Computing Efficiency in Membrane Systems

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Summary

- Membrane Systems: ideas and definitions
- Membrane Systems with Active Membranes
- Computing Power of Membrane Systems
- Attacking Computationally Hard Problems
- Space Complexity in Membrane Systems with Active Membranes
Membrane Systems: a Bio-inspired computing model

- G. Paun, 1998 (P Systems): computational model inspired from the structure and functioning of the cell
  - Discrete
  - Non-deterministic
  - Maximally parallel application of the rules

- Main components:
  - Cellular structure
  - Chemical substances
  - Cellular reactions
  - Communication of substances
Cell Structure
Membrane structure

- Each membrane defines a REGION (compartment) in the membrane structure.
- The most external membrane separates the system and the environment. It is called SKIN.
- Some substances are communicated through the membranes.
- A membrane is identified by means of a label.
Membrane Structure

Skin Membrane
Elementary Membrane
Non-elementary Membrane
Membrane Systems: Chemicals and Reactions

- Chemicals - Ions, molecules, proteins: multisets of symbols over an alphabet
  - Multiset: each symbol can be present in one or more copies in a region
  - E.g. \( a^5, b^3, c \): five copies of chemical \( a \), three of \( b \), and one of \( c \) are present in a region

- A reaction is described by a CF rewriting rule and target indication
  - Chemical on left replaced by chemicals on right
  - Obtained chemicals communicated according to target indication
  - Special Symbol \( \delta \): membrane is dissolved
  - E.g. \( a \rightarrow (x, here)(y, out)(z, in_3)\delta \)
Membrane System

A A A

A >> (A, here) (B, out)

Objects

Evolution Rules
Definition: Membrane System

\[ \Pi = (V, \mu, M_1, \ldots, M_n, (R_1, \rho_1), \ldots, (R_n, \rho_n), i_0) \]

- **V**: Alphabet
- **\( \mu \)**: Membrane structure (Ex. \([ [ ]_2 [ ]_3 [ [ ]_5 [ ]_6 ]_4 ]_1 \))
- **\( M_i \)**: Multisets of symbols (or strings) in \( V \)
- **\( R_i \)**: Finite sets of evolution rules \( x \rightarrow y \), \( x \in V^* \), \( y = y' \) or \( y = y' \delta \) where \( y' \) is a string over \((V \times \text{tar}) \), \( \text{tar} \in \{\text{here, out, inj}\} \)
- **\( \rho_i \)**: Partial order relations over \( R_i \)
- **\( i_0 \)**: Output Membrane. If empty, then the output region is the environment
Evolution

- $M_1, \ldots, M_n$: initial configuration
- Rules are applied following the given priorities
- Rules are applied in a non-deterministic way
- All objects evolve in parallel
- All regions evolve in parallel
- Rules can move objects through membranes
  - *here*: the object is not moved
  - *out*: the object is sent to the adjacent external region
  - *$in_j$*: the object is sent to the inner membrane with label $j$
Computation

- **Computation**: Sequence of transitions between two configurations (by means of rules). A computation halts when no further rule can be applied

- **Output**:
  - Objects in \( i_0 \) (or outside the skin) when the computation halts
  - \( \emptyset \) if the computation never stops
Active Membranes: active role in the computation

- Polarizations: electrical charges (positive +, negative -, or neutral 0) are associated with the membranes.
- Rules are applied according to polarizations
- Membranes can be dissolved
- New membranes can be created by division of existing ones. Objects in the divided membrane are duplicated:
  - Division for elementary membranes
    \[[h \ A]_h^\alpha \rightarrow [h \ B]_h^\beta [h \ C]_h^\gamma\]
  - Division for non-elementary membranes
    \[[h_0 \ [h_1 ]_{h_1}^+ \cdots [h_k ]_{h_k}^+ [h_{k+1} ]_{h_{k+1}}^- \cdots [h_n ]_{h_n}^- ]_h^\alpha \rightarrow\]
    \[[h_0 \ [h_1 ]_{h_1}^+ \cdots [h_k ]_{h_k}^+ ]_h^\beta [h_0 \ [h_{k+1} ]_{h_{k+1}}^- \cdots [h_n ]_{h_n}^- ]_h^\gamma\]
Definition: Membrane Systems with Active Membranes

\[ \Pi = (V, H, \mu, M_1, \ldots, M_n, R) \]

- \( V \): Alphabet
- \( H \): set of labels for membranes
- \( \mu \): Membrane structure (Ex. \([ [ ]_2 [ ]_3 [ [ ]_5 [ ]_6 ]_4 ]_1\))
- \( M_i \): String over \( V \), initial multiset of symbols in region \( i \)
- \( R \): Finite sets of evolution rules
- Membranes are marked using polarization: \( \{+, -, 0\} \)
Developmental Rules

Assume $a \in V$, $w \in V^*$, $h \in H$, $\alpha_i \in \{+, -, 0\}$

- **Object evolution:** $[a \rightarrow w]_{h}^{\alpha_1}$
- **IN communication:** $a [ \ ]_{h}^{\alpha_1} \rightarrow [b]_{h}^{\alpha_2}$
- **OUT communication:** $[a]_{h}^{\alpha_1} \rightarrow [ \ ]_{h}^{\alpha_2} b$
- **Dissolution:** $[a]_{h}^{\alpha_1} \rightarrow b$
Division Rules

- **Elementary division:**
  \[ [a]_{h}^{\alpha_1} \rightarrow [b]_{h}^{\alpha_2} [c]_{h}^{\alpha_3} \]

- **Non-elementary division:**
  \[
  \begin{array}{c}
  [[[ ]_h^+ \cdots [ ]_{h_k}^+]_{h_{k+1}}^- \cdots [ ]_{h_n}^-]^{\alpha_1}_{h} \rightarrow \\
  [[[ ]_h^+ \cdots [ ]_{h_k}^+]^{\alpha_2}_{h} \\
  [[[ ]_{h_{k+1}}^- \cdots [ ]_{h_n}^-]^{\alpha_3}_{h}
  \end{array}
  \]

- **Non-elementary division:** Membranes with neutral polarization are duplicated
Application of the rules

- Maximal parallel semantics
- At each step, each object and membrane can be the subject of only one rule
- If two conflicting rules can be applied: non–deterministic choice
- When a membrane divides, its content is replicated unchanged in the new copy
- OUTPUT: Symbols that exit from the skin in a halting computation
Computing Power of Membrane Systems

- Systems using a single membrane can only generate length sets of context-free languages.
- Computing power cannot be extended by using an unlimited number of membranes.
- Allowing the dissolution of membranes increases computing power, when at least two membranes are used; universality is not reached.
- To obtain universal systems, further features must be considered: cooperative (non context-free) rules, priorities defining the order of rules application, or structured objects.
- Membranes are necessary to reach universality (one membrane does not suffice).
SAT - Satisfiability for boolean formulas: a boolean formula $\Phi$ in CNF, with

- $n$ boolean variables $x_1, x_2, \ldots x_n$
- $m$ clauses

Question: is there a truth assignment for $x_1, x_2, \ldots x_n$ such that $\Phi$ is true?

Brute force algorithm requires exponential time

SAT is NP–complete
Solving SAT in linear time

\[ [[z_1 \ a_1 a_2 \ldots a_n]_{2}]_1 \]
Solving SAT in linear time

- $[[z_1, a_1a_2\ldots a_n]_2^0]_1^0$
- $[[z_2, T_1, a_2\ldots a_n]_2^0 [z_2, F_1, a_2\ldots a_n]_2^0]_1^0$
Solving SAT in linear time

\[
\begin{align*}
\mathbf{z}_1 & \begin{bmatrix} a_1 & a_2 & \ldots & a_n \end{bmatrix}_0^0 \\
\mathbf{z}_2 & \begin{bmatrix} T_1 \quad a_2 & \ldots & a_n \end{bmatrix}_2^0 \quad \begin{bmatrix} z_2 & F_1 \quad a_2 & \ldots & a_n \end{bmatrix}_2^0 \\
\mathbf{z}_3 & \begin{bmatrix} T_1 \quad T_2 \quad a_3 & \ldots & a_n \end{bmatrix}_2^0 \quad \begin{bmatrix} z_3 & T_1 \quad F_2 \quad a_3 & \ldots & a_n \end{bmatrix}_2^0 \\
& \quad \begin{bmatrix} z_3 \quad F_1 \quad T_2 \quad a_3 & \ldots & a_n \end{bmatrix}_2^0 \quad \begin{bmatrix} z_3 \quad F_1 \quad F_2 \quad a_3 & \ldots & a_n \end{bmatrix}_2^0
\end{align*}
\]
Solving SAT in linear time

- \([[[z_1 \ a_1 a_2 \ldots a_n]_2^0]_1^0]\)
- \([[[z_2 \ T_1 \ a_2 \ldots a_n]_2^0 \ [z_2 \ F_1 \ a_2 \ldots a_n]_2^0]\_1^0]\)
- \([[[z_3 \ T_1 T_2 \ a_3 \ldots a_n]_2^0 \ [z_3 \ T_1 F_2 \ a_3 \ldots a_n]_2^0 \ [z_3 \ F_1 T_2 \ a_3 \ldots a_n]_2^0 \ [z_3 \ F_1 F_2 \ a_3 \ldots a_n]_2^0]\_1^0]\)
- In \(n\) steps we generate all possible truth assignments
In one step we change the polarization of the membranes using $z_n$

\[ [[T_1 T_2 \cdots T_n]_2^+ [T_1 T_2 \cdots T_{n-1} F_n]_2^+ \]
\[ \cdots [F_1 F_2 \cdots F_n]_2^+ ]_1^0 \]
Solving SAT in linear time

- In one step we change the polarization of the membranes using $z_n$
- $\left[ [T_1 T_2 \ldots T_n]^+ [T_1 T_2 \ldots T_{n-1} F_n]^+ \right]_2^+$
  $\ldots \left[ F_1 F_2 \ldots F_n]^+_2 \right]_1^0$
- In one step every symbol $T_i$ (resp. $F_i$) is replaced by some symbols $R_{h_i}$
- $1 \leq h_i \leq m$ is the index of a clause satisfied by setting $x_i = $TRUE (resp. $x_i = $FALSE)
- We obtain, for example,
  $\left[ [R_1 R_3 R_1 R_4 \ldots R_6]^+ [R_7 R_3 R_2 R_3 \ldots R_2]^+ \right]_2^+$
  $\ldots \left[ R_2 R_5 R_1 R_5 \ldots R_1]^+_2 \right]_1^0$
Solving SAT in linear time

- In $2m$ steps we check whether or not a membrane contains all $R_j$, where $1 \leq j \leq m$
- $\begin{bmatrix} [...]_2^- & [...]_2^+ & \cdots & [...]_2^- T & T \end{bmatrix}_1^0$
Solving SAT in linear time

- In $2m$ steps we check whether or not a membrane contains all $R_j$, where $1 \leq j \leq m$
- $[[\ldots]_2^- \ [\ldots]_2^+ \ \ldots \ [\ldots]_2^- T \ T]_1^0$
- After $n + 2m + 2$ steps, eventually a symbol $T$ appears in the skin membrane
- $[[\ldots]_2^- \ [\ldots]_2^+ \ \ldots \ [\ldots]_2^- T]_1^- \ YES$
- If after exactly $n + 2m + 3$ computation steps we obtain a $T$, then a symbol YES is sent out through the skin; otherwise a symbol NO is sent out.
Features of the Solution

- Requires linear time
- Requires exponential space
- The solution proposed is said to be **Semiuniform**: 
  - Every input instance requires a specific membrane system to be computed
  - Given an input instance $x$ of length $n$, the membrane system used to solve it can be generated by a deterministic Turing machine in polynomial time w.r.t. $n$

- The solution is said to be **CONFLUENT**
Determinism vs Non–determinism

- A Membrane System $\Pi$ is said to be **deterministic** if there is at most one possible transition from a configuration to the following one, for all possible configurations.

- A **non–deterministic** Membrane system $\Pi$ is said to be **confluent** if the computations of $\Pi$ are either all accepting or all rejecting. Such a system *accepts* in the former case and *rejects* in the latter.

- When not all computations necessarily agree on the result, the system is called **non-confluent**. Non-confluent systems are said to *accept* when there exists an accepting computation, and to *reject* otherwise.
Complexity classes for **confluent** Membrane systems

\[(N)PMC_T\] : languages decided **IN POLYNOMIAL TIME** by (non–)confluent Membrane systems in the class \(T\)

- \(T = AM\) : systems with both division for elementary and non–elementary membranes
- \(T = EAM\) : systems with division for elementary membranes only
- \(T = NAM\) : systems without membrane division
Basic properties

- $\text{PMC}_T \subseteq \text{NPMC}_T$
- $\text{PMC}_{\text{NA}} \subseteq \text{PMC}_{\text{EA}} \subseteq \text{PMC}_{\text{A}}$
- $\text{NPMC}_{\text{NA}} \subseteq \text{NPMC}_{\text{EA}} \subseteq \text{NPMC}_{\text{A}}$
CONFLUENT P systems without division rules

- $P \subseteq PMC_{\mathcal{N},AM}$
  - "Trick": the DTM deciding $L \in P$ is used to solve DIRECTLY the problem in polynomial time
  - Then, we build a P system with a single membrane containing either an object YES, whenever an input $x \in L$ is given, or NO, otherwise. This requires polynomial time.
  - The P system send out the object in a single step
The opposite is also true:

- \( PMC_{\mathcal{NAM}} \subseteq P \)
  - Idea: simulation of a generic P system \( \Pi \) without membrane division using a DTM \( M \), with a polynomial slowdown
  - We keep track of the NUMBER OF OCCURRENCES of each symbol in each membrane
  - The application of a rule in \( \Pi \) can be simulated by modifying the counters used in \( M \)
We have already seen that SAT is solvable by a family of Membrane systems that make use only of elementary membrane division. It follows: \( NP \subseteq PMC_{EAM} \)

SQRT-3SAT (PP–complete problem) can also be solved by such systems. Hence: \( PP \subseteq PMC_{EAM} \)

Confluent P systems with elementary membrane division can be simulated by Deterministic Turing machines using polynomial space: \( PMC_{EAM} \subseteq PSPACE \)
CONFLUENT systems with both types of division rules

- $PMC_{AM} \subseteq PSPACE$ : can be simulated by DTM in polynomial space

- Quantified SAT (QSAT) - SAT using quantifiers: consider a Boolean expression $\Phi$ in CNF. Question:
  $\exists x_1 \forall x_2 \exists x_3 \forall x_4 \ldots \exists x_n \forall x_n \Phi$?

  - QSAT is PSPACE–complete
  - QSAT $\in PMC_{AM}$
  - $PSPACE \subseteq PMC_{AM}$

- $PSPACE = PMC_{AM}$

- What if we remove dissolving action and polarizations?
  $P = PMC_{AM}(n\delta, nPol)$!!!
Introducing space complexity classes

- Idea: both objects and membrane need physical space
- Let $C_i$ be a configuration of a P system $\Pi$
- $size(C_i)$ is the sum of number of membranes in $\mu$ and the total number of objects they contain
- The space required by a halting computation $C = (C_0, C_1, \ldots, C_m)$ of $\Pi$ is $size(C) = \max\{size(C_0), \ldots, size(C_m)\}$
- The space required by $\Pi$ itself is $size(\Pi) = \max\{size(C) : C \text{ is a halting computation of } \Pi\}$
Some basic result concerning space complexity classes

From results concerning time complexity, it follows immediately:

- \( P \subseteq \text{MCSPACE}_{NAM}(O(1)) \)
- \( NP \cup \text{co-NP} \subseteq \text{EXPMCSPACE}_{EAM} \)
- \( PSPACE \subseteq \text{EXPMCSPACE}_{AM} \)
Space Complexity Results

- **PSPACE**–complete problem Quantified–3SAT can be solved by Membrane–systems with active membranes using a polynomial amount of space
- Membrane–systems with active membranes using a polynomial amount of space can be simulated by Turing machines using polynomial space
- Hence, $PSPACE = PMCSPACE_{AM}$
- Similarly, $EXPSPACE = EXPPMCSPACE_{AM}$
- What about sublinear space?
Sublinear Space Membrane Systems

- Two distinct alphabets: *INPUT* alphabet and *WORK* alphabet
- Input objects cannot be rewritten and do not contribute to the size of a configuration
- Size of a configuration: number of membranes + total number of working objects
- Weaker uniformity condition: $DLOGTIME$-uniformity ($DLOGTIME$ Turing machines)
Power of Sublinear Space Membrane Systems

- Idea: compare with logarithmic space Turing machines (or other equivalent models)
- Two problems if we use "standard" techniques:
  - Need for a polynomial number of working objects (violates log–space condition)
  - Need for a polynomial number of rewriting rules (violates uniformity condition)
- Solution: use polarization both to communicate objects and store information
Power of Sublinear Space Membrane Systems

Each Log–space DTM $M$ can be simulated by a $DLOGTIME$-uniform family $\Pi$ of Membrane systems with active membranes in logarithmic space having:

- A state object $q_{i,w}$: $M$ is in state $q$, input–head on $i$-th symbol, work–head on $w$-th symbol
- $O(\log(n))$ nested membranes (INPUT tape membranes) containing, in the innermost one, the input symbols of $M$
- $O(\log(n))$ membranes to store the work tape of $M$ (WORK tape membranes).
- Two sets of membranes, which size depends on the dimensions of the input and the working alphabets of $M$ (SYMBOL membranes).
To simulate a computation step of $M$

- The state object enters the INPUT membranes: the bits corresponding to the actual position of the INPUT head of $M$ are stored in the polarizations of the INPUT membranes.
- Only the object corresponding to the INPUT symbol actually read can reach the skin.
- The state object identifies the symbol actually under the WORK head.
- The transition of $M$ can be simulated using the SYMBOLS membranes.
Power of Sublinear Space Membrane Systems

- Only a logarithmic number of objects and membranes are required (besides the input objects)
- The family $\Pi$ is $DLOGTIME$-uniform
- Thus: $L$ (class of problems solved by log–space Turing machines) is contained in the class of problems solved by $DLOGTIME$-uniform, log–space Membrane systems with active membranes.
Main resources

► BOOKS:
  ► P. Frisco, Computing with Cells. Advances in Membrane Computing, Oxford University Press, 2009
  ► G. Paun, G. Rozenberg, A. Salomaa (eds.), The Oxford Handbook of Membrane Computing, Oxford University Press, 2010

► INTERNET: P systems web page: http://ppage.psystems.eu