Networks of Bio-Inspired Processors. An introduction

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Networks of Bio-Inspired Processors. An introduction

A NBP is a computational model which

... is inspired by biological aspects (darwinian evolution, DNA recombination, etc.)

... is computationally complete (it has the computation power of a Turing machine)

... is parallel and distributed

... solves NP-complete problems in "polynomial" time

Networks of Bio-Inspired Processors. An introduction

Devetome

NRDe

	r systems	NDFS
Computationally complete and universal	OK	OK
Parallel and distributed	OK	OK
Works with strings	OK	OK
Hardware implementations	OK+KO	OK + KO
Works with multisets of data	OK	OK
Software simulators	OK	OK + KO
In vitro/in vivo implementations	KO	KO
Efficient solutions to hard problems	OK	OK

From NEPs to P Systems → Evolutionary P systems (Mitrana, Sempere 2009)
From P Systems to NBPs → Open problem

Some bioinspired operators over strings and languages

Insertion Insert a symbol into a string

aaaaa 🛨 aabaaa

Deletion Delete a symbol from a string

aabaaa 🗕 aaaaa

Substitution (mutation) Substitute a symbol into a string

aaaaa 🗲 aabaa

Splicing Splicing rules $r=(u_1#u_2$v_1#v_2)$

r=(a#a\$b#b) (abcdaa,bbabcd) → (abcdababcd,ba)

Crossover Full massive splicing with empty context | $aa \bowtie bb \rightarrow \lambda$, bb, abb, aabb, aab, ...

Hairpin completion Hairpin completion from folded strings

Superposition Complementarity completion from double stranded strings

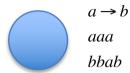
loop and double loop recombination DNA recombination based on gene assembly

inversion, duplication and transposition DNA fragments modification (operations on substrings)

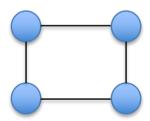
... etc, etc.

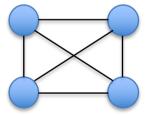
The ingredients to define a Network of Bioinspired Processors

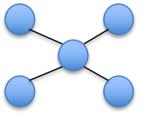
A finite set of processors that apply operations over strings which have been inspired by biomolecular functions and operations in the nature. The processors work with a multiset of strings.



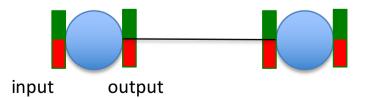
A connection topology between processors in the form of a network.

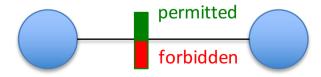






A set of (input/output) filters which can be attached to the processors or to the connections.

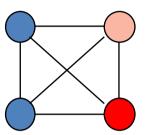




How does the network work?

(I) Evolutionary/genetic/splicing steps

$$C_i \Rightarrow C_{i+1}$$



- Every rule that can be applied is massively applied
- No competition between rules. All the rules are applied by using different copies

(II) Communication steps

$$C_i \mapsto C_{i+1}$$

- Every processor sends all the filtered strings to its neighbours
- Every processor receives and stores filtered strings
- Strings that are sent but not received are lost

(III) Network at work

$$C_0 \Rightarrow C_1 \mapsto C_2 \Rightarrow C_3 \mapsto C_4 \dots$$

Towards a full general model ...

First: Generalize the operations in the processors



Second: Generalize the filter positions



Towards a full general model ...

A <u>bio-inspired processor</u> over *V* is a 5-tuple (*op,PI,FI,PO,FO*), where:

op is a biologically inspired operation over stringsPI,FI⊆ V are the input permitting/forbidding contexts of the processor

PO,FO⊆ V are the output permitting/forbidding contexts of the processor

- op encapsulates the operation parameters
- PI,FI,PO and FO can be empty so the filters are attached to the connections

Accepting Networks of Bio-Inspired Processors

$$\Gamma = (V, U, G, N, \beta, \gamma, x_I, x_O)$$

where

V and U are the input and network alphabets $G=(X_G,E_G)$ is an undirected graph without loops $N: X_G \to BP_U$ associate a bio-inspired processor to every node in $G \to \{s,w\}$ associates a filter predicate to every node $\gamma: E_G \to 2^U \times 2^U$ associates a filter (P_e,F_e) to every edge in the graph x_I,x_O are the input and output nodes

References

Networks of Evolutionary Processors

- J.Castellanos, Carlos Martín-Vide, Victor Mitrana, José M.Sempere. Networks of evolutionary processors.
 Acta Informatica 39, pp 517-529. 2003.
- M. Margenstern, V. Mitrana, M.J. Pérez-Jiménez. Accepting hybrid networks of evolutionary processors. In Proceedings of the International Meeting on DNA Computing, DNA 10, LNCS Vol. 3384, pp 235-246.
 Springer. 2005.

Networks of Splicing Processors

- F. Manea, C. Martín-Vide, V. Mitrana. Accepting networks of splicing processors. In Proceedings of the First Conference on Computability in Europe, CiE 2005, LNCS Vol. 3526, pp 300-309. Springer. 2005.
- F. Manea, C. Martín-Vide, V. Mitrana. Accepting networks of splicing processors: complexity results.
 Theoretical Computer Science 371, pp 72-82. 2007.

Networks of Genetic Processors

- M. Campos, José M. Sempere. Accepting networks of genetic processors are computationally complete Theoretical Computer Science Vol. 456, pp 18-29. 2012
- M. Campos, José M. Sempere. A Characterization of Formal Languages through Networks of Genetic Processors (submitted)