A multi-scale extensive Petri net model of the bacterial–macrophage interaction

Rafael V. Carvalho, Jetty Kleijn, Fons J. Verbeek

Leiden Institute of Advanced Computer Science, Leiden University, Niels Bohrweg 1, 2333 CA Leiden, The Netherlands
{r.carvalho; h.c.m.kleijn; f.j.verbeek}@liacs.leidenuniv.nl

Abstract. ***Mycobacterium tuberculosis*** **is considered one of the most efficient intracellular pathogens responsible for chronic infection, resulting in over 1.3 million of deaths a year. Exploring the host-cell signalling pathways, the bacteria evade host immune responses and enhance the infection inside the macrophage. Understanding how the bacteria interact with the immune system is an important step in the development of new therapies for** ***mycobacterium*** **pathogen. The aim of this paper is to present a prototype draft of a Petri Net model that highlights the interference strategies used by mycobacteria to achieve intracellular survival. The hierarchical model presents an overview of the important host-cell signalling pathways that occur at multiple (molecular, intracellular and intercellular) scales.**

Keywords: mycobacterial infection, host-cell signalling pathways, extended Petri Net, multi-scale modelling

1 Introduction

Tuberculosis (TB) is the second greatest killer disease worldwide due to a single infectious agent: *mycobacterium tuberculosis* (Mtb) [1]. Effective vaccination against tuberculosis is a challenge; a better understanding of the host-pathogen relationship provides an important key for new treatments. The host innate immune response is the first line of defence against invading microbes. It recognises the pathogen in the first stage of infection and initiates an appropriate immune response. Therefore it has been the subject of much scientific research involving mycobacterial infection [2–7] .

The complex interactions between bacteria and the immune cell involve various structures and processes that control, activate and inhibit proteins and signalling pathways in a dynamical system that determines the outcome of an infection [8]. A systematic approach to modelling these interactions should help to comprehend the events that occur between the host and pathogen [9]. Different methods have been used to model the mycobacterial infection process: Gammack *et al*. [10] provided a mathematical model based on Ordinary Differential Equation (ODE) to investigate the early and initial immune response to Mtb. Such work has inspired Segovia-Juarez *et al*. [11] to implement the ODEs that regulate the interaction between host and path-

M. Heiner (Ed.): BioPPN 2014, a satellite event of PETRI NETS 2014,
CEUR Workshop Proceedings Vol. 1159, 2014.

ogen using an agent-based approach, and Warrender *et al*. [9] use the CyCells simulator tool to simulate the interactions in Early *mycobacterium* infection.

Mathematical models, like those based on differential equations, are difficult to obtain and analyse when the number of interdependent variables grows and when the relationship depends on qualitative events. The computational models used for this problem offer an additional avenue for exploring the infection dynamics through the visualization of a specific behaviour simulation. However in both cases the interactions between bacteria and the immune cells and their structures are not intuitively described. The interactions are embedded in programing code and/or described in rules which are not straightforward to interact and comprehend their relationship.

A graphical representation of the interactions and influences among the various molecular and cellular components that involve the bacteria and host immune cells that also captures the dynamics of the system should be very useful. The framework of Petri nets represents a well-established technique in computer science for modelling distributed systems [12] and they have been successfully used to model biological behaviour. Heiner *et al*. [13] propose a methodology of incremental modelling using Petri Nets. They develop and analyse a qualitative model of the apoptotic pathway. In our previous work [14] we have developed a qualitative model of the mycobacterial infection process and the innate immune response. We modelled the cell dynamics level, characterized by the steps that are involved in the *Mycobactrium marinum* infection and granuloma formation in zebrafish.

In this paper, we extend our model and focus on interactions between the bacteria and the host immune cells - specifically the macrophages - in a multi-scale model. We identify and connect the important pathways involved in the host-pathogenic interactions that act over different scales (molecular, intracellular, and intercellular) during the innate immune response. The model captures the quintessential functional processes of the macrophage upon exposure to mycobacteria, their interconnections, subsequent signals and activation of the immune response. It provides a visualization of the signalling pathways that the host immune cell utilizes to terminate the infection as well as the way the pathogen exploits the pathways of the macrophages to enhance its intracellular survival persistence. This Petri net model makes it possible to perform "what-if" situations as part of the experimentation, simulating possible pathway disruptions and the consequences to the infection process. In this paper, we demonstrate the power of the Petri net formalism in modelling signalling and metabolic pathways that are involved in the host-pathogen interaction in a multi-scale model. We apply three different dynamics in the animation mode to mimic the alternatives that might occur once a bacterium is phagocytosed by a macrophage and the persistence of infection. As a next step we plan to consider a qualitative validation of the model so as to confirm consistency and correctness of its biological interpretation.

2 Mycobacteria Interaction With Macrophage

Macrophages play rather contradictory roles in infection and disease as they are likely the first host immune cells to respond to invading mycobacteria, and yet aid in subse-

quent dissemination of the bacteria [15]. The successful parasitation of macrophages by mycobacteria involves the inhibition of several host-cell processes, which allows the bacteria to survive inside the host cells. The host processes that are inhibited by the pathogenic bacteria include fusion of *Phagosomes* with *Lysosomes*, antigen presentation, apoptosis and the stimulation of bactericidal response [16].

Mycobacterial cells release a mixture of lipids and glycolipids that interfere on the macrophage response towards elimination and enabling bacterial survival [17]. Mannosylated Lipoarabinomannam (ManLAM) is one of the major modulators of phagosome maturation [18]. It prevents fusion of mycobacterial phagosome with the late endosome and lysosome by inhibiting the Calmoduling-Ca^{2+} phosphotidol-inositol-3 kinase [19]. Ca^{2+} also has influence in the apoptotic pathways since it increases the permeability of mitochondrial membranes releasing pro-apoptotic elements to facilitate apoptosis [16]. ManLAM also influences the apoptosis by phosphorylating the apoptotic protein Bad leaving the anti-apoptotic protein Bcl-2 free which inhibits caspase activity and functions as an anti-apoptotic regulator [20].

Macrophages and T cells produce many cytokines that promote or inhibit protective response to the mycobacterial infection. An important family of cytokines are the interleukin-10 (IL-10) that regulates the pro-inflammatory (PICs) and anti-inflammatory (AICs) cytokines. The bacteria can limit macrophage apoptosis by inducing the production of IL-10 which blocks the synthesis of Tumor-Necrosis Factor (TNF), a stimulator of apoptosis in infected macrophage [21, 22]. It is likely that bacteria prevent apoptosis in the early phase of infection to allow them to replicate efficiently. However, they induce or are unable to prevent cell death in the later phase, which might facilitate their systemic dissemination through uptake into immune cells [16].

2.1 Cell-cell Host Pathogen Interaction

The modulation of host signalling mechanism is a dynamic process requiring mycobacterial components that trigger or inhibit the host response such as the fusion of Phagosomes with Lysosomes, antigen presentation, apoptosis and stimulation of bactericidal responses due to the activation of pathways that leads to the bacterial survival. The immune cells can identify the pathogen through Pattern Recognition Receptors (PRRs), which are found on the cell surface, on the endosomes and on cytoplasm. It triggers a cascade of events that leads to proinflammatory and antimicrobial response through the phagosome maturation pathway. Van der Vaart *et al.* reviewed the PRRs that identify invading microbes, as well as the innate immune effector mechanisms that they activate in zebrafish embryos [23]. The maturation of the phasosome forms the late-phagosome which fuses with the lysosome forming the phagolysosome which can digest the pathogen and leads to the bacterial death [24–26]. The mycobacteria are using several strategies to avoid the maturation of the phagosome and the key contributor is mannosylated lipoarabinomannan (ManLAM), a glycolipid of the mycobacteria cell wall. ManLAM is involved in the inhibition the phagosome maturation by inhibition of calcium (Ca^{2+}) concentration rise in macrophage and also the

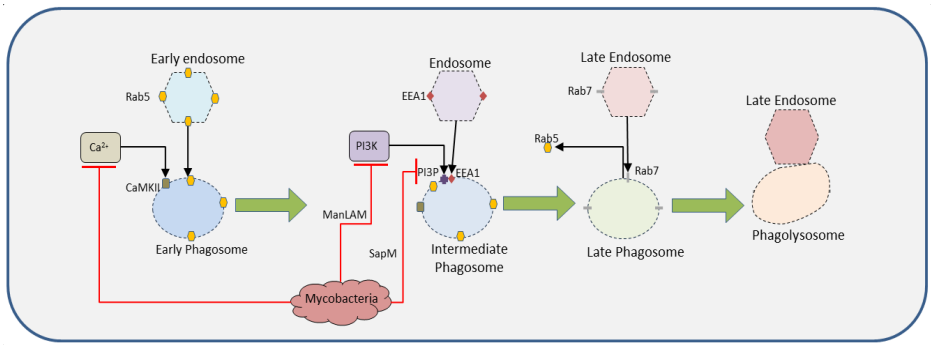

Fig. 1: Schematic overview of the phagosomal maturation pathway blocked by pathogenic mycobacteria according to Koul et al. [16]**. Nascent phagosome acquires Rab5 recruiting PI3K which generate PI3P. Pathogenic mycobacteria block the rise in cellular Ca^{2+}, recruitment of PI3K to the phagosomes and degrading PI3P through Sap-M**

Calmoduling-Ca^{2+} phosphotidol-inositol-3 kinase (PI3K) which is responsible to lead the maturation of the phagosome and drives the fusion with the lysosome [19, 27, 28]. To accomplish complete arrest and prevent the phagosome maturation, a second mycobacterial macromolecule, SapM, is released degrading the existing Phosphatidylinositol 3-phosphate (PI3P), a phospholipid found in the cell membrane involved on the phagosomal maturation [29]. A schematic representation of the phagosomal maturation arresting by the pathogenic mycobacteria is given in **Fig. 1**.

When the immune cell is not able to kill the bacteria through the phagolysosome, the macrophage activates the apoptosis thereby programming its own death and signalling to others defences mechanisms. Once the maturation fails, the apoptotic programme is mainly activated by the extrinsic apoptosis pathway, which is initiated by binding of ligands to death receptors; and the intrinsic pathway, which involves translocation of cytochrome-C from mitochondria to the cytosol. The activation of the caspase cascade and degradation of genomic DNA are characteristics of apoptotic cell death [16]. Mycobacteria alter host apoptotic pathways interfering on the intrinsic death pathway preventing the increasing in cytosolic Ca^{2+} concentration and also inhibit caspase activity and functions by stimulating the phosphorylation of the apoptotic protein Bad [28, 30]. It also limits macrophage apoptosis by inducing the production of cytokines such as interleukin-10 (IL-10) which interferes in one of the apoptosis stimulators of the macrophage in the extrinsic apoptosis pathway, the tumour-necrosis factor-α (TNF- α) [22, 31]. Mycobacteria take advantage of blocking these defence mechanisms of macrophages, phagocytosis and apoptosis, to proliferate inside the cell till a necrosis breakdown and dissemination of infection through the others immune cells that aggregate at that particular infected macrophage to take over the infection. The apoptotic pathway is depicted in **Fig. 2**.

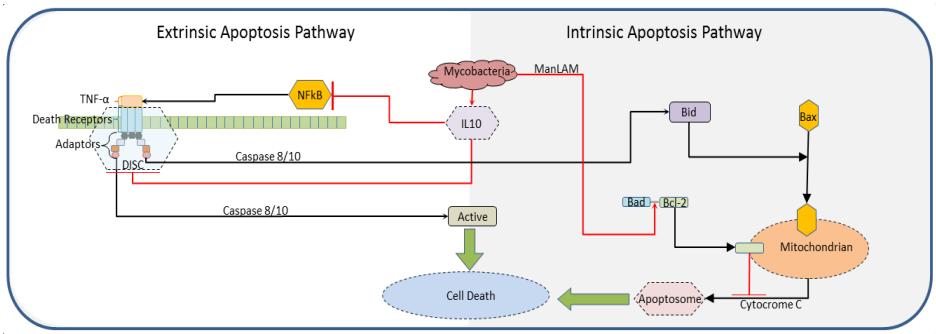

Fig. 2: Apoptotic pathway inhibition by pathogenic mycobacteria according to Koul et al. [16]**. Pathogen mycobacteria interfere in intrinsic apoptotic pathway suppressing Ca^{2+} and releasing Bcl-2. In the extrinsic apoptotic pathway it inhibits binding ligands and DISC formation.**

2.2 Molecular Host Pathogen Interaction

At the molecular level the most important interactions occur in the phagosomal maturation pathway and also in the apoptosis pathway. In both cases, the mycobacteria interfere in different ways to guarantee their survival and proliferation. Ca^{2+} is a key messenger that is released from intracellular storage; an increase in cytosolic Ca^{2+} concentration promotes the phagosomal maturation process by regulating calmodulin and the multifunctional serine/threonine protein kinase CaMKII [28]. CaMKII is important to PI3K activation and recruitment of early endosomal antigen 1 (EEA1) to the phagosomal membrane that is extremely important in the process of phagosomal maturation. PI3K is also essential for the production of the lipid regulator phosphatidylinositol 3-phosphate (PI3P) which form a ligand together with EEA1 leading to an intermediate phagosome which maturates to the late the endosome after EEA1 dissociation and acidic expression due to accumulation of the proton-ATPase [32, 33]. Through releasing ManLAM, the mycobacteria inhibit the rise of the Ca^{2+} concentration in macrophages and also the PI3K activation, preventing the generation of PI3P degrading the existing PI3P by the action of SapM.

Despite the fact that phagosomes fail to fuse with the lysosomes to degrade the bacteria, pathogen-derived material is released in the host cell lysosomes and the cell surface of the infected macrophage which can induce the apoptosis process [34]. Mycobacteria influence the host apoptosis through several mechanisms that interfere in the intrinsic and extrinsic apoptosis pathways. The cytosolic Ca^{2+} facilitates apoptosis by increasing the permeability of mitochondrial membranes that promote the release of pro-apoptotic elements such as cytochrome-C. In the cytosol, cytochrome-C associates with procaspase-9 and apoptosis protease forming a signaling complex called the apoptome which activates the induction of apoptosis [35]. ManLAM interfere in the intrinsic apoptosis pathway not only inhibiting the concentration of Ca^{2+} but also stimulating the phosphorylation of the apoptotic protein Bad that leave BCL-2 free that also prevents the release of cytochrome c.

The extrinsic apoptosis pathway is induced by Toll-like receptors (TLRs) who identify the virulence mycobacterial pathogen and trigger the synthesis of tumor-necrosis factor-α (TNF-α) - a stimulator of apoptosis – trough the TLR signaling pathway. To do so, an important adaptor factor protein, the Myleoid differentiation factor 88 (MYD88) recruits a family of kinases (IRAK) that will form "myddosome" signaling complex that activate nuclear factor kB (NF-kB) to transcript target gene to synthesize TNF-α. The tumor necrosis factor binds with death receptors leading to a cascade of events that will release caspase 8 and 10 and the formation of a death-inducing signal complex (DISC) resulting on the formation of apoptotic vesicles [35, 36]. Pathogen mycobacteria interfere in this process by inducing the production of immunosuppressive cytokine interleukin-10 (IL-10), which inhibit the phosphorylation of NF-kB, therefore the synthesis of TNF-α. It also inhibits the DISC formation and the extrinsic apoptotic pathway failure.

3 Petri Net Model of the Bacterium–Macrophage Interaction

We construct a Petri Net model of the process triggered in the macrophage in response to mycobacterial infection, based on an extensive literature survey and extending our previous model [14]. The model captures the interactions between the immune cell and the pathogen once a bacterium is phagocyte. The model is hierarchical and has three different levels of representations to mimic the signal processing that activates/inhibits the pathways related to the macrophage response to the bacteria. The first level models the overall actions from the system started after the phagocytosis and it represents the cell-cell interaction between the macrophage and the bacteria. The second level representing the intracellular interaction models two important signalling pathways: the Phagosome Maturation which is responsible for the degradation of the infection through antimicrobial components; and the Apoptotic Pathway which is the macrophage mechanism responsible to resolve the infection in response to virulence factors. It represents an alternative way to the phagolysosome. The third level represents the molecule-molecule interactions that occur on the Phagosome Maturation and Apoptotic pathways.

To model the host-pathogen interaction we use an Extended Petri Net implemented in the Snoopy tool [37] with a maximal concurrency semantics. All formal definitions can be found in [38]. The pathways described in section 2 represent a complex process involving various host-bacterial factors in a heavy cross-talk interaction. To get a consistent view of the entire interaction process, we express the most important reactions simplifying the pathways at different levels of abstraction. We define each biochemical compound or receptor as a place. The relations between biochemical substances are represented basically by transitions with corresponding arcs modeling biochemical reactions, inhibitions/degradations (using inhibitor arcs) or signaling/catalytic atomic events (using read arcs). To hierarchically connect the subnets we use coarse transitions and coarse places structuring all the levels as a tree as shown in **Fig. 3**. The top level (the root) models an overall view of the system starting by interactions that occur in the cellular wall and its consequences. It is connected to the sub-

nets (mid-level) through coarse transitions which link to the molecular level modeled in coarse places (the leaves of the tree).

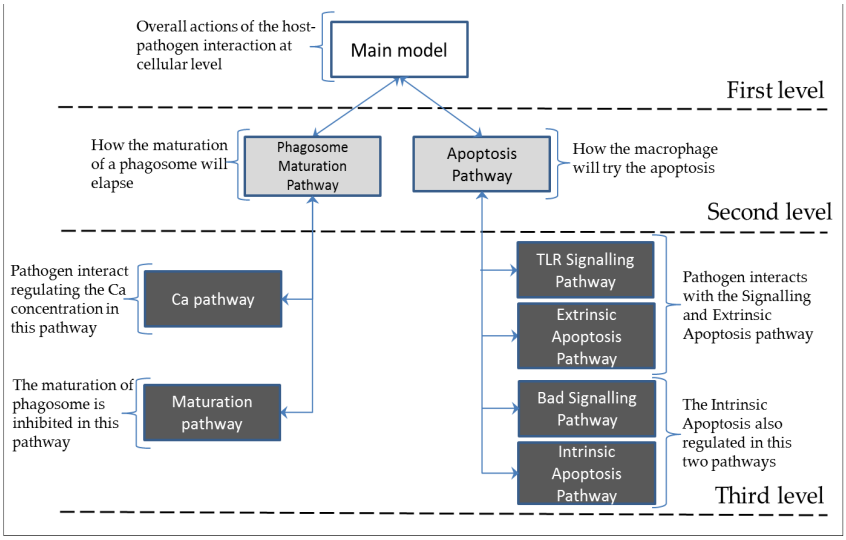

Fig. 3: Hierarchical structure of the net. The three levels are implemented in independent interconnected subnets

3.1 Model Definition

We start the modeling with the interaction between the bacteria inside the macrophage once it is in the host. The first level of our Petri net model is given in **Fig. 4**. The input place ***Infected_macrophage*** represents this situation. The sequence of interaction events happens once there is a bacterium infecting the macrophage (a token is present at the input place) detected by three reading arcs to trigger the interactions. The macrophage uses the PRRs to detect the presence of the pathogen and starts the phagosome maturation process, the bacteria starts its protein secretion system and counter attack by releasing SapM to degrade existing PI3P in the cytosol and ManLAM to interfere in the maturation of the phagosome which is modeled in a lower level by the coarse transition ***Phagosome_Maturation_Pathway***; and in the apoptosis process which is modeled in a lower level in the coarse transition ***Apoptosis_Pathway***. The presence of ManLAM triggers the macrophage production of the cytokine IL10 and also interferes in both pathways. ***Phagosome_Maturation_Pathway*** interacts with ***Apoptosis_Pathway*** releasing calcium and bactericidal material that was not degraded by the maturation.

In our model there are three different scenarios: The phagosome maturation occurs in the ***Phagosome_Maturation_Pathway*** leading to a late phagosome that will fuse with lysosome digesting the bacteria and turning the macrophage healthy. The second scenario can occur if the maturation fails but the apoptosis process in the ***Apopto-***

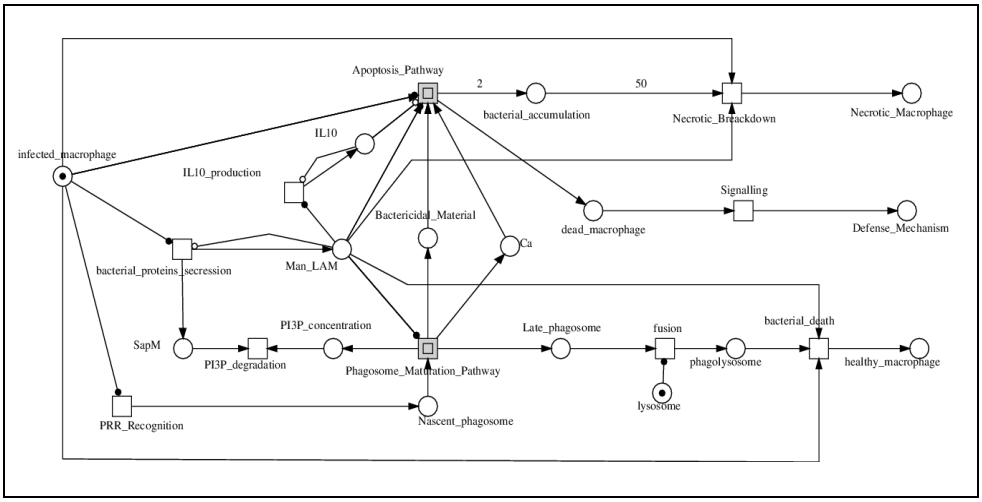

Fig. 4: Petri Net of host-pathogen interaction at the top (root) level. The coarse transitions: *Phagosome_Maturation_Pathway* and the *Apoptosis_Pathway* contain the second level of the model and are represented here by a double square.

sis_Pathway, leading to a dead macrophage, which will signal for another defense mechanism. The third scenario occurs when both pathways are failing at the molecular level, in that case the bacteria proliferate and accumulate in the macrophage till a necrosis breakdown, releasing all the pathogenic material to the surrounding cells. To represent the proliferation and accumulation of bacteria, we use weighted arcs that double the amount of bacteria (accumulated in the place: ***Bacterial_accumulation***). The breakdown of the macrophage occurs when it reaches a threshold of 50 bacteria (a weighted arc fires the transition ***Necrotic_breackdown***). Here we should note that the weighted arcs (with weights 2 and 50) are examples to express the idea of bacterial proliferation.

Following the hierarchical tree, we have at the second level: ***Phagosome_Maturation_Pathway*** and ***Apoptosis_Pathway***, two subnets which basically connect the cellular interaction (top level) with the molecular interactions at the biochemical pathways implemented in the coarse places (the leaves of the tree). **Fig. 5** depicts these subnets. At this level we have the signaling started in the cell wall (top level) that will trigger the production/interaction between molecules. For example the production/releasing of calcium is triggered by the PRRs and this process occur at ***Ca_pathway***; the PIP3 concentration and bactericidal material that are not degraded at the ***maturation_pathway*** and interact with the top level. We also have the interaction between the cytokine IL10 from the top level with the pro-inflammatory cytokines that will interfere in the TNF-α in the ***Extrinsic_Apopthosis_Pathway*** and ManLAM interfering in the BCL2 activation, which will act in the ***Intrinsic_Apopthosis_Pathway***.

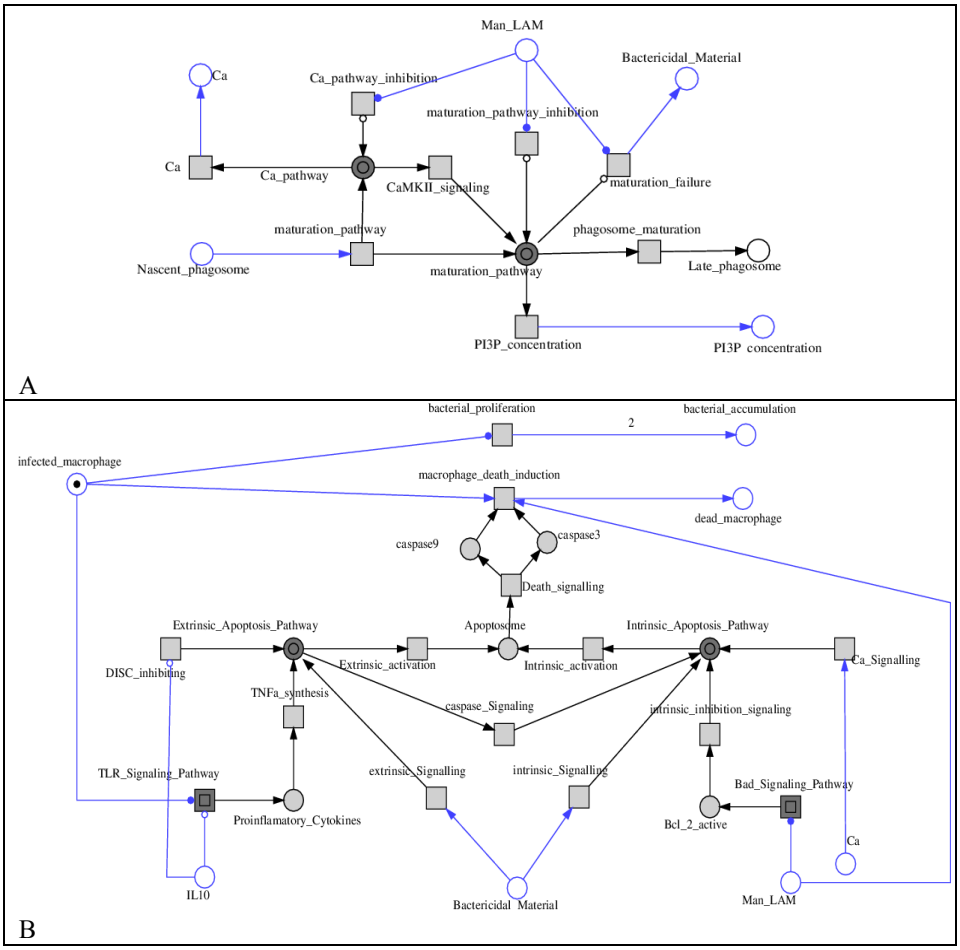

Fig. 5: Second level. A) The *Maturation_Pathway* Subnet which connects the cellular level with the molecular interactions in the production of calcium (*Ca_pathway*) and phagosomal maturation (*Maturation_pathway*) implemented in another subnet level (coarse places). B) *Apoptosis_Pathway* Subnet which connects the cellular level with the molecular interactions in the pro inflammatory cytokines, Bcl2 activation and their influences in the extrinsic and intrinsic apoptosis pathway.

At the lower level of the hierarchical model, we have six related but independent subnets. They represent the important molecular pathways responsible for: the production of calcium/CMKII in ***ca_pathway*** and phagosome maturation and PI3P concentration in ***maturation_pathway,*** both implemented in coarse places; activation of pro-inflammatory cytokines in ***TLR_Signaling_Pathway*** and Bcl2 activation in ***Bad_Signalling_Pathway***, both implemented in coarse transitions; and also the interactions that occur in the intrinsic and extrinsic apoptosis pathways implemented in the

coarse places ***Extrinsic_Apopthosis_Pathway*** and ***Intrinsic_Apopthosis_Pathway*** respecivly. **Fig. 6** depicts all subnets in the leaves of the proposed hierarchical model.

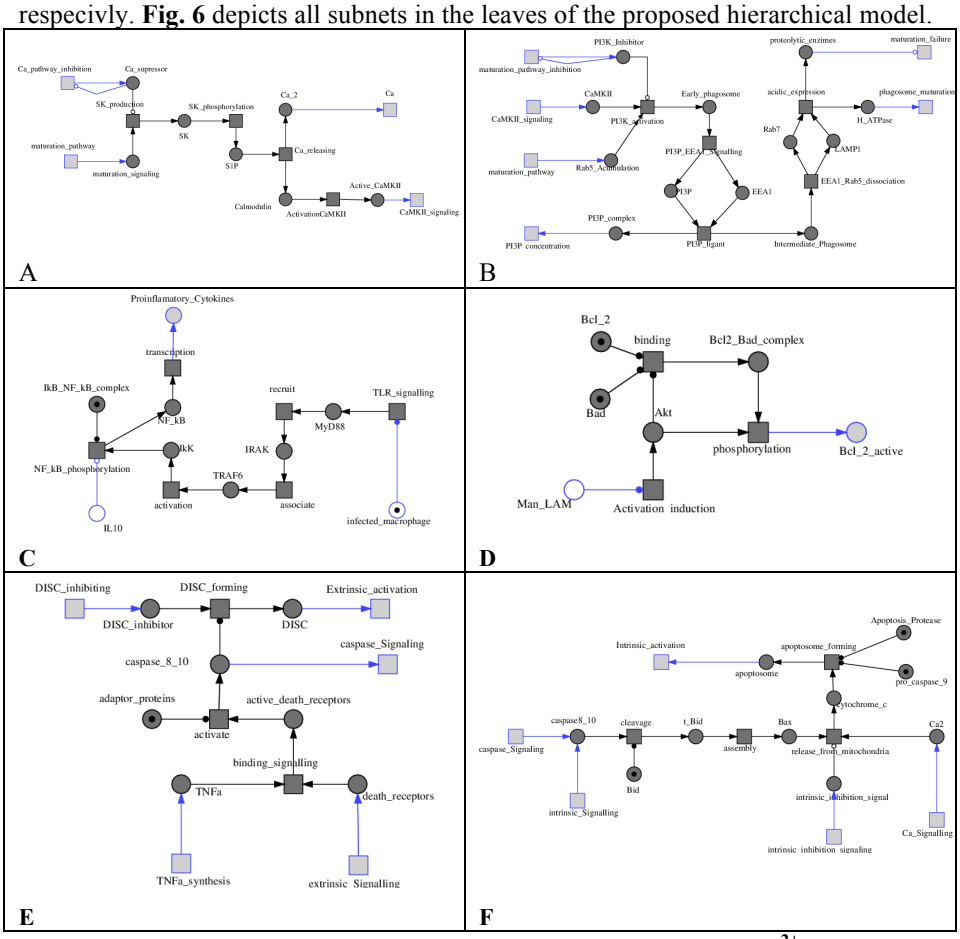

Fig. 6: Subnets that implement the molecular pathway interaction. A) Ca^{2+} and CaMKII production/inhibition model. B) Phagosome maturation pathway (activation and inhibition) and PI3P concentration model. C) TLR signalling and pro-inflammatory cytokines activation/inhibition model. D) Bad/BCL2 complex phosphorylation model. E) Extrinsic apoptosis pathway model. F) Intrinsic apoptosis pathway model

3.2 Animation and Validation

Animation and validation are important tools to provide a consistent model of biological behavior. They allow experimenting with different situations and possibilities of the model as well as checking for integrity and correspondence to the real world. Simulation and analysis for qualitative and quantitative behavior prediction are other steps necessary to certify a useful model. For the model presented here we also performed some animation and validation. For this we employed the Animation mode

available in the Snoopy software. This feature allows animating the token flow of the net through all the subnets, visualizing the causality of the model and its behavior. Three different animations for the scenarios, previously discussed, were performed to experience the events that can occur in the model. For inspection and perusal, the animations can be found at http://bio-imaging.liacs.nl/galleries/epn-infection/.

To validate the model, it is necessary to define validation criteria for a consistency check. To do so, we have to consider that our model is based on a heuristic procedure of collecting information from the literature, perhaps with different interpretations, modeled from the process perspective (top level) down to the molecule perspective (leaves). We built a large model composed of sub-models and to provide a complete analysis, it is necessary to verify each component individually and the system as a whole, which increases the complexity of the validation even with computational support. Basic qualitative behavior properties can be checked using the Charlie analyzer tool [39]. Heiner *et al.* have used as example, p-invariants and t-invariants to analyze case studies in biochemical pathways in [40]. We started to analyze the structural and behavior properties of our model based on results from the Charlie tool which should then be biological meaningful. As a first result, we found that our model is not structurally bounded and not reversible. This implies that indeed the net allows for the proliferation of the bacteria and the infection process is not reversible.

4 Conclusion

In mycobacterial infection, the dynamics of the interactions between the host and bacteria forms a complex system involving numerous activations, inhibitory and control structures that determine the outcome of the infection. A systems approach is essential to comprehend the significance of the multiple events that occur simultaneously among the various molecular and cellular components of the host and pathogen.

Here, we seek to model the interaction of the macrophage upon exposure to pathogen mycobacteria, capturing important functional process and their interconnections including signaling and activation/inhibition of the immune responses on different levels of abstraction. The Petri net formalism has proved to be a useful modeling approach to describe and interconnect different abstract levels into a large and extensive model [13, 41] In our previous work [14] we have developed a Colored Petri net model to explore the early mycobacterial infection and the immune response, modeling the steps that regulates the infection process. In this paper we focus on the lower-scale processes occurring in the cell and descend to molecular interactions relevant to the infection process. Therefore we use an Extended Petri net for the different pathways in subnets, interconnecting them in a hierarchical structured model. The model provides a visualization of the processes occurring at multiple scales using levels that can be operated independently. It also describes the interconnections and signals that influence the host pathogen interaction.

This results in an Extended Petri net model implementation in the Snoopy tool [37]. The model expresses, at different levels of abstraction, the details that are involved in the macrophage-mycobacterium interaction. Information about the proteins

released by the bacteria, their interference in the immune response and the pathways involved in this process are observed in our model. It is possible to visualize the dynamics of the molecular and cellular interaction as well as analyze different scenarios performing "what-if" simulation as part of the experimentation in the animation mode. The model represents the information about host-pathogen interaction available in the literature but the scalability of our model allows extension to a more complete system.

As part of the modelling process, we started to use the Charlie analyzer [39] to check properties of the model and its consistency. As a next step, an extensive analysis of more structural and behavior properties is necessary to validate the model. We also intend to extend to a quantitative model where, with support of experimental data rather than the examples we used until now, we can use analysis techniques for a prediction of qualitative as well as quantitative behavior. This can contribute, for example, in the prediction of results from new experiments and generation of further hypotheses about the innate immune system response to mycobacterial infection. Another challenge is to combine the models implemented in different classes of Petri nets in one system. One solution is to adapt each model in a Hybrid Petri Net, or abstract the models in a Nets-within-Nets approach where the communication of the tokens occurs via predefined interfaces which are dynamically bounded [42].

In summary we have presented in this paper a model that explores the interaction between mycobacterial pathogen and macrophage, modeling the dynamics in three different level of abstraction while interconnecting them in a hierarchical structure. We have checked the structural behavior of our model through an analysis tool. The interplay of hierarchical levels and qualitative/quantitative information has the potential to develop a powerful tool for the research in tuberculosis disease.

5 Acknowledgement

We are grateful to the anonymous reviewers for their constructive criticism which helped us to improve the presentation of this work in progress. This work was partially supported by Erasmus mundus and CNPq.

6 References

1. WHO Report, http://www.who.int/tb/publications/global_report/en/ (2012).
2. Davis, J.M., Clay, H., Lewis, J.L., Ghori, N., Herbomel, P., Ramakrishnan, L.: Real-time visualization of mycobacterium-macrophage interactions leading to initiation of granuloma formation in zebrafish embryos. Immunity. 17, 693–702 (2002).
3. Clay, H., Davis, J.M., Beery, D., Huttenlocher, A., Lyons, S.E., Ramakrishnan, L.: Dichotomous role of the macrophage in early Mycobacterium marinum infection of the zebrafish. Cell Host Microbe. 2, 29–39 (2007).

4. Lesley, R., Ramakrishnan, L.: Insights into early mycobacterial pathogenesis from the zebrafish. Curr. Opin. Microbiol. 11, 277–83 (2008).

5. Stein, C.: Innate immune genes in the zebrafish, Danio rerio. PhD Thesis. Mathematisch-Naturwissenschaftliche Fakultät, Universität zu Köln. Germany. http://kups.ub.uni-koeln.de/volltexte/2011/3308/, (2011).

6. Lalvani, A., Behr, M. a, Sridhar, S.: Innate immunity to TB: a druggable balancing act. Cell. 148, 389–91 (2012).

7. Stanley, S. a, Cox, J.S.: Host-pathogen interactions during Mycobacterium tuberculosis infections. Curr. Top. Microbiol. Immunol. 374, 211–41 (2013).

8. Casadevall, A., Pirofski, L.: Host-pathogen interactions: the attributes of virulence. Journal of Infection Disease. 184, 337–44 (2001).

9. Warrender, C., Forrest, S., Koster, F.: Modeling intercellular interactions in early Mycobacterium infection. Bull. Math. Biol. 68, 2233–61 (2006).

10. Gammack, D., Doering, C.R., Kirschner, D.E.: Macrophage response to Mycobacterium tuberculosis infection. J. Math. Biol. 48, 218–42 (2004).

11. Segovia-Juarez, J.L., Ganguli, S., Kirschner, D.: Identifying control mechanisms of granuloma formation during M. tuberculosis infection using an agent-based model. J. Theor. Biol. 231, 357–76 (2004).

12. Desel, J., Reisig, W., Rozenberg, G.: Lectures on Concurrency and Petri Nets. Springer Berlin Heidelberg, Berlin, Heidelberg (2004).

13. Heiner, M., Koch, I., Will, J.: Model validation of biological pathways using Petri nets--demonstrated for apoptosis. Biosystems. 75, 15–28 (2004).

14. Carvalho, R. V., Kleijn, J., Meijer, A.H., Verbeek, F.J.: Modeling innate immune response to early mycobacterium infection. Comput. Math. Methods Med. 790482 (2012).

15. Flynn, J.L., Chan, J.: What's good for the host is good for the bug. Trends Microbiol. 13, 98–102 (2005).

16. Koul, A., Herget, T., Klebl, B., Ullrich, A.: Interplay between mycobacteria and host signalling pathways. Nat. Rev. Microbiol. 2, 189–202 (2004).

17. Rosenberger, C.M., Finlay, B.B.: Phagocyte sabotage: disruption of macrophage signalling by bacterial pathogens. Nat. Rev. Mol. Cell Biol. 4, 385–96 (2003).

18. Stoop, E.J.M., Mishra, A.K., Driessen, N.N., van Stempvoort, G., Bouchier, P., Verboom, T., van Leeuwen, L.M., Sparrius, M., Raadsen, S.A., van Zon, M., van der Wel, N.N., Besra, G.S., Geurtsen, J., Bitter, W., Appelmelk, B.J., van der Sar, A.M.: Mannan core branching of lipo(arabino)mannan is required for mycobacterial virulence in the context of innate immunity. Cell. Microbiol. (2013).

19. Fratti, R.A., Chua, J., Vergne, I., Deretic, V.: Mycobacterium tuberculosis glycosylated phosphatidylinositol causes phagosome maturation arrest. Proc. Natl. Acad. Sci. U. S. A. 100, 5437–42 (2003).

20. Abarca-Rojano, E., Rosas-Medina, P., Zamudio-Cortéz, P., Mondragón-Flores, R., Sánchez-García, F.J.: Mycobacterium tuberculosis virulence correlates with mitochondrial cytochrome c release in infected macrophages. Scand. J. Immunol. 58, 419–27 (2003).

21. Schluger, N.W., Rom, W.N.: The host immune response to tuberculosis. Am. J. Respir. Crit. Care Med. 157, 679–91 (1998).

22. Moore, K.W., de Waal Malefyt, R., Coffman, R.L., O'Garra, A.: Interleukin-10 and the interleukin-10 receptor. Annu. Rev. Immunol. 19, 683–765 (2001).

23. Van der Vaart, M., Spaink, H.P., Meijer, A.H.: Pathogen Recognition and Activation of the Innate Immune Response in Zebrafish. Advances in hematology. 159807. (2012).

24. Rohde, K., Yates, R.M., Purdy, G.E., Russell, D.G.: Mycobacterium tuberculosis and the environment within the phagosome. Immunol. Rev. 219, 37–54 (2007).

25. Bouley, D.M., Ghori, N., Mercer, K.L., Falkow, S., Ramakrishnan, L.: Dynamic nature of host-pathogen interactions in Mycobacterium marinum granulomas. Infect. Immun. 69, 7820–31 (2001).

26. Booth, J.W., Trimble, W.S., Grinstein, S.: Membrane dynamics in phagocytosis. Semin. Immunol. 13, 357–64 (2001).

27. Vergne, I., Chua, J., Deretic, V.: Tuberculosis toxin blocking phagosome maturation inhibits a novel Ca2+/calmodulin-PI3K hVPS34 cascade. J. Exp. Med. 198, 653–9 (2003).

28. Malik, Z.A., Denning, G.M., Kusner, D.J.: Inhibition of Ca2+ Signaling by Mycobacterium tuberculosisIs Associated with Reduced Phagosome-Lysosome Fusion and Increased Survival within Human Macrophages. J. Exp. Med. 191, 287–302 (2000).

29. Puri, R.V., Reddy, P.V., Tyagi, A.K.: Secreted Acid Phosphatase (SapM) of Mycobacterium tuberculosis Is Indispensable for Arresting Phagosomal Maturation and Growth of the Pathogen in Guinea Pig Tissues. PLoS One. 8, e70514 (2013).

30. Rojas, M., García, L.F., Nigou, J., Puzo, G., Olivier, M.: Mannosylated lipoarabinomannan antagonizes Mycobacterium tuberculosis-induced macrophage apoptosis by altering Ca+2-dependent cell signaling. J. Infect. Dis. 182, 240–51 (2000).

31. Clay, H., Volkman, H.E., Ramakrishnan, L.: Tumor necrosis factor signaling mediates resistance to mycobacteria by inhibiting bacterial growth and macrophage death. Immunity. 29, 283–94 (2008).

32. Fratti, R.A., Backer, J.M., Gruenberg, J., Corvera, S., Deretic, V.: Role of phosphatidylinositol 3-kinase and Rab5 effectors in phagosomal biogenesis and mycobacterial phagosome maturation arrest. J. Cell Biol. 154, 631–44 (2001).

33. Sundaramurthy, V., Pieters, J.: Interactions of pathogenic mycobacteria with host macrophages. Microbes Infect. 9, 1671–9 (2007).

34. Russell, D.G., Mwandumba, H.C., Rhoades, E.E.: Mycobacterium and the coat of many lipids. J. Cell Biol. 158, 421–6 (2002).

35. Lee, J., Hartman, M., Kornfeld, H.: Macrophage apoptosis in tuberculosis. Yonsei Med. J. 50, 1–11 (2009).

36. KEGG PATHWAY: Tuberculosis - Mycobacterium marinum M, http://www.genome.jp/kegg-bin/show_pathway?mmi05152 (2013).

37. Heiner, M., Herajy, M., Liu, F., Rohr, C., Schwarick, M.: Snoopy – A Unifying Petri Net Tool. Petri Nets 2012. pp. 398–407. Springer, LNCS, Hamburg (2012).

38. Blätke, M., Heiner, M., Marwan, W.: Tutorial Petri Nets in Systems Biology. Technical Report, Otto-von-Guericke University, Magdeburg. (2011).

39. Wegener, J., Schwarick, M., Heiner, M.: A plugin system for Charlie. Proc. CS&P. 531–554 (2011).

40. Heiner, M., Koch, I.: Petri net based model validation in systems biology. Applications and Theory of Petri Nets 2004. pp. 216–237. Springer (2004).

41. Marwan, W., Rohr, C., Heiner, M.: Petri nets in Snoopy: A unifying framework for the graphical display, computational modelling, and simulation of bacterial regulatory networks. Bact. Mol. Networks. 1–31 (2012).

42. Heitmann, F., Köhler-Bußmeier, M.: P-and T-Systems in the Nets-within-Nets-Formalism. Appl. Theory Petri Nets. 368–387 (2012).