Control Flow Analysis for Brane Calculi

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Abstract

We introduce a Control Flow Analysis for Brane Calculi. This verification technique allows properties regarding the behaviour of biological systems to be checked. This is an approximate technique that focusses on the static specification of a system, rather than on its dynamics, striving for effectiveness. Examples illustrate the approach.

Keywords: Brane calculi, control flow analysis, systems biology

1 Introduction

Systems biology gives computer scientists the opportunity of providing models and formalisms for describing and analysing complex biological systems. In this regard, well established and founded theories and techniques from formal methods offer a fertile ground.

The underlying idea is that a biological system can be abstractly modelled as a concurrent system [18]. Several approaches – developed to predict the dynamic behaviour of the modelled systems – have introduced the idea of performing in silico experiments to establish which in vitro experiments are more promising.

The behaviour of a system is usually given in terms of its transition system, whose size can be huge, making its exploration computationally hard. Resorting to static techniques offers the possibility of drastically reducing the computational costs, particular high when modelling complex biological systems. The specification of the system is statically analysed in order to obtain information on the dynamic behaviour and to check the related dynamic properties, without actually exploring the whole state space of the associated transition system. The price to be paid is a loss in precision, because usually these techniques can only approximate the actual...
behaviour. Static analysis can be exploited for a sort of preliminary screening of the in silico experiments by efficiently testing different hypothesis and rapidly identifying which in vitro experiments worth to be performed. We first introduce a Control Flow Analysis for the version of Brane Calculi [6,7], called MBD and based on the operations for membrane fusion and splitting. Afterwards, we extend the framework, in order to include also the PEP actions that represent the operations modeling endocytosis and exocytosis. The analysis offers predictions on the contents of membranes: which membranes can be contained in the analysed one and which actions can affect it. This information offers a basis for studying dynamic properties, by suitably handling the over-approximation the static analysis introduces. Having a safe over-approximation of the exact behaviour of a system means that all the valid behaviour are captured. More precisely, all those events that the prediction does not include will never happen, while when included, the events can happen, i.e. they are only possible.

We apply our analysis to two simple examples: (1) a model of the infection due to membrane enveloped viruses, recalling in particular the Semliki Forest Virus [6] and (2) a model of communication via mobile vesicles [19].

The paper follows the tradition initiated by [12,13] and continued with [15,16,3] of applying static techniques and, in particular, Control Flow Analysis to process calculi used for modelling biological phenomena. Our choice of the Brane calculi depends on the fact they have resulted to be particularly useful for modelling and reasoning about a large class of biological systems, such as the one of the eukaryotic cells that, differently from the prokaryiotes, possess a set of internal membranes. Other applications of static analysis techniques have been proposed, like the Abstract Interpretation for BioAmbient in [10]. In a different context, the behaviour of processes is safely approximated and the properties of a fragment of Computation Tree Logic preserved. This makes it possible to address temporal properties and therefore some kinds of causality.

Among the first formalisms used to investigate biological membranes there are the P Systems [14], introduces by Păun, which formalize distributed parallel computations biologically-inspired: a biological system is seen as a complex hierarchical structure of nested membranes inspired by the structure of living cells.

Finally, besides Brane, there are other calculi of interest for our approach, that have been specifically defined for modelling biological structures such as compartments and membranes, e.g. κ-calculus [9], Beta Binders [17] and the Calculus of Looping Sequences [2].

The rest of the paper is organised as follows. In Section 2 we present the MBD version of Brane Calculi. We introduce the Control Flow Analysis in Section 3. In Section 4 the analysis is extended in order to also treat the PEP actions. In Section 5 the new analysis is applied to a model of infective cycle of the Semliki Forest Virus and to a model of communication via a mobile vesicle. Section 6 presents some concluding remarks. Proofs of theorems and lemmata presented throughout the paper are collected in Appendix A.
2 The Calculus

Syntax

The basic structure of Brane Calculi [6] consists of two commutative monoids plus a replication operator, where $\circ$ is used for system composition, with unit $\diamond$, and $|$ is used for membrane composition, with unit $0$. Replication $!$ is used to represent the composition of an unbounded number of instances. We focus here on the version of the calculus without communication primitives and molecular complexes, first introducing the MBD actions and, only afterwards, the PEP ones.

A system consists of nested membranes and membranes consist of collections of actions. The MBD actions are inspired by membrane fusion and splitting. The first is modelled by the mating operation, while the second can be rendered both by budding, that consists in splitting off exactly one internal membrane, and dripping, that consists in splitting off one empty membrane.

$$P, Q ::= \diamond \mid P \circ Q \mid !P \mid \sigma(P)^{\mu}$$

systems $S$

$$\sigma, \tau ::= 0 \mid \sigma|\tau \mid !\sigma \mid a.\sigma$$

membrane processes $B$

$$a, b ::= \text{mate}_n \mid \text{mate}_n^\bot \mid \text{bud}_n \mid \text{bud}_n^\bot(\rho) \mid \text{drip}(\rho)$$

MBD actions $\text{Act}_{MBD}$

Here, $n$ is taken by a countable set $\Lambda$ of names. Membranes are nameless entities, but to facilitate our analysis, we annotate them as in $\sigma(\langle P \rangle)^{\mu}$, in order to distinguish different syntactic occurrences of membranes. We refer to $\mu \in M$ as the identity of the membrane $\sigma(\langle P \rangle)^{\mu}$, where $M$ is the finite set of membrane identities. Still to simplify our analysis, we assume that each considered system is contained in an ideal outermost membrane, identified by a distinguished element $\ast \in M$.

The term $\sigma(\langle P \rangle)^{\mu}$ denotes a system whose behaviour depends on the actions in $\sigma$ and that includes the system $P$: $\sigma$ represents a membrane and $P$ its contents. The term $a.\sigma$ denotes a process that executes $a$ and then behaves as $\sigma$. Actions for mating ($\text{mate}_n$) and budding ($\text{bud}_n$) have the corresponding co-actions ($\text{mate}_n^\bot$, $\text{bud}_n^\bot$ resp.) to synchronise with. The actions $\text{bud}_n^\bot(\rho)$ and $\text{drip}(\rho)$ are equipped with a process $\rho$ to associate with the membrane created by the performed action.

Semantics

The standard structural congruence $\equiv$ on systems and membranes is the least congruence satisfying the following clauses:

- $(S/\equiv, \circ, \diamond)$ is a commutative monoid;
- $!\diamond \equiv \diamond, !(P \circ Q) \equiv !P \circ !Q, \lor P \equiv !P, !P \equiv P \circ !P$;
- $(B/\equiv, |, 0)$ is a commutative monoid;
- $!0 \equiv 0, \lor(\sigma|\tau) \equiv !\sigma||\tau, \lor\sigma \equiv !\sigma, \lor\sigma \equiv \sigma||\sigma$;
- $0(\langle \rangle)^{\mu_0} \equiv \diamond$;
- $P \equiv Q \Rightarrow P \circ R \equiv Q \circ R, P \equiv Q \Rightarrow P \equiv !Q, P \equiv Q \land \sigma \equiv \tau \Rightarrow \sigma(P)^{\mu} \equiv \tau(Q)^{\mu}$;
- $\sigma \equiv \tau \Rightarrow \sigma|\rho \equiv \tau|\rho, \sigma \equiv \tau \Rightarrow !\sigma \equiv !\tau, \sigma \equiv \tau \Rightarrow a.\sigma \equiv a.\tau$. 
\[ P \rightarrow Q \quad \quad P \rightarrow Q \quad \quad P \equiv P' \land P' \rightarrow Q' \land Q' \equiv Q \]

\[
\begin{align*}
(P) & \quad P \circ R \rightarrow Q \circ R \\
(\text{Par}) & \quad P \rightarrow Q \\
(\text{Struct}) & \quad \sigma(P)^{\mu} \rightarrow \sigma(Q)^{\mu}
\end{align*}
\]

\[
\begin{align*}
(Mate) & \quad m\text{at}_e.n.\sigma|\sigma_0(P)^{\mu_P} \circ m\text{at}_e^\perp.n.\tau|\tau_0(Q)^{\mu_Q} \rightarrow \sigma|\sigma_0|\tau|\tau_0(P \circ Q)^{\mu_{PQ}} \\
&Bud) \quad \text{bud}_n^\perp(\rho).\tau|\tau_0(\text{bud}_n.n.\sigma|\sigma_0(P)^{\mu_P} \circ Q)^{\mu_Q} \rightarrow \rho|\sigma|\sigma_0(P)^{\mu_R} \circ \tau|\tau_0(Q)^{\mu_Q} \\
&Drip) \quad \text{drip}(\rho).\sigma|\sigma_0(P)^{\mu_P} \rightarrow \rho|\rho|\sigma|\sigma_0(P)^{\mu_P}
\end{align*}
\]

Table 1
Reduction Semantics for Brane Calculus.

The interleaving semantics is based on the above notion of structural congruence and is composed by the basic reaction rules, valid for all brane calculi (upper part of Table 1) and by the reaction axioms for the MBD version (lower part of Table 1). Observe that, given a system, the set of its membrane identities is finite. Indeed, the structural congruence rule \( !P \equiv !P^!P \) applied to \( !\sigma(P)^{\mu} \) gives \( !\sigma(P)^{\mu} \equiv !\sigma(P)^{\mu} \equiv \sigma(P)^{\mu} \), i.e. no new identity is ever introduced in recursive calls. However, we need a distinguished membrane identity each time a certain action is performed, in order to identify the membrane obtained in the target. More precisely, we need a membrane identity for the membrane resulting from the firing of an action \( m\text{at}_e \), possible whenever a \( m\text{at}_e^\perp \) resides on a membrane identified by \( \mu_P \) (\( \mu_Q \), resp.), with \( \mu_P \) and \( \mu_Q \) included in a membrane identified by \( \mu \). Also we need a single membrane identity for each other possible pair of action/coaction occurring in siblings membranes. The number of such membrane identities is finite, due to the above structural congruence rule. Similarly, we need a distinguished membrane identity for each action \( \text{bud} \) or \( \text{drip} \), i.e. either when a \( \text{bud}_n^\perp \) resides on a membrane identified by \( \mu_P \) (\( \mu_Q \), resp.), with the membrane \( \mu_P \) included in the membrane \( \mu_Q \), in turn included in a membrane \( \mu \), or when a \( \text{drip} \) resides on a membrane identified by \( \mu_P \), included in the membrane \( \mu \). To obtain the needed membrane identities, one can exploit functions that are injective and surjective on their images. These auxiliary functions return fresh membrane identities, depending on the actions and on their syntactic contexts. More precisely:
\[ \text{MI}_{\text{mate}} : \text{Act}_{MBD} \times M \times M \times M \rightarrow M \]

\[ \text{MI}_{\text{bud}} : \text{Act}_{MBD} \times M \times M \times M \rightarrow M \]

\[ \text{MI}_{\text{drip}} : \text{Act}_{MBD} \times M \times M \rightarrow M \]

We dispense from the actual definition of these functions. We just recall that, given a system, the number of needed membrane identities is finite, as finite are the possible combinations of actions and contexts. Therefore, we choose \( M \) such that, given an action and the identities of the membranes on which the action (and the corresponding co-action, if any) reside, \( M \) includes the membrane identity needed to identify the membrane obtained by firing that action.

### 3 Control Flow Analysis

We develop a Control Flow Analysis for analysing Brane calculus systems, borrowing some ideas from [13]. The aim of the analysis is over-approximating all the possible behaviour of a Brane system. In particular, our analysis keeps track of the possible contents of membranes, thus taking care of the possible modifications of the containment hierarchy, due to the dynamics. An approximation of the contents of a membrane or estimate \( I \) is defined as

\[ I : M \rightarrow \wp(M \cup \text{Act}), \]

where \( \wp(S) \) stands for the power-set of the set \( S \) and \( \text{Act} \) is the set of Brane actions. Here, \( \mu' \in I(\mu) \) means that the membrane identified by \( \mu \) may contain the one identified by \( \mu' \); \( a \in I(\mu) \) means that the action \( a \) may reside on and affect the membrane identified by \( \mu \). To validate the correctness of a proposed estimate \( I \), we state a set of clauses operating upon judgements like \( I \models^\mu P \). This judgement expresses that when \( P \) is enclosed within a membrane identified by \( \mu \in M \), then \( I \) correctly captures the behaviour of \( P \), i.e. the estimate is valid also for all the states \( Q \) passed through a computation of \( P \).

Following [13], the analysis is specified in two phases. First, we check that \( I \) describes the initial process. This is done in Table 2, where the clauses amount to a structural traversal of process syntax. These clauses rely on the following auxiliary function that collects all the actions in a membrane process \( \sigma \).

**Definition 3.1** \( A : \mathcal{B} \rightarrow \text{Act} \)

- \( A(0) = \emptyset \);
- \( A(\sigma|\tau) = A(\sigma) \cup A(\tau) \);
- \( A(!\sigma) = A(\sigma) \);
- \( A(a.\sigma) = \{a\} \cup A(\sigma) \);

Note that the actions collected by \( A \), e.g., in \( \sigma = \sigma_0.\sigma_1 \) are equal to the ones in \( \sigma' = \sigma_0|\sigma_1 \), witnessing the fact that the analysis is insensitive to the context and introduces imprecision and approximation.
The clause for membrane system $\sigma\langle P \rangle^{\mu'}$ checks that whenever a membrane $\mu'$ is introduced inside a membrane $\mu$, the relative hierarchy position must be reflected in $I$, i.e. $\mu' \in I(\mu)$. Furthermore, the actions in $\sigma$ that affect the membrane $\mu'$ and that are collected in $A(\sigma)$, are recorded in $I(\mu')$. Finally, when inspecting the content $P$, the fact that the enclosing membrane is $\mu'$ is recorded, as reflected by the judgement $I \models^{\mu'} P$. The rule for $\diamond$ and 0 do not restrict the analysis result, while the rules for parallel composition $\circ$, and replication $!$ ensure that the analysis also holds for the immediate sub-systems, by ensuring their traversal. In particular, the analysis of $!P$ is equal to the one of $P$. This is another source of imprecision.

Secondly, we check that $I$ also takes into account the dynamics of the process under consideration; in particular, the dynamics of the containment hierarchy of membranes. This is expressed by the closure conditions in the lower part of Table 2 that mimic the semantics, by modelling, without exceeding the precision boundaries of the analysis, the semantic preconditions and the consequences of the possible actions. More precisely, the precondition checks, in terms of $I$, for the possible presence of the redexes necessary for an action to be performed. The conclusion imposes the additional requirements on $I$, for the possible presence of the redexes necessary for an action to be performed. The conclusion imposes the additional requirements on $I$, necessary to give a valid prediction of the analysed action. Consider e.g., the clause for $(Mate)$ (the other clauses are similar). We have to make sure that the precondition requirements are satisfied, i.e. that:

- there exists an occurrence of mate action: $mate_n \in I(\mu_P)$;
- there exists an occurrence of the corresponding co-mate action: $mate^\perp_n \in I(\mu_Q)$;
- the corresponding membranes must be siblings: $\mu_P, \mu_Q \in I(\mu)$

If the precondition requirements are satisfied, then the conclusions of the clause express the consequences of performing the transition mate. In this case, we have that $I$ must reflect that

- there may exist a membrane $\mu_{PQ}$ inside $\mu$, with the same father of the membranes $\mu_P$ and $\mu_Q$: $\mu_{PQ} \in I(\mu)$; and that
- the contents of $\mu_P$ and of $\mu_Q$ may also be inside $\mu_{PQ}$, and therefore $\mu_{PQ}$ contains every membrane that is inside $\mu_P$ or $\mu_Q$, while each action affecting $\mu_P$ or $\mu_Q$, affects also $\mu_{PQ}$: $I(\mu_P) \cup I(\mu_Q) \subseteq I(\mu_{PQ})$.

This corresponds to the application of the semantic rule $(Mate)$ that would result in the fusion of the two membranes.

Example 3.2 We illustrate our analysis on a simple example, taken from [5], of which we report one of the possible steps of computation: the $(Mate)$ one.
We can observe that the corresponding conclusion requirements are satisfied as
mate
\[ (\text{Mate}) \quad \text{mate}_n \in \mathcal{I}(\mu_P) \land \text{mate}_n^{\perp} \in \mathcal{I}(\mu_Q) \land \mu_P, \mu_Q \in \mathcal{I}(\mu) \]
\[ \Rightarrow \mu_{PQ} \in \mathcal{I}(\mu) \land (\mathcal{I}(\mu_P) \cup \mathcal{I}(\mu_Q)) \subseteq \mathcal{I}(\mu_{PQ}) \]
\[ \text{where } \mu_{PQ} = \text{MI}_{\text{mate}}(\text{mate}_n, \mu_P, \mu_Q, \mu) \]
\[ (\text{Bud}) \quad \text{bud}_m \in \mathcal{I}(\mu_P) \land \text{bud}_m^{\perp}(\rho) \in \mathcal{I}(\mu_Q) \land \mu_P \in \mathcal{I}(\mu_Q) \land \mu_Q \in \mathcal{I}(\mu) \]
\[ \Rightarrow A(\rho) \in \mathcal{I}(\mu_R) \land \mu_R \in \mathcal{I}(\mu) \land \mu_P \in \mathcal{I}(\mu_R) \]
\[ \text{where } \mu_R = \text{MI}_{\text{bud}}(\text{bud}_m, \mu_P, \mu_Q, \mu) \]
\[ (\text{Drip}) \quad \text{drip} \in \mathcal{I}(\mu_P) \land \mu_P \in \mathcal{I}(\mu) \]
\[ \Rightarrow A(\rho) \in \mathcal{I}(\mu_R) \land \mu_R \in \mathcal{I}(\mu) \]
\[ \text{where } \mu_R = \text{MI}_{\text{drip}}(\text{drip}(\rho), \mu_P, \mu) \]

<table>
<thead>
<tr>
<th>( \mu_{P_0}, \mu_{P_1} \in \mathcal{I}(\mu_P), \mu_P, \mu_Q \in \mathcal{I}(\ast) )</th>
<th>( \mu_{P_0}, \mu_{P_1} \in \mathcal{I}(\mu_{PQ}), \mu_{PQ} \in \mathcal{I}(\ast) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{mate}_n \in \mathcal{I}(\mu_P) )</td>
<td>( \text{mate}_n^{\perp} \in \mathcal{I}(\mu_Q) )</td>
</tr>
<tr>
<td>( \text{bud}<em>m \in \mathcal{I}(\mu</em>{P_0}), \text{bud}_m^{\perp}(\rho_1) \in \mathcal{I}(\mu_P) )</td>
<td>( \text{bud}<em>m^{\perp}(\rho_1) \in \mathcal{I}(\mu</em>{PQ}) )</td>
</tr>
<tr>
<td>( \text{bud}<em>o \in \mathcal{I}(\mu</em>{P_1}), \text{bud}_o^{\perp}(\rho_2) \in \mathcal{I}(\mu_Q) )</td>
<td>( \text{bud}<em>o^{\perp}(\rho_2) \in \mathcal{I}(\mu</em>{PQ}) )</td>
</tr>
<tr>
<td>( \mu_{P_0} \in \mathcal{I}(\mu_{R1}), \mu_{P_0} \in \mathcal{I}(\mu_{R1}') )</td>
<td>( \mu_{P_1} \in \mathcal{I}(\mu_{R2}) )</td>
</tr>
<tr>
<td>( \text{where } \mu_{PQ} = \text{MI}_{\text{mate}}(\text{mate}_n, \mu_P, \mu_Q, \ast) )</td>
<td>( \mu_{R2} = \text{MI}_{\text{bud}<em>o}(\text{bud}<em>o, \mu</em>{P_1}, \mu</em>{PQ}, \ast) )</td>
</tr>
<tr>
<td>( \mu_{R1} = \text{MI}_{\text{bud}_m}(\text{bud}<em>m, \mu</em>{P_0}, \mu_P, \ast) )</td>
<td>( \mu_{R1}' = \text{MI}_{\text{bud}<em>m}(\text{bud}<em>m, \mu</em>{P_0}, \mu</em>{PQ}, \ast) )</td>
</tr>
</tbody>
</table>

satisfied: \( \text{mate}_n \in \mathcal{I}(\mu_P) \) and \( \text{mate}_n^{\perp} \in \mathcal{I}(\mu_Q) \), and the two membranes are siblings. We can observe that the corresponding conclusion requirements are satisfied as well, because both \( \mathcal{I}(\mu_P) \) and \( \mathcal{I}(\mu_Q) \) are included in \( \mathcal{I}(\mu_{PQ}) \), where \( \mu_{PQ} \) identifies the new membrane created by the fusion. Also the transition on \( \text{bud}_m \) is initially possible and this result is actually predicted by the analysis. Instead, we can observe that the transition on \( \text{bud}_o \) cannot be performed in the initial system, because the actions do not reside on two membranes where one is the father of the other. This
is reflected by the analysis; indeed we have that the precondition requirements are not satisfied: \( \text{bud}_o \in \mathcal{I}(\mu_{P_1}), \text{bud}_o^\perp \in \mathcal{I}(\mu_Q) \), but \( \mu_{P_1} \notin \mathcal{I}(\mu_Q) \). Nonetheless, the transition on \( \text{bud}_o \) can be performed, after the mate transition (reported above), as correctly predicted by the analysis, since \( \text{bud}_o \in \mathcal{I}(\mu_{P_1}) \), with \( \mu_{P_1} \in \mathcal{I}(\mu_{PQ}) \) and \( \text{bud}_o^\perp \in \mathcal{I}(\mu_{PQ}) \). Note that the action \( \text{bud}_m \) can be performed in the context in which \( \text{bud}_m \in \mathcal{I}(\mu_{P_0}), \text{bud}_m^\perp \in \mathcal{I}(\mu_{P_0}) \), with \( \mu_{P_0} \in \mathcal{I}(\mu_{PQ}) \). The obtained membranes are therefore differently identified: \( \mu_{R_1} \) in the first case and \( \mu'_{R_1} \) in the second.

**Semantic Correctness**

Our analysis is semantically correct with respect to the given semantics, i.e. a valid estimate enjoys the following subject reduction property with respect to the semantics.

**Theorem 3.3 (Subject Reduction)**

If \( P \rightarrow Q \) and \( \mathcal{I} \models^\mu P \) then also \( \mathcal{I} \models^\mu Q \).

This result depends on the fact that analysis is invariant under the structural congruence, as stated below.

**Lemma 3.4 (Invariance of Structural Congruence)**

If \( P \equiv Q \) and \( \mathcal{I} \models^\mu P \) then also \( \mathcal{I} \models^\mu Q \).

**Existence of the Analysis**

We have previously seen a procedure for verifying whether or not a proposed estimate \( \mathcal{I} \) is valid. We now show that for any given \( P \) there always is a least choice of \( \mathcal{I} \) that is acceptable according to the rules in Table 2, i.e. such that \( \mathcal{I} \models^\mu P \).

**Definition 3.5**

The set of proposed solutions can be partially ordered by setting \( \mathcal{I} \sqsubseteq \mathcal{I}' \) iff \( \forall \mu : \mathcal{I}(\mu) \subseteq \mathcal{I}'(\mu) \).

This suffices for making the set of proposed solutions into a complete lattice; using standard notation we write \( \mathcal{I} \sqcup \mathcal{I}' \) for the binary least upper bound (defined point-wise), \( \cap \mathcal{E} \) for the greatest lower bound of a set \( \mathcal{E} \) of proposed estimates (also defined pointwise), and \( \bot \) for the least element.

**Definition 3.6**

A set \( \mathcal{E} \) of proposed estimates is a **Moore family** if and only if it contains \( \cap \mathcal{F} \) for all \( \mathcal{F} \subseteq \mathcal{E} \) (in particular \( \mathcal{F} = \emptyset \) and \( \mathcal{F} = \mathcal{E} \)).

When \( \mathcal{E} \) is a Moore family it contains a greatest element \( (\cap \emptyset) \) as well as a least element \( (\cap \mathcal{E}) \). The following theorem then guarantees that there always is an estimate satisfying the specification in Table 2.

**Theorem 3.7 (Moore Family)**

For any system \( P \), the set \( \left\{ \mathcal{I} \mid \mathcal{I} \models^\mu P \right\} \) is a Moore family.

Currently, our analysis is not implemented, but it can, along the lines of the Control Flow Analysis for BioAmbients [13]. This means that it is possible, given a process, to compute its least estimate.
4 Extension to the PEP Actions

The presented analysis can be extended (see below) in order to deal with the Phago/Exo/Pino (PEP) version of Brane Calculus. These further operations are used to describe endocytosis and exocytosis processes. The first indicates the process of incorporating external material into a cell, by engulfing it with the cell membrane, while the second one indicates the reverse process. Endocytosis is rendered by two more basic operations: phagocytosis (denoted by phago), that consists in engulfing just one external membrane, and pinocytosis (denoted by pino), consists in engulfing zero external membranes; exocytosis is instead denoted by exo. The detailed extensions to the syntax follow, while the semantics ones are in Table 4.

\[ a ::= \text{phago}_n \mid \text{phago}^\perp_n (\rho) \mid \text{exo}_n \mid \text{exo}^\perp_n \mid \text{pino}(\rho) \]  
PEP actions \( \text{Act}_{PEP} \)

\[ \text{MI}_{\text{phago}} : \text{Act}_{PEP} \times M \times M \times M \rightarrow M \]

\[ \text{MI}_{\text{pino}} : \text{Act}_{PEP} \times M \times M \rightarrow M \]

<table>
<thead>
<tr>
<th>(Phago)</th>
<th>( \text{phago}_n . \sigma \sigma_0 (P)^{\mu_P} \circ \text{phago}^\perp_n (\rho). \tau \tau_0 (Q)^{\mu_Q} \rightarrow \tau \tau_0 (\rho \sigma \sigma_0 (P)^{\mu_P} \circ Q)^{\mu_Q} )</th>
</tr>
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<tbody>
<tr>
<td>where ( \mu_R = \text{MI}_{\text{phago}} (\text{phago}_n, \mu_P, \mu_Q, \mu) ) and ( \mu ) identifies the closest membrane surrounding ( \mu_P ) and ( \mu_Q )</td>
<td></td>
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<tr>
<th>(Exo)</th>
<th>( \text{exo}^\perp_n . \tau \tau_0 (\text{exo}_n . \sigma \sigma_0 (P)^{\mu_P} \circ Q)^{\mu_Q} \rightarrow P \circ \sigma \sigma_0 (\tau \tau_0 (Q)^{\mu_Q} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Pino)</td>
<td>( \text{pino}(\rho) . \sigma \sigma_0 (P)^{\mu_P} \rightarrow \sigma \sigma_0 (\rho)^{\mu_R \circ P)^{\mu_P} )</td>
</tr>
<tr>
<td>where ( \mu_R = \text{MI}_{\text{pino}} (\text{pino}(\rho), \mu_P, \mu) ) and ( \mu ) identifies the closest membrane surrounding ( \mu_P )</td>
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</tr>
</tbody>
</table>

Table 4
Reduction Rules for PEP Actions.

The Control Flow Analysis can be extended by adding the closure conditions in Table 5. Our extended analysis is still semantically correct with respect to the given semantics and the estimates still form a Moore family, therefore guaranteeing the existence of a least estimate satisfying the clauses in Tables 2 and 5. The extended results are handled and proved in the Appendix.

5 The Analysis at Work

In Brane calculi the dynamics of biological membranes is abstracted by means of interactions that lead to modifications of the hierarchy of compartments. Control Flow Analysis gives information on the possible variations of the containment hierarchy. Both examples presented below show why this information is important, as it offers the basis for qualified predictions about the possible dynamic behaviour.
\( (\text{Phago}) \ phago_n \in I(\mu_P) \land phago_n^\perp(\rho) \in I(\mu_Q) \land \mu_P, \mu_Q \in I(\mu) \)

\[ \Rightarrow A(\rho) \in I(\mu_R) \land \mu_R \in I(\mu_Q) \land \mu_P \in I(\mu_R) \]

where \( \mu_R = \text{MI}_{\text{phago}}(phago_n, \mu_P, \mu_Q, \mu) \)

\( (\text{Exo}) \ exo_n \in I(\mu_P) \land exo_n^\perp \in I(\mu_Q) \land \mu_P \in I(\mu_Q) \land \mu_Q \in I(\mu) \)

\[ \Rightarrow A(\sigma), A(\sigma_0) \in I(\mu_Q) \land I(\mu_P) \subseteq I(\mu) \]

\( (\text{Pino}) \ pino(\rho) \in I(\mu_P) \land \mu_P \in I(\mu) \)

\[ \Rightarrow A(\rho) \in I(\mu_R) \land \mu_R \in I(\mu_P) \]

where \( \mu_R = \text{MI}_{\text{pino}}(pino(\rho), \mu_P, \mu) \)

Table 5
Closure Rules for PEP Actions

5.1 Viral Infection

We first refer to the abstract specification introduced in [6] of the viral infection cycle of the Semliki Forest Virus, shown in Figure 1. This is one of the so-called “enveloped viruses”. These viruses possess a lipidic bilayer envelope that surrounds the nucleocapsid, the part of the virus composed by the genome and its protective coat formed by identical protein subunits (capsomers). The viral outer envelope is a modified form of one of the membranes of the host cell, either the cell membrane, or an internal membrane, e.g. the nuclear membrane or endoplasmic reticulum. Noticeably, most enveloped viruses depend on their envelope for their infectivity.

Fig. 1. Viral Infection (highlighted part) and Reproduction. [Adapted from [6] and [1]]

In our example, we consider the first stage of the infective cycle of the Semliki Forest Virus (highlighted part in Figure 1), whose steps can be coded as in Table 6.
The complete evolution of the viral infection is reported in Table 7, while the main analysis entries are in Table 8. The analysis results allow us to predict the effects of the infection. Indeed, the inclusion $\mu_{nucap} \in I(\mu_{memb})$ reflects the fact that, at the end of the shown computation, $nucap$ is inside $membrane$, together with $cytosol$.

### 5.2 Communication via a Mobile Vesicle

In eucaryotic cells a large variety of proteins is targetted to its final destination via mobile transport vesicles, i.e. small membrane-enclosed sacs separated from the cytosol by a lipidic bilayer. Proteins can be contained in the vesicles (e.g. secretory proteins) or embedded in their membrane, e.g. transmembrane proteins.
Through vesicular trafficking, proteins follow routes involving intracellular locations (e.g. endoplasmic reticulum, Golgi apparatus or lysosomes) as well as the plasma membrane, in the case of endo- and exocytosis.

In [19], the PEP Brane calculus, plus the “bud” action, had been used to model a hypothetical scenario of communication via a mobile vesicle. As shown in Figure 2, a vesicle containing (embedded in its membrane) a substance that needs to be shuttled between two compartments, buds from a membrane \( \text{Source} \). Then, it is engulfed by another compartment through phagocytosis and, finally, the mobile vesicle merges with the membrane \( \text{Target} \) releasing the transported substance in it. The encoding of this scenario is in Table 9. There, \( \omega_G \), \( \omega_X \), \( \omega_{\text{Source}} \), and \( \omega_{\text{Target}} \) stand for skin membranes processes (not specified as not relevant at this level of abstraction).

![Diagram of vesicle communication](image)

**Fig. 2.** A vesicle with the substance (rendered as \(|\)) embedded in its membrane, buds from the source membrane (1 and 2). The vesicle is then phagocytated by the target membrane (3 and 4) and merges with it (5 and 6) so delivering the substance to the final destination.

The dynamic evolution is reported in Table 10. The action \( \text{bud}_{n1} \) triggers the communication process, by leading to the gemmation of a vesicle containing the substance \( \omega_X(\phi)^{\mu_X} \) coming from the membrane \( \text{Source} \). The vesicle fuses with membrane \( \text{Target} \), by means of actions \( \text{phago}_{n2} \) and \( \text{exo} \).

The main entries of the Control Flow Analysis are reported in Table 11. The inclusion \( \mu_X \in I(\mu_T) \) reflects that the substance to be transmitted can eventually finish inside the target membrane.
\[ \mu_G \in \mathcal{I}(\ast), \omega_G \in \mathcal{I}(\mu_G); \]
\[ \text{bud}_{n_1}^\perp(\text{vesicle}), \omega_{\text{Source}} \in \mathcal{I}(\mu_S), \mu_S \in \mathcal{I}(\mu_G) \]
\[ \text{bud}_{n_1}, \omega_X \in \mathcal{I}(\mu_X), \mu_X \in \mathcal{I}(\mu_S) \]
\[ \text{phago}_{n_2}^\perp(\text{exo}), \omega_{\text{Target}} \in \mathcal{I}(\mu_T), \mu_T \in \mathcal{I}(\mu_G) \]
\[ \text{phago}_{n_2}, \text{exo} \in \mathcal{I}(\mu_V), \mu_V \in \mathcal{I}(\mu_G), \mu_X \in \mathcal{I}(\mu_V) \]
\[ \text{exo}^\perp \in \mathcal{I}(\mu_E), \mu_E \in \mathcal{I}(\mu_T), \mu_V \in \mathcal{I}(\mu_E) \]
\[ \mathcal{I}(\mu_V) \subseteq \mathcal{I}(\mu_T) \text{ and, in particular, } \mu_X \in \mathcal{I}(\mu_T) \]

Table 11
Communication via a Mobile Vesicle: Analysis Results

6 Conclusion

We have introduced a Control Flow Analysis for the static approximation of the dynamic behaviour of processes, expressed in the MBD + PEP version of Brane calculi.

Like the ones in [12,13,3], our analysis is context-insensitive and also flow-insensitive and these features affect the analysis precision. Future work regards the improvement of our analysis precision, along the lines of [15,16]. Preliminary results make us confident that useful information on the behaviour of the analysed systems can be obtained and used in order to establish biological properties of the systems under consideration. In particular, the properties that can be expressed as reachability properties of the model. Furthermore, we can obtain information on the role played by the various elements composing the investigated system. Therefore, it becomes easier to evaluate the behaviour of the whole system when a single element is added or removed, following an approach similar to [4].

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References


A Proofs

This appendix restates the lemmata and theorems presented earlier in the paper and gives the proofs of their correctness.

To establish the semantic correctness, the following auxiliary results are needed.

Fact A.1 If \( I \models^\mu_1 P \) and \( I(\mu_1) \subseteq I(\mu_2) \), then \( I \models^\mu_2 P \).

Proof. By structural induction on \( P \). This is straightforward, because the membrane identity is only used in recursive calls, to establish a fact like \( \mu \in I(\mu_i) \) or \( a \in I(\mu_i) \). We show just one case.

Case \( P = \sigma(P)^\mu \). We have that \( I \models^\mu_1 P \) is equivalent to \( \mu' \in I(\mu_1) \land A(\sigma) \in I(\mu') \land I \models^\mu_2 P \). Now, \( \mu' \in I(\mu_1) \) and \( I(\mu_1) \subseteq I(\mu_2) \) imply \( \mu' \in I(\mu_2) \), and by induction hypothesis, we have that \( I \models^\mu_2 P \). \( \square \)

Fact A.2 If \( \sigma \equiv \tau \) then \( A(\sigma) = A(\tau) \).
Lemma A.3 (Invariance of Structural Congruence)

If $P \equiv Q$ and $\mathcal{I} \models^\mu P$ then also $\mathcal{I} \models^\mu Q$.

Proof. The proof amounts to a straightforward inspection of each of the clauses defining the structural congruence clauses relative to membranes. We show only two cases, the others are similar.

Case $\sigma_0 | \sigma_1 \equiv \sigma_1 | \sigma_0$. We have that $A(\sigma_0 | \sigma_1) = A(\sigma_0) \cup A(\sigma_1) = A(\sigma_1 | \sigma_0)$.

Case $\sigma \equiv \tau \Rightarrow \sigma | \rho \equiv \tau | \rho$. We have that $A(\sigma | \rho) = A(\sigma) \cup A(\rho)$. Now, since $\sigma \equiv \tau$, we have that $A(\sigma) = A(\tau)$ and therefore $A(\sigma | \rho) = A(\tau) \cup A(\rho)$, from which the required $A(\tau | \rho)$.

Theorem A.4 (Subject Reduction)

If $P \rightarrow Q$ and $\mathcal{I} \models^\mu P$ then also $\mathcal{I} \models^\mu Q$.

Proof. The proof is by induction on $P \rightarrow Q$. The proofs for the rules $(Par)$ and $(Brane)$ are straightforward, using the induction hypothesis and the clauses in Table 2. The proof for the $(Struct)$ uses instead the induction hypothesis and Lemma A.3. The proofs for the basic actions in the lower part of Table 1 and in Table 4 are straightforward, using the clauses in Tables 2 and 5.
Case (Par). Let \( P \) be \( P_0 \circ P_1 \) and \( Q \) be \( P'_0 \circ P_1 \). We have to prove that \( \mathcal{I} \models P \). Now \( \mathcal{I} \models P_0 \) is equivalent to \( \mathcal{I} \models P_0' \land \mathcal{I} \models P_1 \). By induction hypothesis, we have that \( \mathcal{I} \models P_0' \), and from \( \mathcal{I} \models P_0' \land \mathcal{I} \models P_1 \) we obtain the required \( \mathcal{I} \models P \).

Case (Brane). Let \( P \) be \( \sigma(P_0)^{\mu} \) and \( Q \) be \( \sigma(P'_0)^{\mu'} \). We have to prove that \( \mathcal{I} \models P \). Now \( \mathcal{I} \models P_0 \) is equivalent to \( \mu' \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu') \land \mathcal{I} \models P_0' \). By induction hypothesis, we have that \( \mathcal{I} \models P_0' \), and from \( \mu' \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu') \land \mathcal{I} \models P_0' \) we obtain the required \( \mathcal{I} \models P \).

Case (Struct). Let \( P \equiv P_0 \), with \( P_0 \to P_1 \) such that \( P_1 \equiv Q \). By Lemma A.3, we have that \( \mathcal{I} \models P_0 \), by induction hypothesis \( \mathcal{I} \models P_1 \) and, again by Lemma A.3, \( \mathcal{I} \models P \).

Case (Mate). Let \( P \) be \( mate_n.\sigma|\sigma_0(P_0)^{\mu_0} \circ mate_n.\tau|\tau_0(P_1)^{\mu_1} \) and \( Q \) be \( \sigma|\sigma_0|\tau|\tau_0(P_0 \circ P_1)^{\mu_0} \). We have that \( \mathcal{I} \models P \) is equivalent to \( \mathcal{I}(\mu) \land mate_n \in \mathcal{I}(\mu) \land mate_n \in \mathcal{I}(\mu) \land \mu_0, \mu_1 \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \land A(\tau) \in \mathcal{I}(\mu_1) \land A(\tau_0) \in \mathcal{I}(\mu_1) \land \mathcal{I} \models P_1 \). In particular, because of the closure conditions, from (1), we have that \( \mu_0 \in \mathcal{I}(\mu) \land \mathcal{I}(\mu_0) \cup \mathcal{I}(\mu_1) \subseteq \mathcal{I}(\mu_0) \). Since \( \mathcal{I}(\mu_0) \subseteq \mathcal{I}(\mu_0) \) for \( i = 0, 1 \), then, by Fact A.1, we have that \( A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \) and \( A(\tau) \in \mathcal{I}(\mu_0) \land A(\tau_0) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_1 \), and hence the required \( \mathcal{I} \models Q \).

Case (Bud). Let \( P \) be \( bud_n(\rho).\tau|\tau_0(bud_n.\sigma|\sigma_0(P_0)^{\mu_0} \circ P_1)^{\mu_1} \) and \( Q \) be \( \rho(\sigma|\sigma_0)(P_0)^{\mu_0} \circ \tau|\tau_0(P_1)^{\mu_1} \). We have that \( \mathcal{I} \models P \) is equivalent to \( bud_n \in \mathcal{I}(\mu_0) \land bud_n \in \mathcal{I}(\mu_0) \land \mu_0, \mu_1 \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \land A(\tau) \in \mathcal{I}(\mu_1) \land \mathcal{I} \models P_1 \). In particular, because of the closure conditions, from (1), we have that \( \mathcal{I}(\mu) \land \mu \in \mathcal{I}(\mu) \land \mathcal{I} \models P \), and therefore the required \( \mathcal{I} \models Q \).

Case (Drip). Let \( P \) be \( drip(\rho).\sigma|\sigma_0(P_0)^{\mu_0} \) and \( Q \) be \( \rho(\sigma|\sigma_0)(P_0)^{\mu_0} \). We have that \( \mathcal{I} \models P \) is equivalent to \( drip(\rho) \in \mathcal{I}(\mu_0) \land A(\rho) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \). In particular, because of the closure conditions, from (1), we have that \( \mathcal{I}(\mu) \land \mu \in \mathcal{I}(\mu) \land \mathcal{I} \models P \), and therefore the required \( \mathcal{I} \models Q \).

Case (Phago). Let \( P \) be \( phago_n.\sigma|\sigma_0(P_0)^{\mu_0} \circ phago_n(\rho).\tau|\tau_0(P_1)^{\mu_1} \) and \( Q \) be \( \tau|\tau_0(\rho|\sigma_0)(P_0)^{\mu_0} \circ P_1)^{\mu_1} \). We have that \( \mathcal{I} \models P \) is equivalent to \( phago_n \in \mathcal{I}(\mu_0) \land phago_n(\rho) \in \mathcal{I}(\mu_1) \land \mu_0, \mu_1 \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \land A(\tau) \in \mathcal{I}(\mu_1) \land A(\tau_0) \in \mathcal{I}(\mu_1) \land \mathcal{I} \models P_1 \). In particular, because of the closure conditions, from (1), we have that \( \mathcal{I}(\mu) \land \mu \in \mathcal{I}(\mu) \land \mathcal{I} \models P \), and hence the required \( \mathcal{I} \models Q \).

Case (Exo). Let \( P \) be \( exo_n.\tau|\tau_0(exo_n.\sigma|\sigma_0(P_0)^{\mu_0} \circ P_1)^{\mu_1} \) and let \( Q \) be \( P_0 \circ \sigma|\sigma_0|\tau|\tau_0(P_1)^{\mu_1} \). We have that \( \mathcal{I} \models P \) is equivalent to \( exo_n \in \mathcal{I}(\mu_0) \land exo_n \in \mathcal{I}(\mu_0) \land \mu_0, \mu_1 \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \land A(\tau) \in \mathcal{I}(\mu_1) \land A(\tau_0) \in \mathcal{I}(\mu_1) \land \mathcal{I} \models P_1 \). In particular, because of the closure conditions, from (1), we have that \( \mathcal{I}(\mu) \land \mu \in \mathcal{I}(\mu) \land \mathcal{I} \models P \). By Fact A.1, we have that \( \mathcal{I} \models P_0 \) and therefore the required \( \mathcal{I} \models Q \).

Case (Pino). Let \( P \) be \( pino(\rho).\sigma|\sigma_0(P_0)^{\mu_0} \) and \( Q \) be \( \sigma|\sigma_0(\rho)^{\mu_0} \circ P_0)^{\mu_0} \). We have that \( \mathcal{I} \models P \) is equivalent to \( pino(\rho) \in \mathcal{I}(\mu_0) \land \mu_0 \in \mathcal{I}(\mu) \land A(\sigma) \in \mathcal{I}(\mu_0) \land A(\sigma) \in \mathcal{I}(\mu_0) \land \mathcal{I} \models P_0 \). In particular, because of the closure condi-
tions, from (1), we have that $A(\rho) \in \mathcal{I}(\mu_R) \land \mu_R \in \mathcal{I}(\mu_0)$, and therefore the required $\mathcal{I} \models^{\mu} Q$.

\[ \square \]

**Theorem A.5 (Moore Family)**

For any system $P$, the set $\{ \mathcal{I} \mid \mathcal{I} \models^{\mu} P \}$ is a Moore family.

**Proof.** We proceed by structural induction on $P$. Let $E$ be a set of proposed estimates and let $F$ and $\mathcal{I}_j$ such that $F \subseteq E = \{ \mathcal{I}_j \mid j \in F \}$. Next, define $\mathcal{I}' = \cap F$. We have to check that $\mathcal{I}' \models^{\mu'} P$. We just consider one case. The others are similar.

**Case** $(\sigma(P_0)^{\mu'})$. Since $\forall j \in F : \mathcal{I}_j \models^{\mu} \sigma(P_0)^{\mu}$, then

$$\forall j \in F : \mu' \in \mathcal{I}_j(\mu) \land A(\sigma) \in \mathcal{I}_j(\mu') \land \mathcal{I}_j \models^{\mu'} P$$

Using the induction hypothesis and the fact that $\mathcal{I}'$ is obtained in a pointwise way, we then obtain that

$$\mu' \in \mathcal{I}'(\mu) \land A(\sigma) \in \mathcal{I}'(\mu') \land \mathcal{I}' \models^{\mu'} P$$

thus establishing the required $\mathcal{I}' \models^{\mu} \sigma(P_0)^{\mu'}$. \[\square\]