1. **ANTI-MEMBRANES.**

Reminder: rules of types $[]_h \rightarrow []_j []_k$, $[]_h []_{h'} \rightarrow \lambda$; could also be with objects.

A. ALHAZOV, R. FREUND, S. IVANOV: **(Tissue) P Systems with Anti-Membranes**. In Seventeenth Brainstorming Week on Membrane Computing (Orellana-Martín, D.; Păun, Gh.; Riscos-Núñez, A.; Andreu-Guzmán, J. A., Eds.), Sevilla. RGNC report 1/2019, University of Seville, Artes Gráficas Moreno, S.L., 2019, 29-30.
http://www.gcn.us.es/files/17bwmc/029_AntiMembranes.pdf
and
A. Alhazov, R. Freund, S. Ivanov: **P Systems with Anti-Membranes**. In Proceedings of the 20th International Conference on Membrane Computing, CMC20, Curtea de Argeş (Păun, Gh., Ed.). Bibliostar, Râmnicu Vâlcea, 2019, 249-256.
http://membranecomputing.net/cmc20/pdf/procCMC20.pdf#page=250

1) Can we still do anything non-trivial if changing membrane labels is forbidden? Is it possible, e.g., to simulate boolean circuits?
2) What if we forbid changing labels but allow a limited (3?)
number of polarizations? let's say annihilation needs
some form of polarization agreement
3) Descriptional complexity of a small universal NFPAMS
4) Which ingredients are needed to solve SAT with anti-membranes?
5) How we can exploit deeper membrane structures?
For instance, annihilation of nested membranes outside-in performs an ordered sequence of membrane dissolutions.
6) antiMembranes for efficiency? In any way that is not a trivial translation of the previous research from objects to membranes.

2. **CHANNELS.**

For symport/antiport P systems, in tissue case, it is _usually_ assumed that channels do not admit any parallelism. There has been a few exceptions. 1) Some Rudi's talk with PPT slides many years ago, where cells were represented by huge colored circles, I do not remember the title. 2)

A. Alhazov, R. Freund, M. Oswald: **Tissue P Systems with Antiport Rules and Small Numbers of Symbols and Cells**. In: De Felice C., Restivo A. (eds) Developments in Language Theory. DLT 2005. Lecture Notes in Computer Science 3572. Springer, Berlin, Heidelberg, 2005, 100-111.
https://doi.org/10.1007/11505877_9

, where in Ot'P, primed letter t indicated that it was allowed to have distinct channels (i,j) and (j,i). 3) A more recent paper

H. Adorna, A. Alhazov, L. Pan, B. Song: **Simulating Evolutional Symport/Antiport by Evolution-Communication and vice versa in Tissue P Systems with Parallel Communication**. In: Gheorghe M., Rozenberg G., Salomaa A., Zandron C. (eds) Membrane Computing. CMC 2017. Lecture Notes in Computer Science 10725. Springer, Cham, 2018, 1-14.
https://doi.org/10.1007/978-3-319-73359-3_1

relating evolutional symport/antiport with evolution-communication -- in order to make it possible having direct simulation with a slowdown by a factor of a constant, communication needed to be massively parallel. 4) Older research on neural P systems, probably by [Krishna,Rama], long time before spiking… anyway, that last one was quite a different model.
- Parallel VS sequential channels in tP systems.
Improve results with mcre from NP∪co-NP to PSPACE.

3. **GLOBAL** rules,

considered by A.Păun and once briefly by myself. This relates to problem **(Q6)** in Gheorghe's open problem list http://www.gcn.us.es/?q=18bwmc_openproblems . IF membrane structure is static and we do not care about descriptional complexity,

making all rules global does not seem to restrict us at all: objects can always be renamed when moved, so they know where they are ☺
However, the total number of rules in this reduction may increase, and this technique becomes more complicated, or even impossible, with dissolution. BTW, this may open an interesting discussion at solving hard problems in polytime. Besides, not all membranes are ~~created~~ equal: by definition, elementary membrane division is not applicable to membranes that are (currently) non-elementary, and the skin cannot be dissolved or divided (and sometimes it is forbidden for any object to enter it) - this trick _might_ help distinguishing membranes when needed, however, requiring non-determinism or complicated simulation. On the other hand, with sufficient ingredients one working region is already enough, so we should stay in a restricted enough settings.

A. Păun: **On P Systems with Global Rules**. In: Jonoska N., Seeman N.C. (eds) DNA Computing. DNA 2001. Lecture Notes in Computer Science, vol 2340. Springer, Berlin, Heidelberg, 2002, 329-339.
https://doi.org/10.1007/3-540-48017-X_31
A. Alhazov, R. Freund: **On the Efficiency of P Systems with Active Membranes and Two Polarizations**. In: Mauri G., Păun G., Pérez-Jiménez M.J., Rozenberg G., Salomaa A. (eds) Membrane Computing. WMC 2004. Lecture Notes in Computer Science, vol 3365. Springer, Berlin, Heidelberg, 2005,
https://doi.org/10.1007/978-3-540-31837-8_8
A. Alhazov, R. Freund, S. Ivanov: **Length P Systems**. Fundamenta Informaticae 134(1-2), 2014, 17-37.
https://doi.org/10.3233/FI-2014-1088

4. Maximal **CONSISTENCY** modes.
Reminder: here applicability does not only depend on lhs. I have heard about a practical use of this mode in a BWMC2019 discussion from Agustin (though I forgot which application it was for, so I would not know what reference to cite). Usually in membrane computing rule applicability only depends on the left side of the rule (whether all reactants are present in the current configuration, and, possibly, whether some additional conditions are satisfied, e.g., promoters, inhibitors, etc.).

Consider rules changing membrane polarization. Allow to apply multiple rules (maximal parallelism), as long as the polarization in their rhs is the same. Let me call it "polarization agreement". Need to be precise, probably need to choose the polarization corresponding to at least one applied rule, if possible.

Other examples of maximal consistency:

- Parallel string rewriting without conflicts [D. Besozzi], many years ago, reference needed.
- Rudi's target agreement/label agreement, original reference needed.
- Any other shared resource to agree upon?

Overall, I believe this feature deserves more attention.

5. **cP** systems
= P systems with **complex objects**, see [Nicolescu]. Reminder: prolog-like rules using power of term rewriting and unification. Very powerful model, e.g., a solution of the **Travelling Salesman Problem** has been reported with **five** rules only [CooperNicolescu_ACMC2017].
Some longer time ago the colleagues in my institute wanted to attack with P systems the problem of finding Gröbner basis. Unfortunately, the data structures that can be represented and efficiently processed by usual P systems are limited, and hence they are not suited well to work, e.g., with **dynamic ordered lists of strings** (a solution via Turing machine is not elegant). It turns out that cP systems are much more flexible in representing and efficiently processing complicated data structures.

Some problems that have been addressed besides universality/computational completeness and NP-hard problems, by usual P systems:
- sorting https://doi.org/10.1007/3-540-29937-8_8 ,
- dictionary search and update http://univagora.ro/jour/index.php/ijccc/issue/download/44/pdf_165 ,
- inflections http://www.math.md/publications/csjm/issues/v17-n2/10082/ ,
annotating affixes https://doi.org/10.1007/978-3-642-54239-8_7 ,
- firing squad synchronization problem https://doi.org/10.1007/978-3-540-95885-7_9
(more problems and solutions can be found in Applications of Membrane Computing, 2005 and Membrane Computing Handbook).

Need: more problems that are practical, well defined and sufficiently simple (simpler than Gröbner basis), to be attacked by cP systems, but not completely trivial (needing, say, more than two rules).