 2 with the previous version of the tool. As ANIMO 2 provides the biologist with a proper access to the formal technique of model checking [35], we tested the model performances also in this setting. We will show that the performance improvement is even more significant in the case of model checking, making the use of Timed Automata as formal foundation for modeling biological processes both more accessible and more profitable.

The case study we use as a testbed is shown in Figure 1, and is a model of signalling events downstream of growth factors EGF (epidermal growth factor) and NGF (nerve growth factor) in PC12 cells. The topology for this network was proposed in [36], and it was analyzed with an ANIMO model, reproducing the experimentally observed ERK (extracellular signal-regulated kinase) activity changes [37]. In particular, a 10 minutes stimulation with EGF resulted in transient behavior (i.e. peak-shaped, see also the graph in Fig. 1), while NGF stimulation led to sustained activity (see Fig. 6).

Simulation-based analysis

The simplest analysis that can be performed with ANIMO is based on simulating the behavior of the network during a given period of time (see also the analyses of the Drosophila and TNF- α /EGF models above). As this type of analysis is also normally used when looking for a match between model parameters and experimental data, the computation speed of a simulation run deeply affects the level of interactivity perceived by the user. In order to make the modeling approach in ANIMO as smooth as possible, it is desirable to decrease dead times, i.e. significantly reduce simulation costs. Our first performance test compares the execution time for simulation runs on the Timed Automata models generated by ANIMO applying the old (i.e., ANIMO 1.0) and new (ANIMO 2) modeling approaches to the case study. To define the initial state of the model, we consider the starting condition to be the treatment with 50 ng/ml NGF, which translates into setting the initial activity level of nodes NGF to 15/15, and EGF to 0/15. We have chosen this configuration as the model is expected to continue reacting indefinitely (sustained ERK activity), without reaching a deadlock state where all reactions are inactive. This makes the model more demanding when generating the state space because having more reactions occur means having more states in the transition system underlying the Timed Automata model. Table 1 illustrates the computation time and memory usage when performing 100 simulation runs on each of the two considered models. Computing the simulation runs took about 92% less time with the new version of ANIMO, using 87% less memory. This decrease in computation time for long simulation runs brings the approach nearer to the idea of interactive exploration of a network. This advantage is particularly noticeable when analyzing more complex networks. [[Add also lines for drosophila and TNFa-EGF models, that are larger and make the performance increment look even more impressive]]

A good reason to use formal methods: model checking

To show why one should use a formal model like Timed Automata, we demonstrate the application one of the biggest advantages of Timed Automata: model checking [35].

The technique of model checking consists in verifying the truth of some properties that describe the behavior of a model. This is usually done by exploring every possible execution path of the model starting from its initial configuration. The set of all the configurations that can be reached by a model during all its possible executions is called *state space*. The properties on the evolution of the model are usually expressed in a formal language such as computation tree logic (CTL, [38]), which allows to formally describe how and when a property should hold. Examples of such properties can be expressed in natural language as: “the activity of node A stays always above 20”, “it is possible to reach a state where the activity of both nodes A and B is at least 60”, “whenever the activity of node A surpasses 20, the activity of node B will eventually reach at least 40”.

Model checking performances in ANIMO 2 have been tested using the case study of EGF-NGF signaling as reference. We compared the execution times and memory requirements in ANIMO and ANIMO 2 for a number of interesting queries:

- (1) and (2): `A[] not deadlock`. The model continues to execute indefinitely (`A` refers to all possible paths in the transition system of the model, and `[]` asks the property to always hold along a path).
- (3): `RKIP < 10 --> ERK >= 40`. After RKIP (Raf kinase inhibitory protein) activity has been lowered, ERK activity increases. As in the model RKIP has 20 levels of granularity and ERK has 100 levels, `RKIP < 10` means that RKIP is less than half active, and `ERK >= 40` means that ERK activity is at least 40%.
- (4): `E<> RKIP < 10`. Find a point when RKIP is low (`E` asks for the existence of at least one path for which the property holds, while `<>` requires the property to hold at least once along a given path). This query is expected to generate a trace, the last point of which will be used as initial configuration for model checking queries (5) and (6).
- (5): `A[] ERK < 70` and (6): `A[] ERK > 35`. Once RKIP activity has significantly decreased, ERK activity is sustained at an intermediate level.

The initial conditions are:

- (1): $\text{EGF} = 15/15$ and $\text{NGF} = 0/15$, all others as the original configuration, corresponding to the treatment condition with 100 ng/ml EGF.
- (2) - (4): $\text{EGF} = 0/15$, $\text{NGF} = 15/15$, all others as the original configuration, corresponding to the treatment condition with 50 ng/ml NGF^[1].
- (5) and (6): all activities as in the last state of the trace computed from query (4).

The analysis of query (1) returned false and all other queries returned true. In particular, query (1) confirms that under EGF treatment no other activity is observed in the model after the initial peak, while query (2) confirms that with NGF activity continues indefinitely. Moreover, queries (3) - (6) confirm the result of the

^[1]In the laboratory experimental setting, NGF is used at a lower concentration than EGF, but it is still enough to saturate all NGF receptors, which are rarer than EGF receptors.

simulations shown in [37], with NGF treatment leading to sustained ERK activity. The model checking performance of UPPAAL comparing the two versions of ANIMO is shown in Table 2.

Analysis of the results

Note that we focus most of our attention on the NGF treatment, as with this configuration the model was hypothesized to keep reacting permanently (sustained ERK activity). The results from queries (1) and (2) show that this is indeed the case, as EGF treatment leads to all reactions dying out after a number of steps. This means that the queries (3) - (6) deal with a larger state space, leading to presumably lower model checking performances. Requesting a full inspection of the state space as we do when using a query of the type $A[]\phi$ returning true in cases (5) and (6), allows us to indirectly compare the state space size of the two model versions. As the hundreds-fold computation time improvements in Table 2 show, the new model produces indeed a noticeably smaller state space, allowing for a higher level of interactivity also when performing non-trivial model checking.

Moreover, our experiments point out that ANIMO 2 considerably lowers the memory requirements for the model. Further investigation on this point (see Methods section) makes us believe that the main gain is indeed due to the new modeling perspective used in ANIMO 2.

Note that while the network we consider for the case study is not particularly large, the gain in performances is still considerable and promising in the perspective of analyzing more complex networks. [[Add some example queries also for the TNFa-EGF model??]]

Model checking for bigger models

When a model becomes particularly complex, its state space tends to grow considerably, dramatically increasing the model checking times. The most prominent cases of such state space growth offer the so-called *state space explosion* challenge: in such cases, it is often necessary to find other approaches to conventional model checking. One of such approaches is based on statistical considerations and allows to obtain approximated answers with a given confidence level in far less time than most exact model checking techniques: it is called statistical model checking. The newer versions of UPPAAL include also a statistical model checking engine [39], enabling us to obtain approximate answers for the bigger Timed Automata models, when exploring the whole state space would cost too much. Models that particularly benefit from statistical model checking usually represent non-deterministic behavior by defining probabilistic distributions for the choice of alternative evolution paths. Such paths are potentially infinite in number, and their exhaustive exploration would be mostly impossible using exact model checking.

Basic models built in ANIMO are deterministic, i.e. they will always exhibit the same behavior. However, ANIMO 2 now allows to define the k -value representing the scale factor for an interaction with a coupled *uncertainty* level. For example, consider an interaction $A \rightarrow B$ described by scenario 1 (i.e., its speed depends only on the activity level of A), with parameter $k = 0.02$. If the model behaves as expected but we want to test it for robustness, we can “relax” the value of k by

letting it be equally possibly inside a $\pm 5\%$ interval around the original value. Setting the uncertainty for the k -value of $A \rightarrow B$ at 5% induces a uniformly distributed choice on that k -value in the underlying Timed Automata model. The value for k is chosen as a first step at the beginning of the evolution of the model, sampling from a uniform random distribution in the interval $[0.95 \times k, 1.05 \times k]$, and using the chosen value along the rest of that model's execution path. Another way to add non-determinism to ANIMO 2 models is to let the initial activity of one (or more) nodes range inside user-defined bounds. For example, the initial activity of A could be chosen among values ranging from 20/100 to 70/100. Similarly to what is done with uncertainty in k -values, the underlying Timed Automata model will make a starting choice for the initial activity of A based on an uniform distribution on the interval $\{20, 21, \dots, 69, 70\}$. If using both the non-deterministic settings described in the example, two simulations could use settings of $k = 0.0202$ ($k + 1\%$), $A = 25$ or $k = 0.0194$ ($k - 3\%$), $A = 55$ with equal probability, generating different simulation courses.

While uncertainty for k -values can be used to test a model's robustness against parameter variations, the possibility to add non-determinism in the choice of initial activities can be used in ANIMO 2 as a basic *dosage-based therapy*. Assuming that some inputs to an ANIMO model represent drugs, we can let their initial activity (which may represent drug concentration) range over different intervals, and then interrogate ANIMO with model checking queries to understand whether it is possible to obtain a desirable state in the network.

Please note that having included non-deterministic behavior in a model does not imply that only statistical model checking is feasible. It is however true that non-determinism can significantly increase the size of the state space: for example, if we let the initial activity of $\text{TNF}\alpha$ in the model of Figure 4A vary in the interval $\{1, \dots, 100\}$, the size of the state space for that model increases by a factor of 100. In that case, it is indeed true that exact model checking cannot visit the whole state space without increasing the level of abstraction in the model. It is however still possible to obtain (true) answers to reachability-based queries in a small amount of time: if in the setting of the example we ask the query "It is possible to reach a state in which MK2 is active for more than 40/100 within 30 minutes", the answer is found to be true in 0.6 seconds. However, no answer can be found in reasonable time if the query asks for an activity of 90/100. This query would be evaluated to false: as we know from the behavior of the deterministic version of the model with 100 ng/ml $\text{TNF}\alpha$ as input, MK2 activity never goes above 50 (see Suppl. Figure S9). In order to find the negative answer to that second query, the model checker would need to explore the whole state space, which would require a large amount of computational resources. Still, an approximated answer for both queries can be found within 4 seconds if formulated in a probabilistic way "What is the probability to reach a state in which MK2 is active for more than X/100 within 30 minutes?". In the first case (MK2 activity > 40), the answer would be a probability in the interval $[0.90, 1]$, while in the second case (MK2 activity > 90) the probability would be in $[0, 0.05]$.

User interface for model checking in ANIMO 2

In order to allow a non-expert user to profit from the power of model checking, we have implemented a template-based user interface to define queries directly inside the ANIMO Cytoscape plug-in: Figure 7 shows the interface for composing a model checking query in ANIMO. The mappings between user interface templates and actual model checking queries are inspired on the ones proposed in [40], and are shown in Table 3.

If the answer to a model checking query contains a (counter-) example trace, the trace is automatically parsed by ANIMO and presented to the user in form of a graph of activity levels, in the same fashion as is normally done with simulation runs. Finally, a button positioned near the time slider under a simulation graph allows the user to easily change the initial activity levels of the whole network by setting them as in the currently selected time instant. This feature was used after executing query (4) to set the initial conditions for queries (5)-(6). Such an addition makes it easier to inspect the behavior of a network by using a sequence of model checking interrogations.

Discussion

Final remarks on the models

In the Results section, we described the construction of an ANIMO model of the circadian clock in *Drosophila Melanogaster*. This model captured the dynamics of the regulatory network and led to similar conclusions as an ODE model that had been published previously [Fathallah-Shaykh et al., 2009]. This finding supports the use of the series of modeling abstractions on which ANIMO is based. The biggest difference between the construction of these models is that the model by [Fathallah-Shaykh et al., 2009] is constructed by writing a system of mathematical equations, together with an algorithm for simulation. In ANIMO, instead, a number of network nodes is drawn for the molecules involved. These nodes are then linked by directed interactions that represent cause-and-effect relationships, with a single parameter that defines the strength of each interaction. This is a more intuitive approach to construct a model. Further contributing to an interactive modeling process is the compositionality of the model. Each node in the network can be disabled at any time by the user, or extra nodes can be added, without having to change any of the existing interactions.

In the Results section we also showed the construction of an executable model of signaling events downstream of TNF α and EGF in human colon carcinoma cells. This data set has been used for previous modeling studies, based on partial least-squares regression and fuzzy logic [41, 42]. The partial least-squares regression model describes an abstract data-driven model that uses statistical correlations to relate signal transduction events to various cellular decisions. This type of modeling is very useful in uncovering new and unexpected relations. It is also successful in making predictions, but gives little direct insight in the dynamic behavior of the network. Fuzzy logic analysis led to a model that gave a better fit to the dynamic network behavior than discrete logic (Boolean) models. Inspection of the inputs to the logical gates that were used to model protein behavior led to the prediction of novel interactions between proteins, showing the usefulness of this approach. For most of the proteins,

such as JNK1, time was used as an input parameter. For example, the logical gates “if TNF α is high *AND* time is low, then JNK1 is high” and “if TNF α is high *AND* time is high, then JNK1 is low” were used to describe the dynamic behavior of JNK1. Although this leads to a representative description of the dynamic behavior of JNK1, peaks in protein activity at early time points were not reproduced by the fuzzy logic model. Moreover, it gives no insight in the molecular interactions that are involved in activation or inhibition.

In this study, we used the same data set and performed a single round of the empirical cycle. This cycle starts off with the experiments carried out by [28]. We used the resulting experimental data, together with knowledge from curated databases [26, 27] to construct an executable model of the biological system. In contrast with the two approaches described above, ANIMO is aimed at the construction of more mechanistic models, mimicking biochemical interactions *in silico*. This way of modeling gives a different type of insight. In the process of model construction, we extended a prior-knowledge network with time-dependent extracellular crosstalk that has been reported previously [Janes et al., 2006]. To come up with possible explanations for a disagreement between the model and the experimental data, two additional layers of crosstalk were introduced, at the signal transduction and transcriptional level. These modifications improved the fit of the model to the data and can be interpreted as novel testable hypotheses. Finally, we proposed new experiments that could be carried out to test these hypotheses, closing the empirical cycle. Together, our model sheds more light on the intricate entanglement between the TNF α and EGF pathways at multiple cellular levels. But above all, the model provides an excellent starting point for further investigation.

Comparison between ANIMO and other modeling tools

Different formalisms are in use in the field of computational modeling of biological systems, each with their specific characteristics. Many of these formalisms have been implemented into software tools to support modeling efforts. In order to compare ANIMO with existing tools, we have selected a number of mathematical formalisms, each connected to a supporting tool. With an emphasis on the modeling process rather than the final model, we compared these tools on the basis of the following parameters:

- 1 **Hidden formalism:** a knowledge of the underlying formalism is not required in order to use the tool
- 2 **Visual modeling:** the tool allows the user to model using a visual interface, and is not exclusively founded on formula-, text- or table-based input forms
- 3 **Qualitative parameters:** parameters for reactions can be input as approximated estimations, and not exclusively as numbers
- 4 **Tight coupling with topology:** models are tightly and clearly coupled to the networks they represent, showing the visual representation of the model in a shape similar or comparable to the representation currently used by biologists for signaling pathways
- 5 **User-chosen granularity:** if discretization is applied during the modeling process, the user can change the granularity with which such discretization is made, possibly for each component of the model separately

Table 4 shows the comparison between ANIMO and the selected tools.

Going beyond the user interface, there are a number of “pros and cons” for using ANIMO and Timed Automata in the biological context. First and foremost, being Timed Automata an executable formal language, a state space can be derived from a Timed Automata model. This means that state space-related analyses such as model checking can be performed on Timed Automata: as explained in the Results section, this can be done directly in ANIMO, bypassing the need for a deeper understanding of Timed Automata as ANIMO acts as an intermediary towards the powerful model checking tool UPPAAL.

The smaller amount of parameters needed to build an ANIMO model, if compared e.g. to a differential equation-based approach, makes the modeling process faster, allowing the biologist to obtain interesting results in less time. However, a less parameter-intensive modeling approach is also less precise: in our case we abstract sequences of biochemical reactions into activation or inactivation interactions, simplifying any relation between two entities in a network as either activating or inhibiting. While this allows for some simplifications in the networks and the underlying formal models, it does not allow to represent in full detail more specific concepts such as reactant concentration or reaction affinity. In case such concepts are of primary importance, we encourage the interested reader to turn to more precise modeling approaches, such as those based on differential equations.

All reactants modeled in ANIMO are assumed to be present at the same (unitary) concentration. While this assumption is not always applicable, it encourages abstract thought: many biological processes can be represented as networks driven by *activity-based* interactions. Even if with a limited scope, ANIMO can be applied also in the analysis of metabolic processes, considering the production of protein *A* as the activation of node *A*, with degradation being represented as inhibition. As stated before, it cannot be expected from such models to be a completely realistic representation of their target biological processes, but they can still be a useful tool. This can be seen for example in the Drosophila model in the Results section, where mRNA and protein concentrations were abstracted to activity-driven processes in the ANIMO model.

Conclusions

ANIMO is not the first modeling tool to provide an interface to a modeling formalism. Such interfaces exist in many other tools (as shown in Tab. 4). With its focus on user-friendliness and intuitive modeling, ANIMO’s main contribution lies in making computational modeling more accessible to experts in biology. Making use of the visual interface provided by Cytoscape, network representations subscribe to biological conventions. Model parameters are kept to a minimum and can be directly accessed by mouse-clicking on nodes and edges. Because of the automatic translation of the network topology and user-defined parameters into an underlying formal model, training in the use of formal methods is not needed.

ANIMO 2

We have presented here how the new and improved ANIMO 2 provides an interactive approach to model analysis and a way of exploiting the power of model checking.

Thanks to the increased performances, we are able to obtain answers to model checking queries in a matter of seconds. Coherently with the user friendliness of the tool, we ensure that the biologist can access the features of model checking without the need to directly deal with Timed Automata models. In this way, ANIMO acts as an intermediary between the biologist and a formal representation of biological signaling pathways, letting the experts concentrate on investigating the mechanisms of cellular responses.

Future plans

In order to enforce the concept of user interaction as a primary focus of the tool, we plan to extend ANIMO by adding support for parameter sensitivity analysis and automatic parameter sweeps. We already allow for only one numeric parameter per reaction, but an automatic way of adjusting such parameters to fit experimental data will allow the user to concentrate more on defining a sensible topology for a pathway. Such an automatic search could be limited by setting specific bounds on reaction rates based on previous knowledge, or on a trade-off with performances. Moreover, inspired by works on automata learning [43], we plan to add also the possibility to automatically derive a network topology based on experimental data and user-defined restrictions based on previous knowledge.

We aim at widening the available set of model checking queries, in order to allow biologists to perform in silico experiments on an already fitting model and to obtain answers to more relevant questions. This would increase the usefulness of a model as a help to drive wet-lab investigation. In order to allow for meaningful in silico experiments, we plan to purposefully introduce user-defined non-deterministic parts in our models, which would allow for drug dosage investigations through model checking. This can be done e.g. through the definition of intervals for the values of some reaction kinetic constants, adding considerable uncertainty in the timing of those reactions. A model of this type could then be interrogated with queries like “How much X, Y and Z do we need to provide, and at which time points, in order to obtain targets A, B and C to be active?”. More useful results can be achieved through proper application of the statistical model checking part of UPPAAL [39] to an extended version of our model to include realistically significant stochastic behavior. Finally, in order to further improve performances, the applicability a multi-core model checking approach based on the works by Dalsgaard et al. [44] is under study.

Methods

A new way of modeling signaling pathways with Timed Automata

We propose here a novel model to represent signaling pathways with Timed Automata. We define the model currently used in ANIMO to be *reaction-centered*, as for each reaction in the network an instance of a Timed Automaton template is generated to mimic the occurrences of that reaction. Observing that signaling networks tend to be highly connected, containing noticeably more reactions than reactants, we propose to shift the focus on reactants instead, achieving what we call a *reactant-centered* model. This change of view is inspired by the classical way in which biological events are modeled with ordinary differential equations (ODEs) [45].

Reactant-centered model

The reactant-centered model presented here is based on the concept of *net effect* of a set of reactions on a reactant: instead of considering each reaction in isolation, we consider their combined influence on each reactant. As an example, consider a reactant A activated by reactions R_1 and R_2 , and inhibited by reaction R_3 (see Fig. 5A). The net effect of these three reactions on A defines the *net reaction* $R_A = R_1 + R_2 - R_3$. Applying a concept similar to the definition of an ODE, where the rate of change of each reactant depends on the rate of the reactions influencing it, the rate of R_A is computed as the sum of the rates of the reactions influencing A :

$$r_A = r_1 + r_2 - r_3$$

where r_i is the rate of reaction R_i and is defined as follows. Consider R_1 to be the reaction $B \rightarrow A$ with kinetic constant k_1 . Suppose the settings in the ANIMO network for R_1 make its rate depend only on the activity level of B . Then we compute the rate of R_1 as $r_1 = [B] \times k_1$, with $[B]$ the current activity level of B . We do similarly for the reactions R_2 and R_3 .

As with ODEs, if r_A is positive the activity level of A will increase; otherwise, A will decrease its activity level. The absolute value of r_A determines the speed with which such change happens. The value of the reaction rate is thus translated into a time value to be used as time bound in the Timed Automaton representing R_A (see Fig. 5B) by computing

$$T_A = \frac{1}{\text{abs}(r_a)}$$

with $\text{abs}(r_a)$ the absolute value of r_a . In order to represent a natural variability in the timing of reactions, we relax the exact value of T_A by defining bounds of $\pm 5\%$:

$$\begin{aligned} tL &= T_A \times 0.95 \\ tU &= T_A \times 1.05 \end{aligned}$$

Analogously to the reaction-centered model of [37], we will call tL the *lower time bound* and tU the *upper time bound*.

Timed Automata model

The behavior of the Timed Automaton representing the net reaction R_A is defined as follows: after a number of seconds variable inside the continuous interval $[tL, tU]$ (measured with the local clock c), the activity level of A will increase or decrease by one step, depending on the sign of r_A ; then new values for r_A , tL and tU will be computed based on the (possibly) changed conditions.

The process described in Section to compute the values of tL and tU is an instance of the function called `update()` in the Timed Automaton template of Figure 5B. The computation of `update()` is the first step taken when initializing a new model taking the transition from the initial location `start` (identified by two concentric circles) to `updating`. Location `updating` is then used to decide whether R_A can be executed or not (functions `can_react()` and `cant_react()` used as guards for the transitions exiting from `updating`). This decision is based on the computed value for r_A and

the current activity level of A : if $r_A > 0$ and A is already completely active (or $r_A < 0$ and A is completely inactive), no update to A can be applied, so the automaton switches to location `not_reacting`. Moreover, r_A can be 0: this means that the reactions influencing A balance each other to complete cancellation, so also in this case R_A cannot occur and the next location will be `not_reacting`. Otherwise (i.e. if `can_react()` is true), the activity level of A can be changed, so the next location will be the one labeled `waiting`, which is reached after having made sure that its clock invariant is respected (committed location between `updating` and `waiting`).

When in location `waiting`, the local clock c is let run until enough time has passed for the reaction to occur: this is obtained by using $c \geq tL$ as guard for the transition from `waiting` to `updating`. Because of the invariant $c \leq tU$ on `waiting`, we ensure that the reaction occurs after no more than tU seconds have passed. The transition to `updating` leads to an update to the activity level of A (call to `react()`), together with the computation of new values for r_A , tL and tU (function `react()` calls `update()`). Moreover, we see in Figure 5B that a communication is sent on channel `reacting[0]` (0 is the index assigned to reactant A): this is used to warn the other automata that the activity level of A has just changed, possibly changing the conditions for other reactions.

During the course of a model simulation, one of the reactants influencing a reaction on which A depends may change its activity level before R_A can occur: this event may have an influence on the value of r_A , so a re-computation of r_A , tL and tU is needed. In the template of Figure 5B, the indexes of the influencing reactants are 1, 2 and 3, corresponding respectively to B , C , D in Figure 5A. Whenever a communication on one of the channels corresponding to an influencing reactant is received while in location `waiting`, the automaton moves to location `stubborn`. This location was introduced to avoid unwanted non-deterministic behavior^[2] in the model. In the example, this could happen when the activity level of B is updated concurrently (in the same instant) with the activity level of A . As B influences A through reaction R_1 , any change in the activity level of B causes a change in r_1 , thus requiring a re-computation of r_A , tL and tU . Due to the interleaving nature of Timed Automata semantics, only one automaton may change location for the Timed Automata system to change state. This means that, should the activity level of B be changed first, the conditions for R_A would be recomputed, possibly preventing the update to A to occur. Vice versa, should the activity level of A be changed first, both A and B could change their activity levels. In such a situation, the non-deterministic order in which the updates are computed decides the behavior of the model. To avoid this, we ensure that if a reaction can occur in a given instant (i.e. $c \geq tL$), it will not consider the concurrent updates to influencing reactants (in the example, having the clock reach tL ensures that R_A occurs, independently from any concurrent update to B). Performing a check on the current value of the clock c with respect to the reaction lower time bound allows an automaton to detect the case of a concurrent update, remaining “stubborn” in its resolution of reacting with the current configuration: the guard $c \geq tL$ on the transition returning from `stubborn` to `waiting` is the same as the guard on the transition from `waiting` to `updating` and

^[2]The term *unwanted* refers to a non-determinism that is not related to actual biological concepts, but to the semantics of the modeling paradigm.

implies that the transition could occur in the current time instant. If no conflict is found, i.e. $c < tL$, a new time limit for the reaction is computed via function `update()` while moving to location `updating`. Note that the clock c is not reset when moving from `stubborn` to `updating`: should the new conditions only change the value of tL and tU without disabling the reaction, the “partial work” of the reactions is not discarded.

Finally, location `not_reacting` is used to avoid reacting when not necessary (see the description of `cant_react()` above), and to respond to changes in those reactants which can influence the value of r_A . Should one of such reactants change its activity level, the conditions are updated and the local clock is reset, moving to `updating` to check whether the reaction can now occur.

Computations on the fly

Reaction rates are all computed at run-time by function `update()`, and are based on the user-chosen scenarios, their kinetic constant k and the activity level of the involved reactants. As such computations require floating-point precision but UPPAAL only provides integer variables and operators, we use a significand-and-exponent notation with 4 significant figures, which allows for an error in the order of 0.1% while avoiding integer overflow in UPPAAL’s engine. As an example of such a notation, consider the two floating-point numbers $a = 1.23456$ and $b = 0.00023456$, and their sum $c = a + b = 1.23479456$. The corresponding representations in our integer-based notation will be:

$$\begin{aligned} a &= \langle 1235, -3 \rangle = 1235 \times 10^{-3} \\ b &= \langle 2346, -7 \rangle = 2346 \times 10^{-7} \\ a + b &= \langle 1237, -3 \rangle = 1237 \times 10^{-3} \end{aligned}$$

In this case, the number representing the sum $a + b$ differs from the exact result by $c - 1237 \times 10^{-3} = 0.001456$. The interested reader can find the UPPAAL definitions and functions needed to compute rate and time values for the Timed Automata templates inside any UPPAAL model file generated by ANIMO with a reactant-centered model type.

Notes on the Timed Automata model

We note that replacing all the existing reactions with the net reactions relative to each reactant in a model does change the behavior of the model in the sense that continuous oscillations of activity levels around an equilibrium point are less frequent. However, this does not mean that the behavior of two models using the two different approaches will diverge: the equilibrium points are still the same. From the user’s point of view, graphs will look smoother while still exhibiting the same qualitative behavior, as can be seen in Figure 6. The Timed Automata templates in Figure 5 show that the main difference between the two approaches is indeed due to the choice of lumping all the reactions influencing A into the single reaction R_A . In the Results session we have shown that having less oscillations leads in practice to better analysis performances. The significant decrease in memory usage is partly

due to the absence of the (possibly large) precomputed time tables of the reaction-centered model, which could store up to ten thousand elements in each table.^[3] But that is not the only cause. Indeed, this point was further investigated by implementing a reaction-centered model which avoids the use of tables and instead makes on-the-fly computations of the time bounds with the same number representation as in the reactant-centered model. This resulted in improved performances in the cases of reachability and simulation-based queries, with memory requirements similar to the ones for the reactant-centered model. However, in all other cases a much larger amount of memory (more than 2 Gb) was used with respect to the table-based implementation of the same model, without leading to appreciable benefits in terms of execution time: in some cases performances were noticeably deteriorated. These findings support the intuitive idea that the new reactant-centered approach leads in general to a smaller state space.

Experimental setup for simulations and model checking

All experiments described in the Results section were carried out on an Intel® Core™ i7 CPU at 2.80GHz equipped with 4 Gb RAM and running Ubuntu GNU/Linux 12.10 64bit. UPPAAL version 4.1.11 was used to compute the result of the queries, asking for “some trace” with random depth-first search order when an execution trace was expected to be produced. All options for simulation queries were left at their default values.

Competing interests

The authors declare that they have no competing interests.

Author's contributions

S.S. designed and performed the experiments, developed the Cytoscape integration, wrote the manuscript; J.S. conceived, designed and performed the experiments, wrote the manuscript; P.E.vdV. initiated the study, conceived the Cytoscape implementation, supervised the project; M.K. designed experiments, analyzed data and wrote the manuscript; R.L. Contributed to the methodology and supervised the project; J.vdP. contributed to the strategy and methodology in the manuscript, in particular the connection with formal methods; J.N.P. designed experiments, analyzed data sets, contributed in particular to the application of ANIMO for large biological data, wrote the manuscript, and supervised the project.

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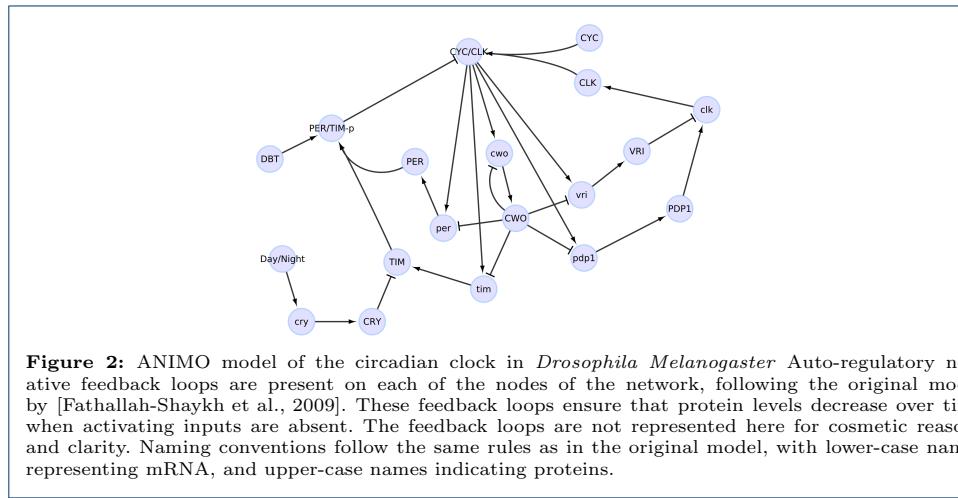
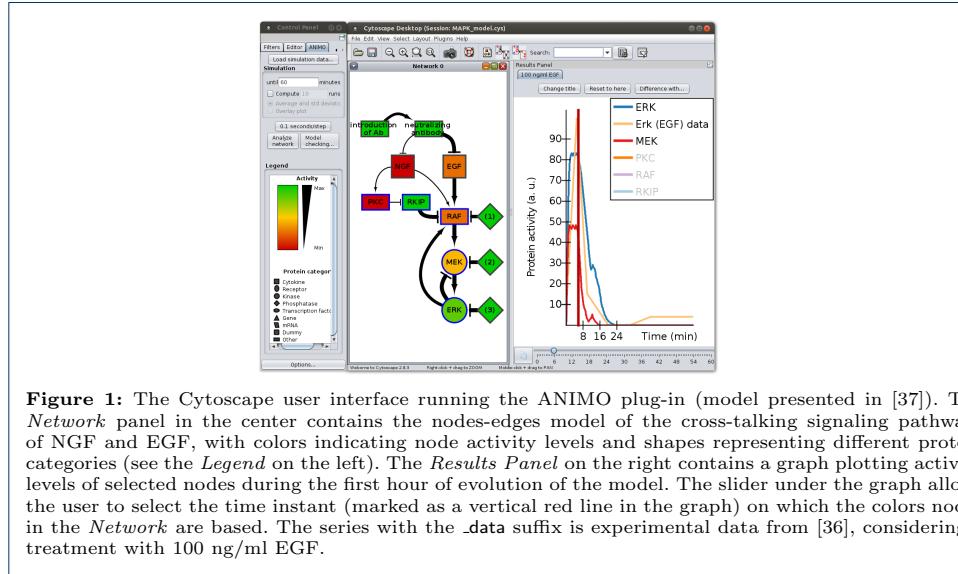
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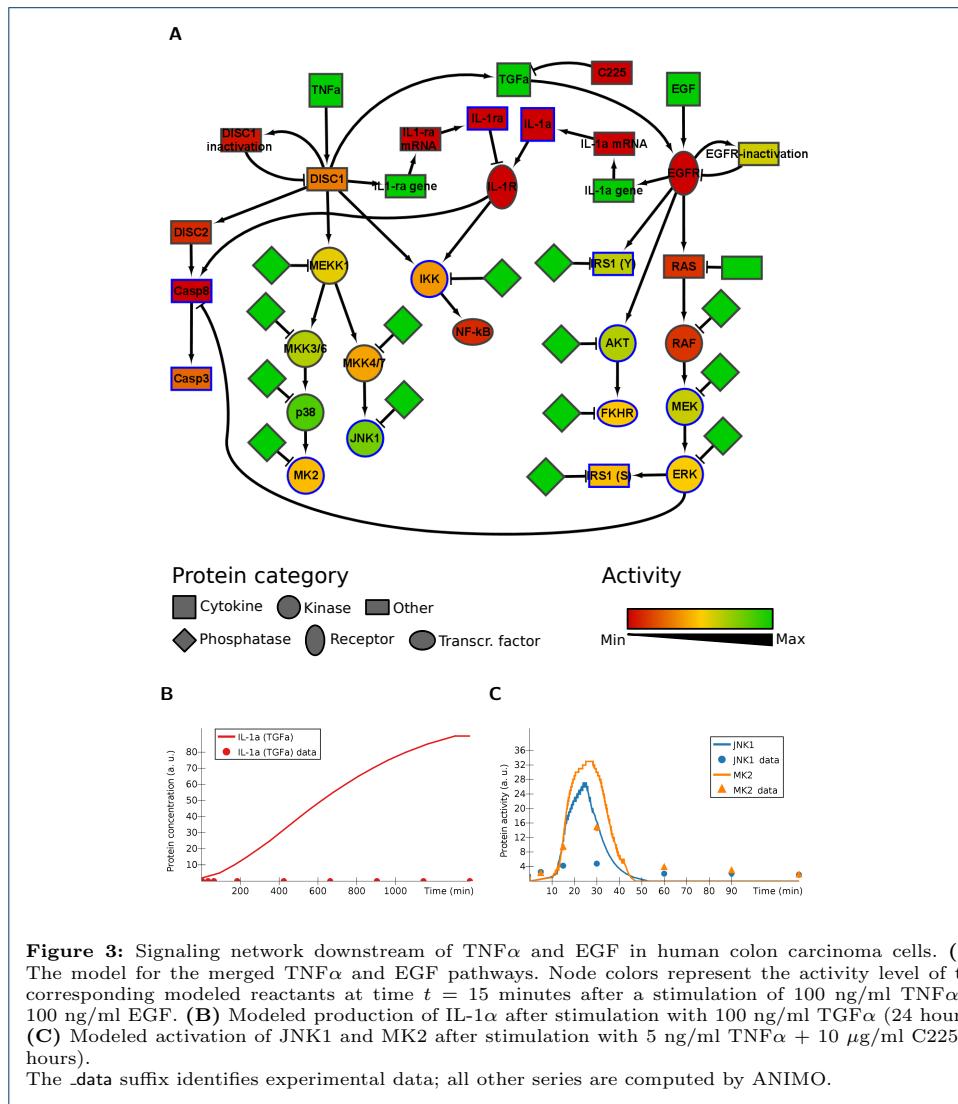
^[3]In the model used in ANIMO 1.0, having a reaction depend on two 100-levels reactants lead to the generation of two time tables containing $100 \times 100 = 10\,000$ elements each.

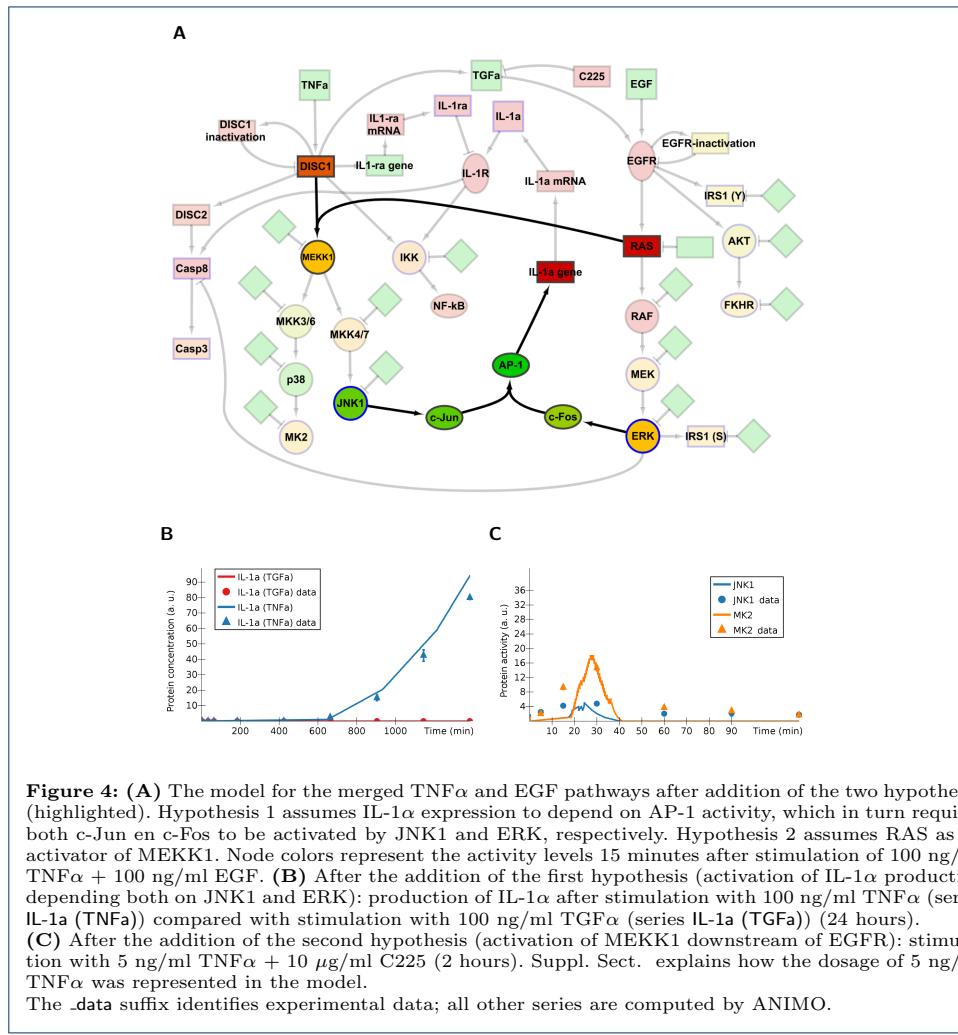
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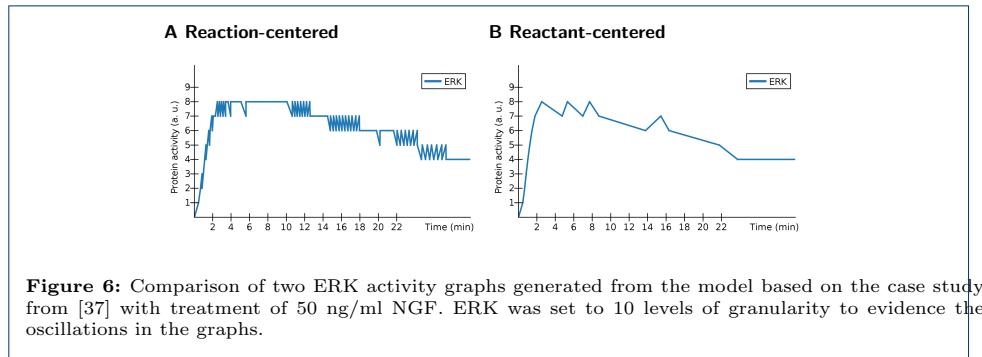
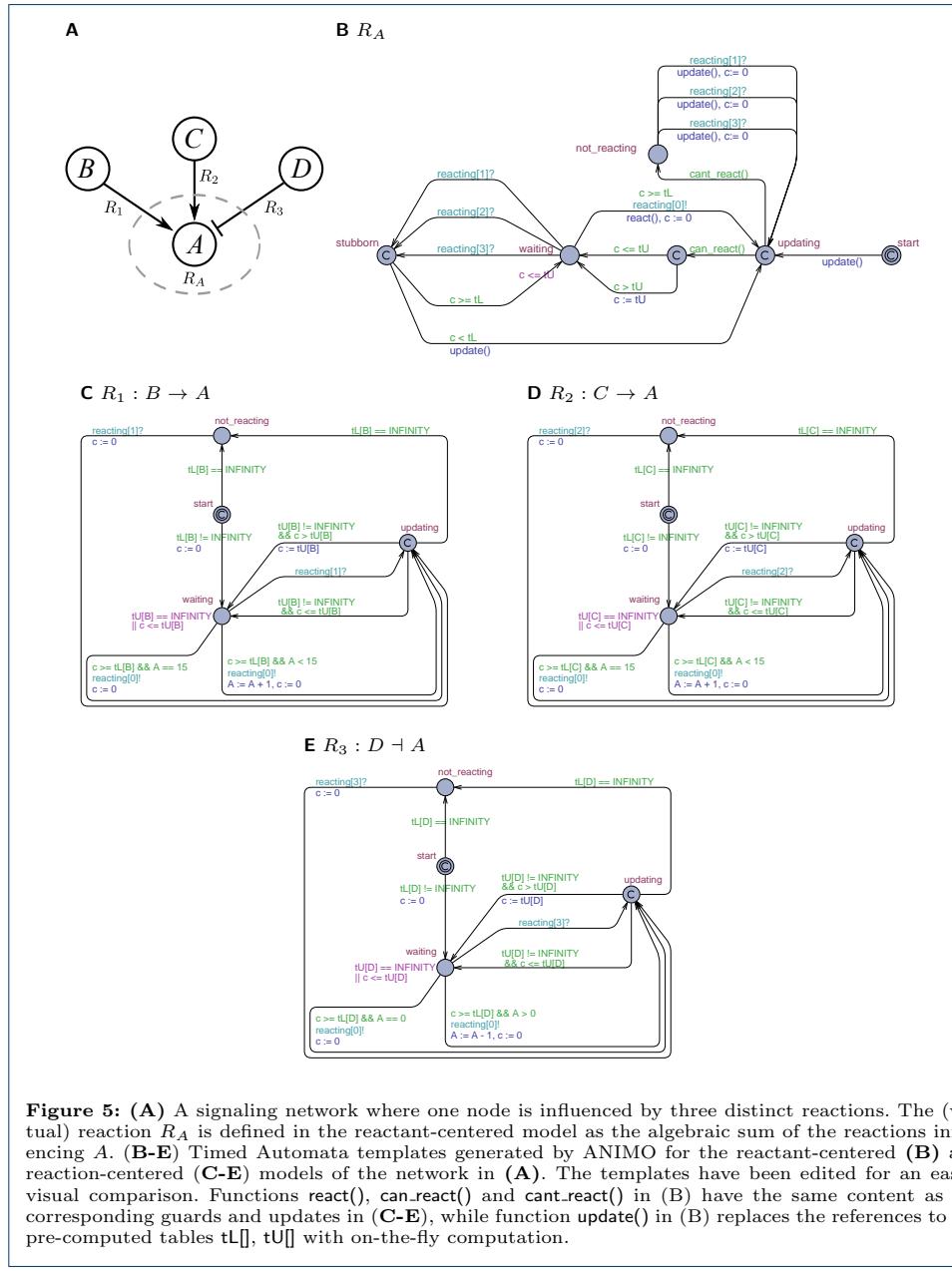
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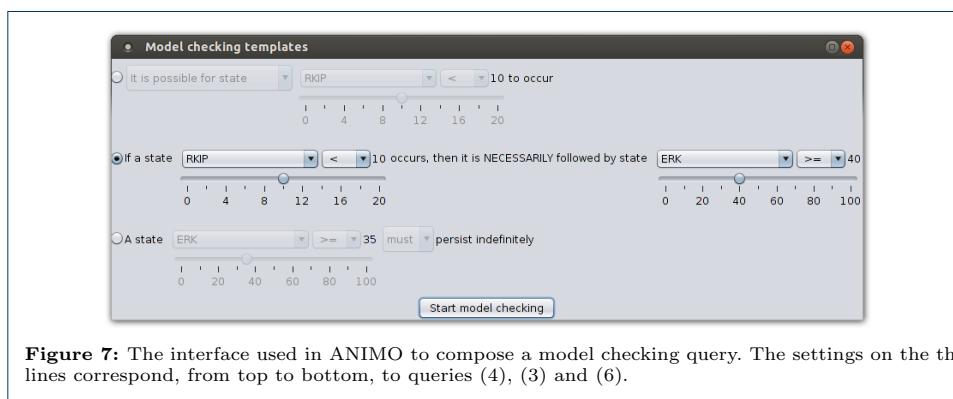
Figures











Tables

ANIMO Version	Time (s)	Memory (peak KB)
ANIMO 1.0	37.14	257,928
ANIMO 2	2.83	33,464

Table 1: UPPAAL processor time and memory usage for reaction- and reactant-centered modeling approaches when computing the query `simulate 100 [≤36000] { R1, R2, ..., R11 }` on the model from [37] with starting condition $\text{NGF} = 15/15$, $\text{EGF} = 0/15$, corresponding to a treatment with 50 ng/ml NGF. The query asks for 100 time series of the activity levels of all reactants in the model over the first 60 minutes of execution. This means that, on average, it takes 0.37 seconds to perform one simulation of the behavior of the EGF/NGF model with ANIMO 1.0 and 0.028 seconds to compute the same result with ANIMO 2.

Query	ANIMO 1.0		ANIMO 2		Improvement	
	Computation time (s)	Memory usage (peak KB)	Computation time (s)	Memory usage (peak KB)	Time (n-fold)	Memory (n-fold)
(1)	127.248	351 804	1.415	25 716	90	14
(2)	167.635	269 932	1.932	26 112	87	10
(3)	150.901	318 460	1.439	26 136	105	12
(4)	2.154	216 920	0.113	25 316	19	9
(5)	470.560	311 568	2.223	26 648	212	12
(6)	453.900	357 980	2.229	26 652	204	13

Table 2: UPPAAL processor time and memory usage for ANIMO 1.0 and ANIMO 2 when computing the given queries on the case study from [37].

ANIMO template	UPPAAL formula
It is possible for state ϕ to occur	$E\phi$
State ϕ never occurs	$E\phi$
If a state ϕ occurs, then it is necessarily followed by a state ψ	$\phi \rightarrow \psi$
A state ϕ can persist indefinitely	$E[]\phi$
A state ϕ must persist indefinitely	$A[]\phi$

Table 3: Mapping between queries as presented in ANIMO user interface and the corresponding model checking queries in UPPAAL syntax. State formulas indicated by ϕ and ψ are all in the form $R \bowtie n$, with R the identifier of a reactant in the model, $\bowtie \in \{<, \leq, =, \geq, >\}$ and $n \in [0, g(R)]$ a valid activity level value between 0 and the granularity (number of discrete levels) of R .

Tool	Formalism	Hidden formalism	Visual modeling	Qualitative parameters	Tight coupling with topology	User-chosen granularity
ANIMO [37]	Timed Automata	Yes	Yes	Yes	Yes	Yes
Bio-PEPA Work-bench [Ciocchetta et al., 2009]	Bio-PEPA	No	No	No	No	Yes
Cell Illustrator [Nagasaki et al., 2011]	Petri Nets	Yes	Yes	No	Yes	No
COPASI [Mendes et al., 2009]	ODE, stochastic models	No	No	No	No	No
COSBI LAB ¹	BlenX	Yes	Yes	No	Yes	No
GINsim [Chououiya et al., 2003]	Boolean Networks	No	Yes	Yes	Yes	Yes ²
GNA [de Jong et al., 2003] Rhapsody ³	PLDE Statecharts	No No	Yes Yes	Yes Yes	Yes No ⁴	Yes ² No

Table 4: Comparison between ANIMO and some existing approaches to modeling biological systems. A “Yes” under a column indicates that the modeling tool (mostly) fulfills the parameter, “No” indicates very limited or no fulfillment.

¹ COSBILab web page <http://www.cosbi.eu/index.php/research/cosbi-lab>

² The user can choose the number of levels for each reactant, allowing to define multi-level models based on Boolean reaction dynamics.

³ IBM Rational Rhapsody web page <http://www-01.ibm.com/software/rational/products/rhapsody/designer>

⁴ Statecharts represent more closely the so-called *transition system* of the model as opposed to the components and interactions occurring among them.

Additional Files

Additional file 1 — Sample additional file title

Additional file descriptions text (including details of how to view the file, if it is in a non-standard format or the file extension). This might refer to a multi-page table or a figure.

Additional file 2 — Sample additional file title

Additional file descriptions text.

Bringing biological networks to life with ANIMO

Additional Materials

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Naming conventions

Table S1 explains the abbreviations used in the paper.

Table S1: Explanation of the abbreviated names referring to molecular species in the main text.

Abbreviation	Full name	
Akt	protein kinase B	P31749
AP-1	activator protein 1	heterodimer of c-Jun and c-Fos
Casp3	caspase 3	P42574
Casp8	caspase 8	Q14790
c-Fos	proto-oncogene-protein c-fos	P01100
c-Jun	Jun activation domain binding protein	P05412
CLK	clock	O61735
CRY	cryptochrome	O77059
CWO	clockwork orange	Q9VGZ5
CYC	cycle	O61734
CYC/CLK	cycle-clock complex	
DBT	double-time kinase	O76324
DISC1	death-inducing signaling complex 1	
DISC2	death-inducing signaling complex 2	
EGF	epidermal growth factor	P01133
EGFR	EGF receptor	P00533
ERK	extracellular regulated kinase	P27361
FKHR	forkhead box protein O1	Q12778
IKK	inhibitor of nuclear factor kappa-B kinase	O14920
IL-1a	interleukin 1 α	P01583
IL-1R	interleukin 1 receptor	P14778
IL-1ra	interleukin 1 receptor antagonist	P18510
IRS1 (S)	insulin receptor substrate 1 (Serine 636)	P35568
IRS1 (Y)	insulin receptor substrate 1 (Tyrosine 896)	P35568
JNK1	c-Jun N-terminal kinase 1	P45983
MEK	MAPK ERK kinase	Q02750
MEKK1	MAPK/ERK kinase kinase 1	Q13233

Table S1 - continued from previous page

Abbreviation	Full name	
MK2	mitogen-activated protein kinase-activated protein kinase 2	P49137
MKK3/6	dual specificity mitogen-activated protein kinase kinase 3/6	P46734 / P52564
MKK4/7	dual specificity mitogen-activated protein kinase kinase 4/7	P45985 / O14733
NF-kB	nuclear factor kappa-B	P19838
p38	mitogen-activated protein kinase p38	Q16539
PDP1	par-domain protein 1	Q9TVY0
PER	period	P07663
PER/TIM-p	phosphorylated period-timeless complex	
RAF	Raf	P04049
RAS	Ras GTPase-activating protein	P01112
TGF α	transforming growth factor α	P01135
TNF α	tumor necrosis factor- α	P01375
TNFR	TNF receptor	P19438
TIM	timeless	P49021
VRI	vrille	O18660

Normalizing experimental data for use with ANIMO

Document S1 in the Supplemental Data of the work by [Janes et al., 2006] contains three tables, named Replicates, Averages and DPLSR dataset. The data we use to compare the results computed with ANIMO are based on the values from the Averages table. In particular, we compute activity data by performing a normalization on a 0...100 scale using this formula

$$v_{\text{norm}} = \frac{v}{v_{\text{max}}} \times 100$$

where v is the datum to be normalized taken from the column v in the Averages table, v_{norm} is the normalized value and v_{max} is the maximum value over the whole column v in the Replicates table. For each series, we compute also the standard deviation using the triplicate measurements present in table Replicates. The standard deviation is also normalized using the formula presented for the average. Each table produced with this process contains a subset of the columns from the Averages table, and refers to one treatment condition only. A column with time references is added to the table in first position. Finally, a column named *Number_of_levels* containing only the value 100 (see the instructions on page ??) is added at the rightmost position. The tables are all exported in .csv format to be used with ANIMO, and are included in the *Model_and_data.zip* file in the additional materials of the present work.

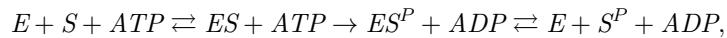
ANIMO and Timed Automata

Modeling abstractions

In living cells, cascades of chemical and physical interactions enable propagation of signals through molecular networks. In this process, the activity of upstream molecules induces a change in the concentration or activity of downstream molecules. For many reactions, the values of the kinetic parameters are unknown or difficult to collect. This lack of knowledge hampers the feasibility of computational models that describe molecular networks in fine mechanistic detail, especially for larger networks. As a solution to this problem, we propose the construction of models at a higher level of abstraction, thereby reducing the number of parameters involved. In choosing a suitable abstraction level, it is important to retain enough descriptive power to give a meaningful formal description of the topology and the associated dynamic behavior of biological networks.

As a first abstraction in ANIMO models, the active and inactive forms of each network component are represented together by a single node in the network. Each of these nodes is characterized by its *activity level*, which represents the fraction of active molecules of that molecular species. When a molecule is known to be constitutively active, changes in concentrations of that molecule are treated as changes in its activity level. Activity levels are discretized into integer variables with a user-defined granularity, ranging from Boolean (2 levels) to near-continuous (100 levels).

Detailed biochemical reaction mechanisms are abstracted to *interactions*, which can represent either activations (\rightarrow) or inhibitions (\dashv). This aggregation of elementary reactions into single interaction steps reduces the number of kinetic parameters involved, while preserving cause-and-effect relationships. For example, consider a reaction in which enzyme E phosphorylates and activates substrate S , transferring a phosphate group from a molecule of ATP to a molecule of S . Biochemically, this reaction can be represented as



with conservation condition $S + S^P = \text{constant}$ and $ATP + ADP = \text{constant}$.

Under the assumption of ATP constantly being replenished by the cell, this reaction is abstracted in ANIMO to the corresponding interaction



Each occurrence of the interaction $E \rightarrow S$ will increase the activity level of S by one discrete step. Since the activity level is defined as the active fraction of a molecular species, an increase in the active fraction implies a decrease in the inactive fraction. Hence, the original conservation condition is automatically satisfied. The interaction rate, R , depends on the activity levels of the reactants involved and on a single kinetic parameter k that is set by the user. The three available interaction scenarios can be interpreted as abstracted kinetic rate laws:

- 1 $R = k \times [E]$: the interaction rate depends only on the activity level of the upstream node.

- 2 $R = k \times [E] \times [1 - S]$ (activations) or $R = k \times [E] \times [S]$ (inhibitions): the rate depends on the activity levels of both the upstream and downstream participants. Activations depend on the presence of inactive substrate, $[1 - S]$, whereas inhibitions depend on the level of active substrate, $[S]$.
- 3 $R = k \times [E_1] \times [E_2]$: this scenario can be used when the activation or inhibition of a downstream node depends on the simultaneous activity of two upstream nodes. This scenario is comparable to an *AND-gate* in Boolean logic.

We will show in Section that the abstraction proposed here preserves ample expressivity to capture the dynamic behavior of a biological network.

Modeling interactions with Timed Automata

Timed Automata have been shown to be a powerful formalism to model biological processes [10, 11, 12]. A timed automaton consists of locations and transitions between these locations (see Fig. ??), and a system of timed automata can be used to model a system of interacting molecules. At any time, each automaton is in a specific location, and together these locations represent the current state of the biological system. Each timed automaton can have one or more local clocks associated to it, allowing temporal control of transitions between locations. These transitions are used to represent interactions between molecules. Fast interactions take less time than slow interactions to perform an activation or inhibition step. We have previously described in detail how the scenarios presented in Section can be used to calculate the timing of molecular interactions to give a description of network dynamics [Schivo et al., 2012]. Figure ?? presents a small example that illustrates the basic properties of TA. This model describes the activation of ERK by MEK^[4].

ANIMO

The modeling approach described in Section and Section is implemented in the software tool ANIMO (Analysis of Networks with Interactive MOdeling, [Schivo et al., 2012]) as a plug-in to the network visualization tool Cytoscape [Killcoyne et al., 2009]. The visual interface of Cytoscape makes the construction, expansion and rewiring of a network topology a fast and user-friendly process.

When a new node is added to the network, it has to be initialized with the number of activity levels and its initial activity. For each interaction, a scenario needs to be selected, together with the corresponding kinetic parameter and the interaction type: activation or inhibition. All settings can be readily adapted by double clicking, or via a table of nodes or interactions.

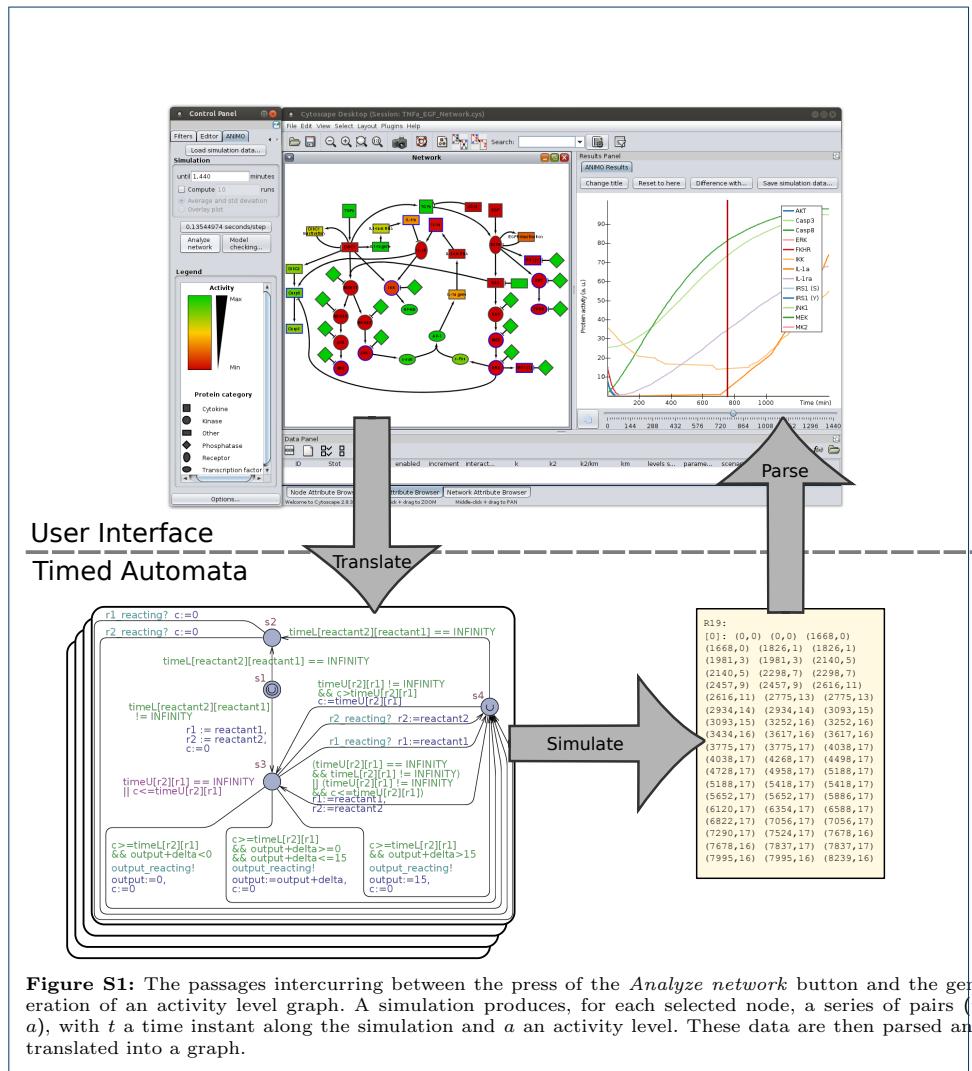
ANIMO automatically translates the user input to a TA model, which is then simulated with the model checking tool UPPAAL [Larsen et al., 1997]. The results are subsequently parsed and translated to a graph that shows the dynamic behavior of nodes in the network. A schematic overview of this process is given in Supplementary Section . No training or prior knowledge on the use of TA or UPPAAL is needed in order to benefit from ANIMO. Nevertheless, the TA model and the model checking process in UPPAAL can be accessed when desired by the user.

^[4]All acronyms used in this paper and their corresponding UniProt IDs are listed in Suppl. Sect. .

The dynamic behavior of a model can be interactively explored by moving a time slider underneath the graph to highlight time points in a simulation. In the network view, each node will be colored according to its activity level at the selected time point. Experimental data can be compared to the model by importing and superposing these data upon an output graph from the model (Figure ?? B,D,F). The ANIMO user workflow and the features described above are illustrated in Suppl. Video 1.

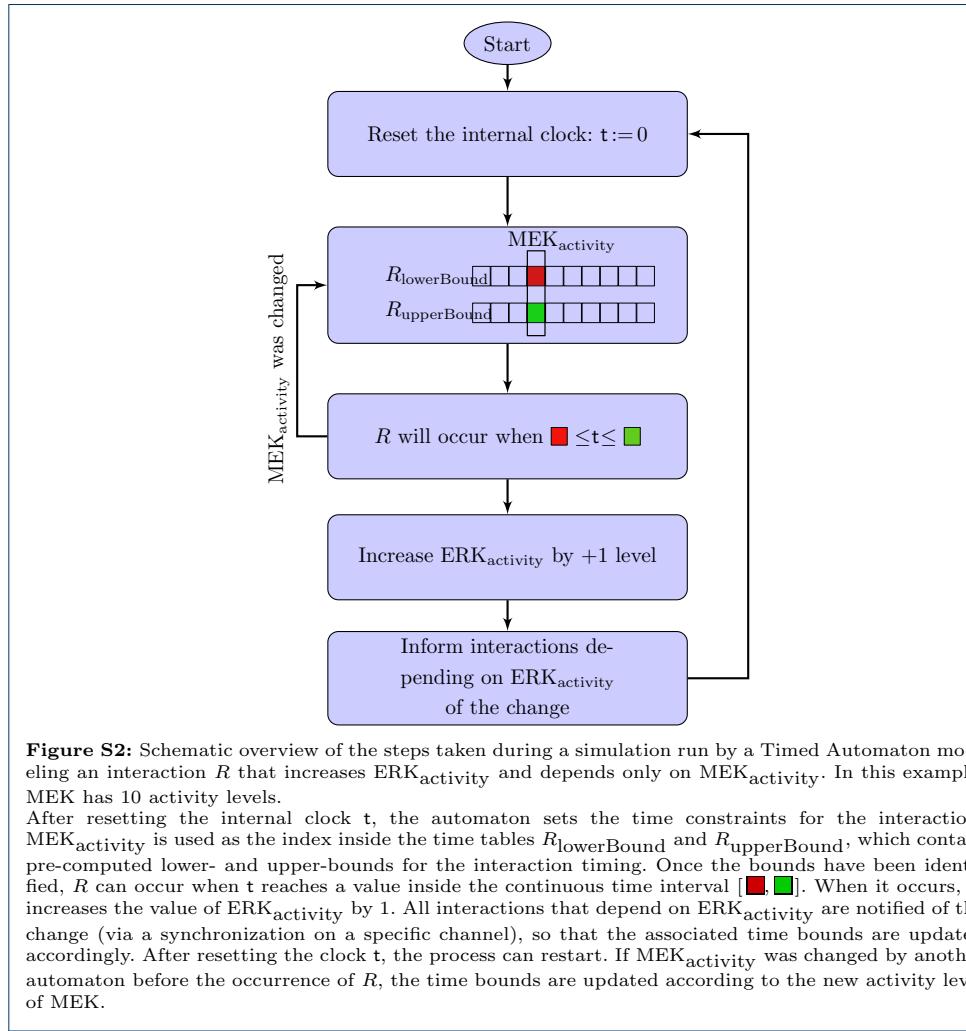
Timed Automata model

The Timed Automata (TA) model underlying an ANIMO network is generated whenever an analysis is requested by the user. Starting from the network represented in the Cytoscape-based user interface, ANIMO automatically generates a TA model to be used with UPPAAL. The analysis result is then parsed and properly presented to the user, for example as a graph of reactant activity levels. This workflow is described in Figure S1.



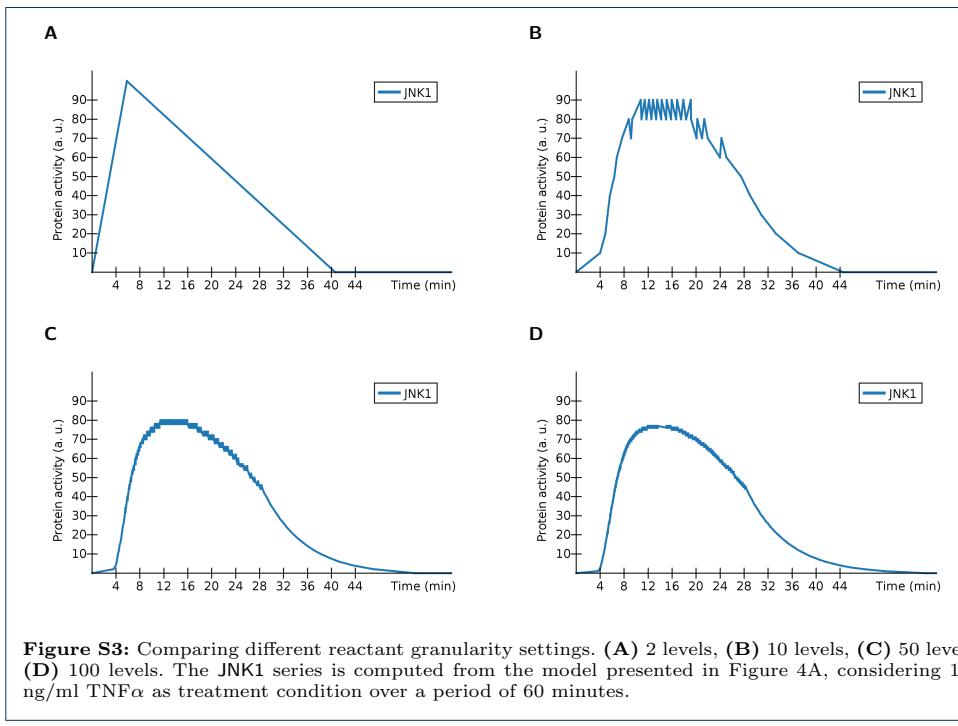
Each TA model generated by ANIMO contains one automaton for each interaction (activation or inhibition) in the network. A TA representing an interaction performs a cyclic series of steps, continuously updating the target of the interaction it represents, and adapting the timing of the next update according to the user-defined dynamics. Synchronizations between different automata occur when the activity level of a network component (e.g. ERK) changes: this allows the automata depending on that component to update their time settings.

The abstract behavior of the interaction $\text{MEK} \rightarrow \text{ERK}$ in the TA model used in ANIMO is described in Figure S2. There, the activity levels of MEK and ERK are represented by variables called, respectively, $\text{MEK}_{\text{activity}}$ and $\text{ERK}_{\text{activity}}$. A more detailed description of the TA model underlying ANIMO was presented in the IEEE Journal of Biomedical and Health Informatics [Schivo et al., 2012].



Granularity of an ANIMO network node

Figure S3 shows the differences between different choices for the number of levels of a node. This allows to adapt a model to the quality of experimental data.



Additional notes

Simulating the day-night cycle

The model presented in Figure 2 contains a node labeled Day/Night. That node abstracts our representation of the cyclic alternation of day and night, which causes the variations in cryptochrome (*cry*): these oscillations allow the network to synchronize to a time zone. Note that the network oscillates also when the node *cry* is not included in the model.

The alternation between day and night is represented in our model with a repressilator-like [Elowitz, 2000] subnetwork, as can be seen in Figure S4. In the model by [Fathallah-Shaykh et al., 2009] a specific function was introduced in the equations to approximate the experimental data from [Kadener et al., 2007].

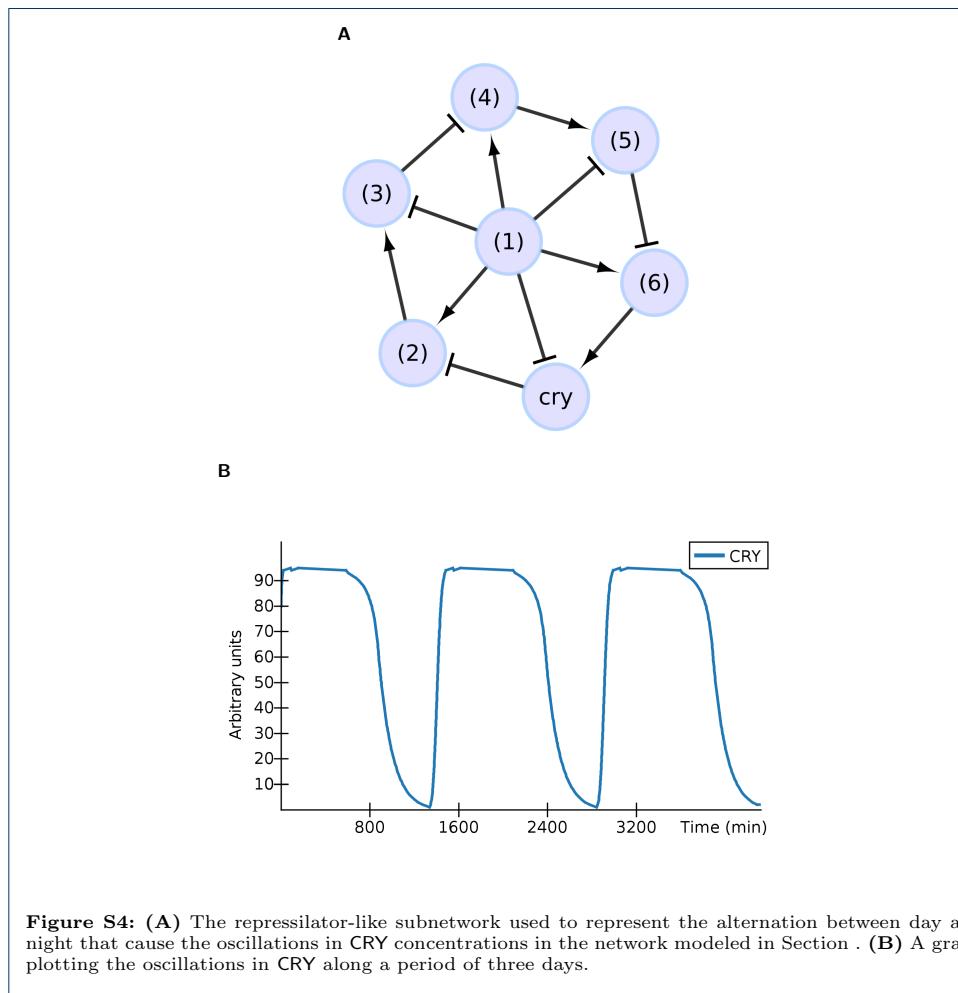


Figure S4: (A) The repressilator-like subnetwork used to represent the alternation between day and night that cause the oscillations in CRY concentrations in the network modeled in Section . (B) A graph plotting the oscillations in CRY along a period of three days.

ANIMO model of the Drosophila circadian clock

We compared the simulation results from the ANIMO model presented in Figure 2 with the ODE model described by [Fathallah-Shaykh et al., 2009]. The raw data coming from the two models were aligned to have a roughly close initial point, and all amplitudes were normalized following the procedure described in Suppl. Sect. . The results of this comparison can be seen in Figure S5.

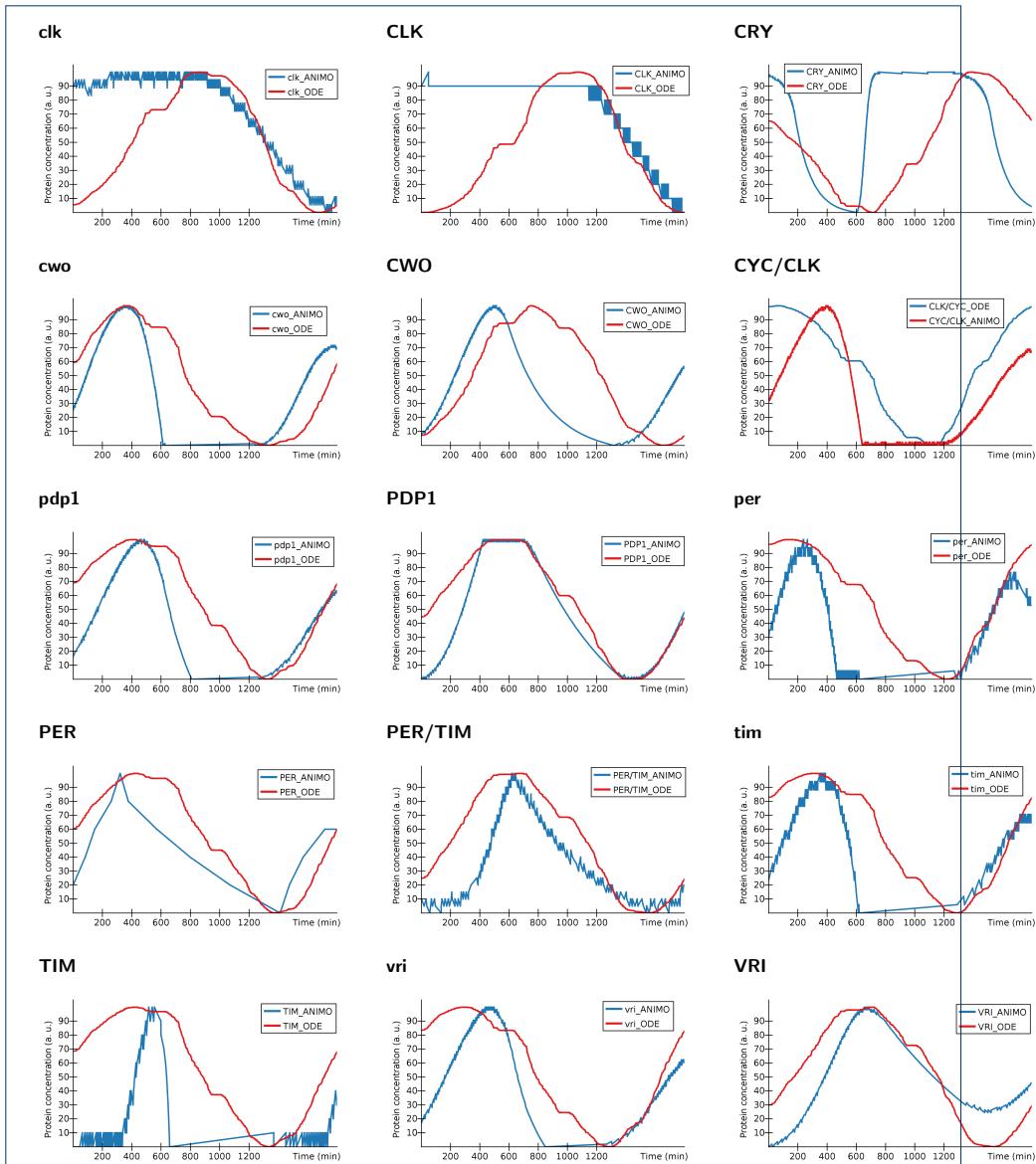


Figure S5: Comparing the simulation results from the ANIMO and ODE models of *Drosophila Melanogaster* circadian clock. Blue lines (ANIMO series) represent data from the ANIMO model in Figure 2, while red lines (ODE series) represent data from the ODE model by [Fathallah-Shaykh et al., 2009].

Most of the molecules represented in the two models evolve with the same period and phase. CLK and clk in the ANIMO model have a small oscillation range (their values change by around 10% during a simulation), so their behavior match the continuous model less precisely.

Note on the parameters in the TNF α -EGF model

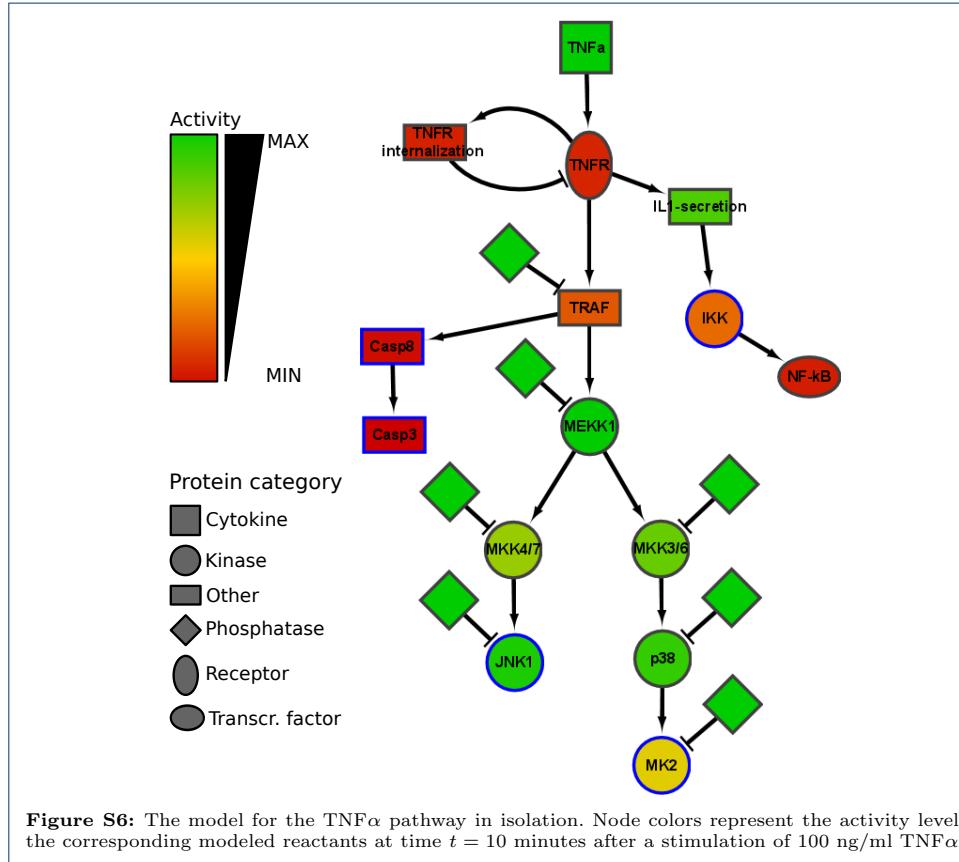
The parameters in the model in Figure 4A have been set by fitting the model to the experimental data for conditions with 100 ng/ml TNF α . In the model we have set the starting level of TNF α at 100 out of 100 for these conditions. This level is a dimensionless quantity that indicates the maximum activity level in the

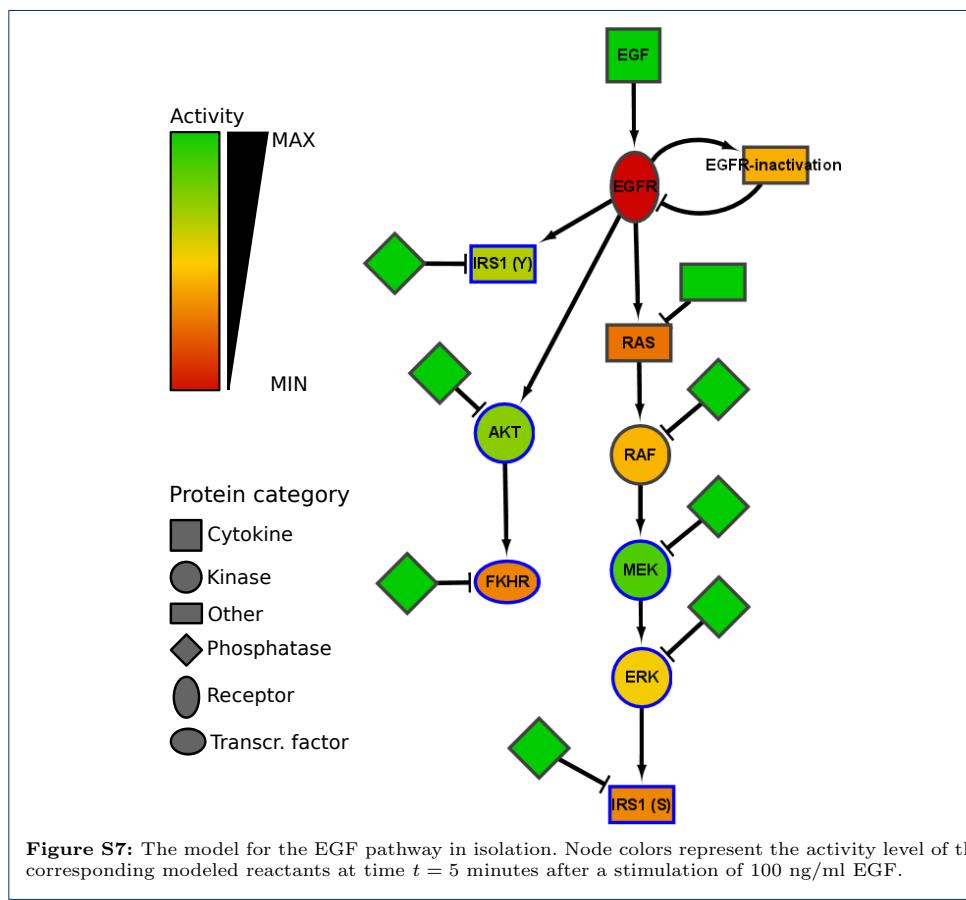
data set. We found that setting the initial level of TNF α at level 8 out of 100 gave slightly better results for the condition with 5 ng/ml TNF α than level 5 out of 100. We believe that this has to do with the fact that 100 ng/ml is a highly supra-physiological concentration of TNF α , that will rapidly cause activation of all receptors present. Fitting the model to this experimental condition may have resulted in slight deviations in the parameter values. Nevertheless, the modeling results illustrate that building a model with basic kinetic rate laws can give useful predictions over a range of concentrations. Figures 3C and 4C show the modeling results with TNF set at 8 out of 100.

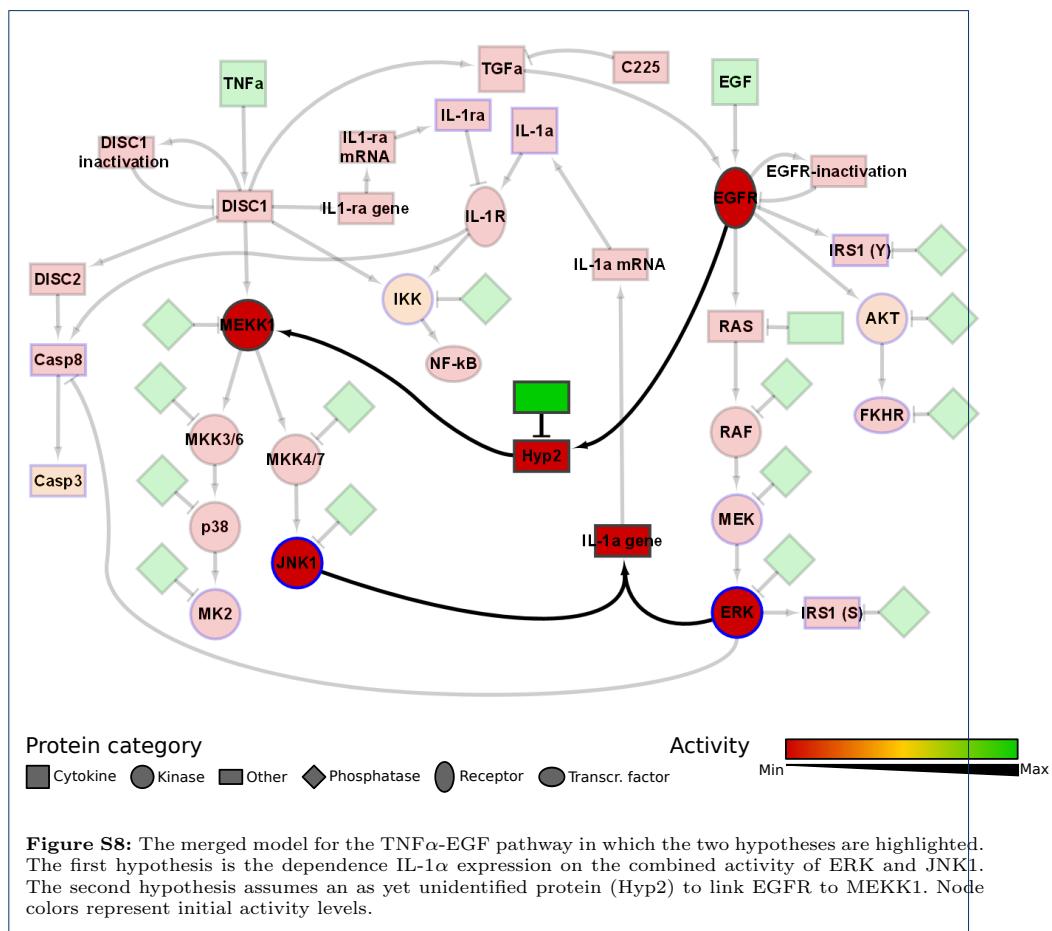
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Supplementary figures







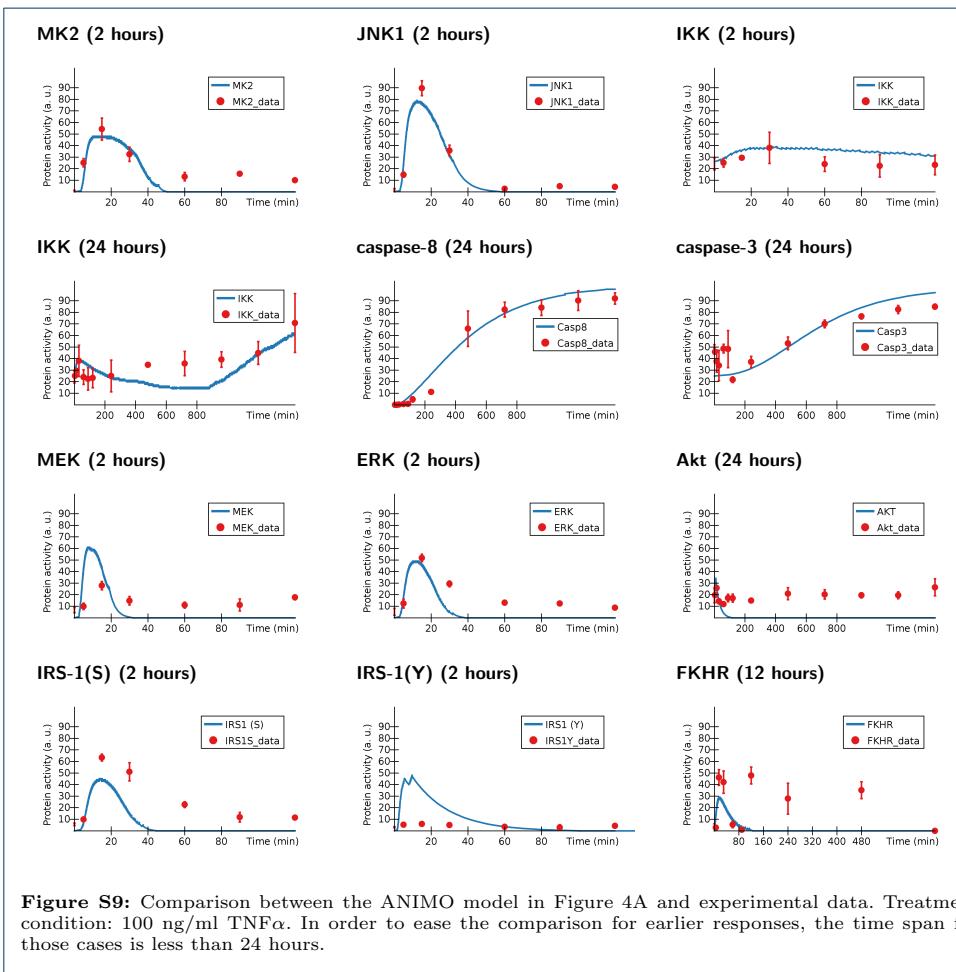
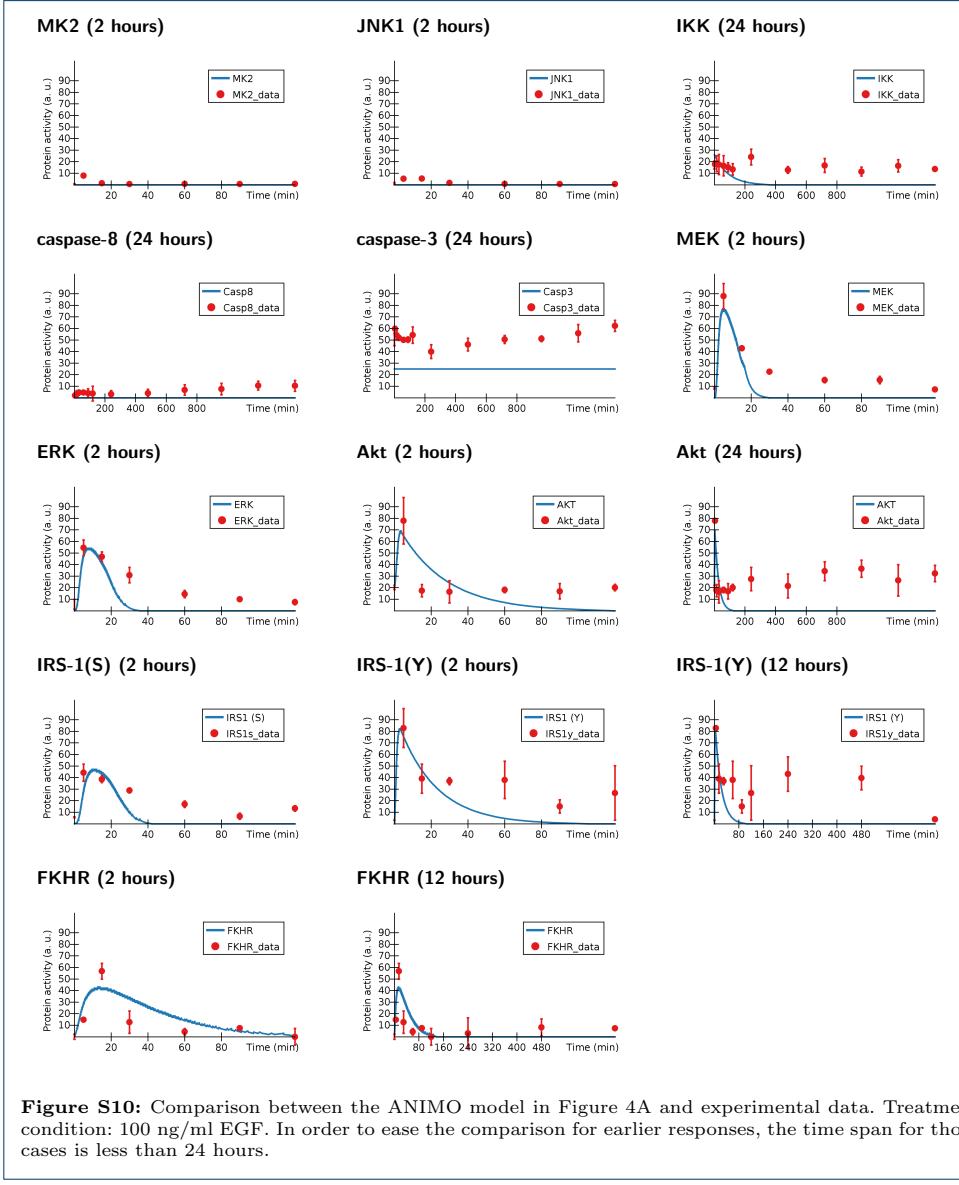


Figure S9: Comparison between the ANIMO model in Figure 4A and experimental data. Treatment condition: 100 ng/ml TNF α . In order to ease the comparison for earlier responses, the time span for those cases is less than 24 hours.



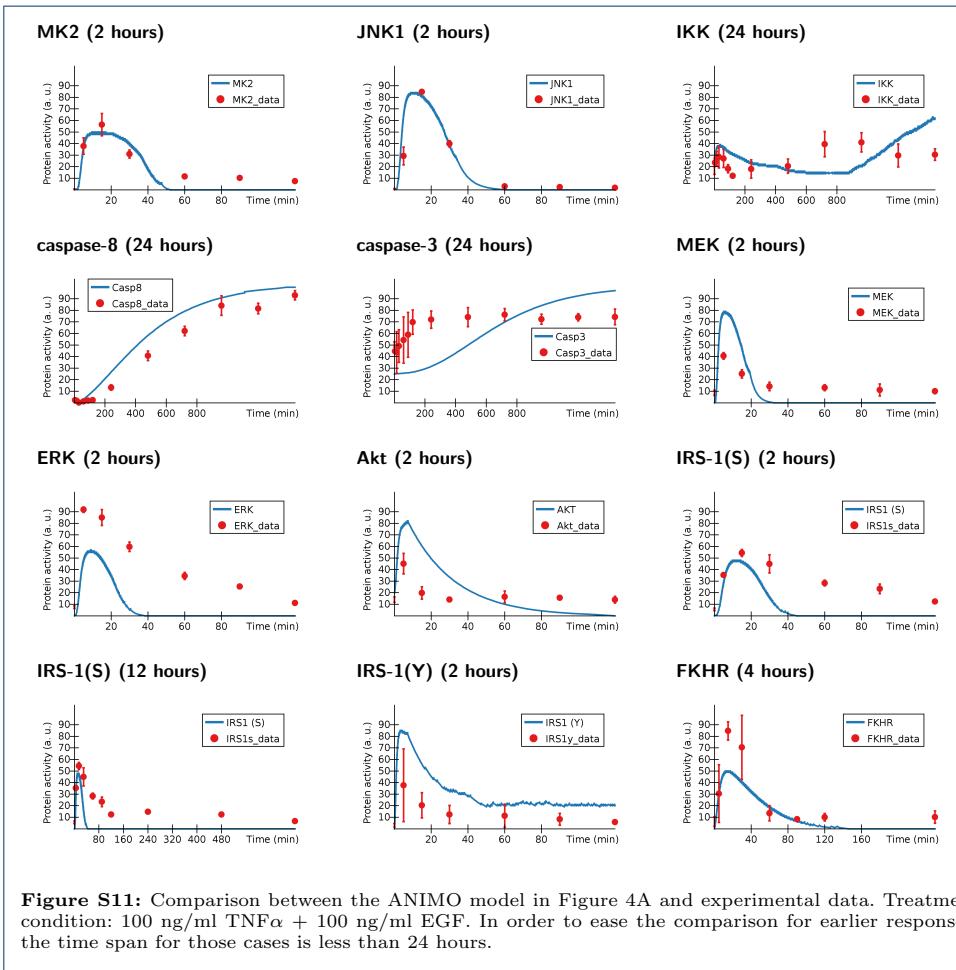


Figure S11: Comparison between the ANIMO model in Figure 4A and experimental data. Treatment condition: 100 ng/ml TNF α + 100 ng/ml EGF. In order to ease the comparison for earlier responses, the time span for those cases is less than 24 hours.