

Svetlana Cojocaru
(in honour of her 60th anniversary)



Our colleague, Vice Editor-in-Chief of the Computer Science Journal of Moldova and director of the Institute of Mathematics and Computer Science of Academy of Sciences of Moldova, dr.hab. Svetlana Cojocaru accomplishes in July a beautiful age. All her career is linked to the Institute, where she came after graduating from State University of Moldova, reaching today the head of the institute. She is known as a profound scientist, with extensive interests in computer science and mathematics.

Even at the first steps of research she achieved important results, which find their application today too. She is an honest person, friendly and well-wishing. We are confident that these qualities have helped her to become a recognized leader in the domains that she professes.

At editorial board' call several colleagues from different countries presented papers to form an edition dedicated to Mrs.dr.hab. Svetlana Cojocaru. To our gladness, there have been so many papers and they are so good, that we decided to publish them in two consecutive numbers (N2 and N3, V.20, 2012).

We address cordial greetings to our colleague and wish her new achievements and successes.

Editorial board of the "Computer Science Journal of Moldova"

Languages and P Systems: Recent Developments

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Abstract

Languages appeared from the very beginning in membrane computing, by their length sets or directly as sets of strings. We briefly recall here this relationship, with some details about certain recent developments. In particular, we discuss the possibility to associate a control word with a computation in a P system. An improvement of a result concerning the control words of spiking neural P systems is given: regular languages can be obtained as control words of such systems with only four neurons (and with usual extended rules: no more spikes are produced than consumed). Several research topics are pointed out.

1 Introduction

Basically, membrane computing is associated with multiset processing in the compartments defined by a membrane structure, hence with handling *numbers* encoded in a *unary* manner, by means of the multiplicity of given objects, represented by symbols of an alphabet. However, from the very beginning, [22], also P systems were considered whose objects are strings. While the multisets of objects are processed by biochemical or biological inspired rules (similar to reactions taking place among the chemicals in a cell, or by other operations, such as symport and antiport), the string objects should be processed by specific rules, such as rewriting, splicing (from DNA computing), replication. However, also in the case of symbol objects we can “compute” (generate, accept or translate) strings and languages, and we find this case particularly

interesting, taking into account the qualitative difference between the “internal data structure”, the multiset, and the “external data structure”, the string (hence with a positional information). That is why in what follows we only discuss this case, of symbol objects P systems handling languages.

For P systems with string objects we refer to the corresponding chapter of [31] and to the current bibliography of membrane computing from [38]. It is important to note, however, that P systems with string objects can have interesting applications in natural language processing; we refer only to [1], but researches of the same group should be followed in this respect.

In what follows, we assume that the reader is familiar with basic facts in membrane computing, including definitions of the main classes of P systems: cell-like P systems with symbol objects (called here *transition P systems*), P systems with active membranes, symport-antiport P systems, spiking neural P systems (in short, SN P systems). Details can be found in [23], [31], and at [38]. We also assume some familiarity with basic elements of formal language theory, e.g., from [34]. Some notations will be also given below; we only mention now that *REG*, *LIN*, *CF*, *CS*, *RE* denote the families of regular, linear, context-free, context-sensitive, and recursively enumerable languages, respectively, and that V^* is the set of all strings over the alphabet V , the empty string, λ , included.

Informal presentations of the four classes of P systems are given below, in order to facilitate the understanding of the subsequent sections.

A *transition P system* uses rules of the form $u \rightarrow v$, where u and v are strings over a given alphabet O of objects, representing multisets; the intuition is that the objects in the multiset [represented by] u are consumed and those in v are produced, like in a (bio)chemical reaction. The objects in v can have associated *target indications*, in the forms $(a, here)$, (a, in) , (a, out) ; the meaning is that the object a produced by applying the rule remains in the same compartment of the membrane structure if *here* is associated with it, it goes to a mem-

brane immediately inside the compartment where the rule is used, or it goes outside this compartment, in the surrounding compartment, if the indications *in* or *out* are associated, respectively. Note that the objects are processed inside compartments, by local rules, but they can travel across membranes, due to the target indications. In particular, an object (a, out) produced in the external membrane of a P system (also called skin membrane) leaves the system and it “gets lost” in the environment.

Rules of the general form $u \rightarrow v$ are called *cooperative*. If u consists of a single object, then the rule is said to be *non-cooperative*. The intermediate case of rules $ca \rightarrow cv$, where a and c are objects, with c taken from a distinguished subset C of O , is the *catalytic* case.

In *P systems with active membranes*, the membranes themselves are part of rules and can evolve during a computation. The objects can evolve inside compartments (by cooperative, catalytic or non-cooperative rules) and can pass across membranes, while membranes can get divided, dissolved, separated, etc.

In P systems with symport-antiport rules the objects pass across membranes by rules of the forms (u, in) , (u, out) (symport rules), and $(u, out; v, in)$ (antiport rules), where u, v are strings in O^* (representing multisets of objects). The rules are associated with the membranes, the objects are never modified, they are just moved from a compartment to another one.

Starting from an initial configuration (the membrane structure and the multisets placed in its compartments), and using the rules in a specified way (synchronously or unsynchronously, in the maximally parallel way, sequentially, etc.), we get *transitions* among configurations; a sequence of transitions forms a *computation*; a computation which reaches a configuration where no rule can be applied is said to be *halting*. In all the previous cases, the most natural result of a computation is a number, for instance, of objects present in the halting configuration in a specified membrane.

In what follows, always the P systems work in the maximally parallel manner.

Finally, an *SN P system* consists of a set of *neurons* placed in the nodes of a directed graph and sending signals (*spikes*, denoted in what follows by the symbol a) along *synapses* (arcs of the graph). The objects evolve by means of *spiking rules*, which are of the form $E/a^c \rightarrow a; d$, where E is a regular expression over $\{a\}$ and c, d are natural numbers, $c \geq 1, d \geq 0$. The meaning is that a neuron containing k spikes such that $a^k \in L(E), k \geq c$, can consume c spikes and produce one spike, after a delay of d steps. This spike is sent to all neurons to which a synapse exists outgoing from the neuron where the rule was applied. There also are *forgetting rules*, of the form $a^s \rightarrow \lambda$, with the meaning that $s \geq 1$ spikes are forgotten, provided that the neuron contains exactly s spikes. If rules can produce more than one spike, i.e., they are of the form $E/a^c \rightarrow a^p; d$, with E, c, d as above and $1 \leq p \leq c$, then the system is said to be *extended*. (Note that the number p of produced spikes cannot be greater than the number c of consumed spikes.) In the initial configuration, each neuron contains a given number (it can be zero) of spikes.

The system works in a synchronized manner, i.e., in each time unit, the rule to be applied in each neuron is non-deterministically chosen, each neuron which can use a rule should do it, but the work of the system is sequential in each neuron: only (at most) one rule is used in each neuron. One of the neurons is considered to be the *output neuron*, and its spikes are also sent to the environment. The moments of time when a spike is emitted by the output neuron are marked with 1, the other moments are marked with 0. This binary sequence is called the *spike train* of the system – it might be infinite if the computation does not stop. The *result of a computation* can be the spike train itself (a binary string if the computation halts, or an infinite sequence otherwise) or a number (e.g., the distance between the first two spikes sent into the environment by the output neuron of the system).

If a spiking rule $E/a^c \rightarrow a * p$ has $L(E) = a^c$, then we write it in the simpler form $a^c \rightarrow a^p$ (and we call it *finite*).

Four ways to associate a language with a P system were considered so far:

1. external output,
2. using a P system in the accepting mode,
3. following the trace of a distinguished object through the membrane structure,
4. control words.

We shortly present them below, with some details in the case of control words, and then we propose some ideas for further research.

It should be noted that the references we give here are not meant to be complete or to indicate the first place where a notion was introduced, but only to offer a good introduction to this research area.

A *general research topic* can already be formulated here: consider systematically the 4×4 combinations of (basic) types of P systems and ways to associate a language with a P system. Not all of these 16 possibilities were explored (but we cannot say in advance that any of them is of no interest). In particular, equivalences between some of the 16 combinations would be nice to be found.

2 External Output

Introduced already in [30], for transition P systems, the idea is simple: because objects can exit a P system (of any type), we (the user, the observer) can “wait in the environment” and arrange the symbols which leave the system in a sequence. If the computation halts, then we obtain a string, if not, we obtain an infinite sequence. An important detail: we have to decide what to do in the case when several objects leave the system at the same time. In [30] and several subsequent papers, all permutations of the symbols are allowed, hence several strings are associated with the same computation. An interesting possibility is to disregard certain symbols and/or to associate a single symbol to a multiset (by means of a given “interpretation mapping”), like in [12].

Somewhat surprisingly, in spite of its simple definition, defining a language in the external output manner was not too much investigated

– at least not until last years, when a systematic study was started in [3], [4], mainly for transition P systems with non-cooperative rules (and no further ingredients; in [30], catalytic rules and membrane dissolution rules are used, as well a priority relation among them). The obtained family lies in between *REG* and *CS* and has interesting (combinatorial) properties.

The spike train of an SN P system can also be considered as the result of a computation defined in the external mode, but, having only one object, we have to assign different symbols to the time units when (at least) a spike exits the system and to the time units when no spike is emitted. In this way, a binary string (or sequence, when the computation does not stop) is obtained. There are several papers in the SN P systems area dealing with such languages.

The external output is not very much investigated for symport-antiport systems, and we know no paper of this kind dealing with P systems with active membranes. Also, as far as we know, the case when only computations which send out at most one object in each step was not investigated (this condition imposes a restriction on the accepted computations, hence the computing power of P systems can be altered in this way).

3 P Automata

This is indeed a much investigated topic in membrane computing – but mainly for the symport-antiport case. The idea is simple (symmetric to the external output): we arrange in a sequence the symbols which enter a P system, again with the two possibilities, to consider all permutations of symbols which enter in the same step (see [21] and its bibliography), or to consider an encoding of multisets by symbols (see a survey and references in [12]).

For symport-antiport P systems the “reading” of symbols from the environment is naturally defined by means of symport and antiport rules associated with the skin membrane. This is also provided by rules with active membranes, but we know no study about this issue for such systems. For transition P systems and for SN P systems we have to

input symbols in an “external manner” (an external user provides a string, symbol by symbol, according to its wish). In most cases, a string is accepted if the computation halts (there are also other ways to define successful computations, such as local halting, reaching final configurations, but we do not discuss them here).

This way of using P systems is also related to the use of P systems to solve decidability problems, where an input is introduced in the system and the problem (an instance of it) has a positive answer if the computation halts (and a special object is sent to the environment), however, in this case the input (an encoding of the instance of the problem) is introduced in the form of a multiset, placed in a distinguished membrane. Details can be found in [32].

A recent variant of P automata was introduced in [26], called *dP automata*: several (symport-antiport) systems are connected to each other by means of antiport-like rules; they read separately strings from the environment, process them, also communicating, and if the computation halts, then the concatenation of the input strings is accepted. This is a way to introduce more distribution in P systems, making explicit the splitting of a problem among the components of the dP automaton. There are several papers devoted to this topic, see, e.g., [27], [28], [37]. The idea was extended also to SN P systems, in [19]; in this context, also a dual of spiking rules is introduced, in the form of *request rules* (depending on the contents of a neuron, spikes can be brought in from the environment, that is, the spikes come in *by request*, not introduced by an external user).

4 Traces

The idea was introduced in [18] for symport-antiport P systems, investigated in a couple of papers (see [17] and its bibliography), and extended to SN P systems in [7]: distinguish an object and follow its path across membranes; the sequence of membrane labels visited by that object provides a string (in the case of SN P systems, one single spike is distinguished, it is always used by a spiking rule applied in the neuron where the marked spike resides and one of the produced spikes

becomes marked). We know no paper dealing with traces in transition P systems and in P systems with active membranes.

5 Control Words

Finally, the fourth way to associate a string with a computation is to consider *control words*, as sequences of labels of rules used in the steps of a computation.

This is a well investigated topic in formal language theory, especially for Chomsky grammars, because in each step such grammars use only one rule. Each derivation produces a control word; the set of all control words associated with all terminal derivations in a grammar is called the *Sziland* language associated with (generated by) the grammar. The things become more complicated in the case of parallel computing devices, when several rules are used simultaneously.

This is the case also in membrane computing, and probably this is the reason why control words were, up to our knowledge, never considered in this area (until the special case proposed in [33]). However, a sort of bidimensional control word was introduced already in [10], under the name of *Sevilla carpet*, as a way to describe the rules used in a computation and their multiplicity in each step, but not as a way to define a control language associated with the computations in a P system.

A possible solution to the above difficulty is to consider a sequence of multisets of labels, those labels associated with all rules applied in a given step. Then, a string of symbols can be obtained following the ideas also used for accepting P systems: take a function from multisets to strings and build the string(s) obtained by concatenating the strings associated with the multisets. For instance, all permutations of the labels in a multiset can be considered, as in [21], or only one specific string (maybe a symbol) associated with the multiset, like in [12].

Another idea was recently introduced in [33], starting from the following restriction: all rules used in a computation step should have the same label, or they can also be labeled with λ .

The definition in [33] is given for SN P systems, but it works for any type of P systems.

Indeed, let us consider a P system Π , of any type, with the total set of rules (the union of all sets of rules associated with compartments, membranes, neurons – as it is the case) denoted with R . Consider a labeling mapping $l : R \rightarrow B \cup \{\lambda\}$, where B is an alphabet. We consider only transitions $s \xRightarrow{b} s'$, between configurations s, s' of Π , which use only rules with the same label b and rules labeled with λ . We say that such a transition is *label restricted*. With a label restricted transition we associate the symbol b if at least one rule with label b is used; if all used rules have the label λ , then we associate λ to this transition. Thus, with any computation in Π starting from the initial configuration and proceeding through label restricted transitions we associate a (control) word. The language of control words associated with all label restricted halting computations in Π is denoted by $Sz_\lambda(\Pi)$. The subscript indicates the fact that λ steps are permitted; in the opposite case, we write $Sz(\Pi)$ (the label restricted transitions which cannot use only rules with label λ are called λ -label restricted).

We give here two results for symport-antiport P systems. The family of languages $Sz(\Pi)$ associated with symport-antiport P systems with at most m membranes is denoted with $SzSAP_m$; when λ moves are allowed, we write $Sz_\lambda SAP_m$, and if the number of membranes is not bounded, then the subscript m is replaced with $*$.

In what follows we need the characterizations of regular languages by means of *regular grammars*. Such a device is a construct $G = (N, T, S, P)$, where N, T are disjoint alphabets (the nonterminal and the terminal one, respectively), $S \in N$ (the axiom), and P is a finite set of rewriting rules of the forms $A \rightarrow aB, A \rightarrow a$, where $A, B \in N$ and $a \in T$; a rule $S \rightarrow \lambda$ can be added, if we also want to generate the empty word. The language generated by G is denoted with $L(G)$. Without any loss of generality we may assume that the grammar is *reduced*: each $A \in N$ can be reached from S and can derive a terminal string.

When comparing two language generating or accepting devices G_1, G_2 , the empty string is ignored, that is, $L(G_1)$ is considered equal

to $L(G_2)$ as soon as $L(G_1) - \{\lambda\} = L(G_2) - \{\lambda\}$. Thus, no λ -rule is necessary in our regular grammars.

Theorem 5.1 $REG \subset SzSAP_1$.

Proof. The inclusion is easy to prove: for a regular grammar $G = (N, T, S, P)$ with $N = \{A_1 = S, A_2, \dots, A_n\}$, we consider the antiport rules $b : (A_i, out; A_j, in)$ associated with $A_i \rightarrow bA_j \in P$ and the symport rules $b : (A_i, out)$ associated with $A_i \rightarrow b \in P$. Initially, the single membrane of the system contains the object A_1 . Clearly, each terminal derivation in G corresponds to a halting computation in the system we have constructed, and conversely.

The inclusion is strict; actually, we have a stronger result: $SzSAP_1 - CF \neq \emptyset$. A P system proving this assertion is

$$\begin{aligned} \Pi &= (O, []_1, e, O, R_1), \text{ where:} \\ O &= \{a_1, a_2, e, f, g, h\}, \\ R_1 &= \{a : (e, out; ea_1a_2, in), a : (e, out; fa_1a_2, in), \\ &\quad b : (fa_1, out; f, in), b : (fa_1, out; g, in), \\ &\quad c : (ga_2, out; g, in), c : (ga_1, out; h, in), \\ &\quad d : (ha_1, out; ha_1, in), d : (ha_2, out; ha_2, in)\}. \end{aligned}$$

The ‘‘carrier’’ e brings inside $n \geq 1$ copies of a_1 and a_2 , then f and g remove copies of a_1 and a_2 , respectively. Eventually, the object h is introduced in the system. If any copy of a_1 or a_2 is still present in the system, then the computation never halts, because the rules with label d can be used forever. Therefore, the control words associated with terminal computations are of the form $a^n b^n c^n$, for some $n \geq 1$, hence $Sz(\Pi)$ is not context-free. \square

If steps when only rules with label λ are allowed, then all one-letter recursively enumerable languages can be generated.

Theorem 5.2 *If $L \subseteq a^*$, $L \in RE$, then $L \in Sz_\lambda SAP_1$.*

Proof. A language $L \in a^*$ is in *RE* if and only if its length set is a recursively enumerable set of numbers. Symport-antiport P systems with one membrane (and rules with no restricted complexity) can generate all recursively enumerable sets of numbers, [31]. Take such a system Π , namely, one which simulates a register machine $M = (n, H, l_0, l_h, I)$ (the number of registers, the set of instruction labels, the label of the initial instruction, the label of the halt instruction, the set of instructions, labeled with elements of H ; simulating register machines is the usual way to prove the universality of symport-antiport P systems, so the reader is assumed to be familiar with such proofs). In the halting configuration, the system contains k copies of a symbol a_1 , which encodes the contents of register 1 of M , the one where the number is generated, as well as the object l_h , for $k \in N(M)$. Assume that all rules of Π are labeled with λ , and add the following rules $a : (l_h a_1, out; l_h, in)$. This rule must be used for each copy of a_1 present in the system, hence the control word of the computation in the augmented system – let us denote it by Π' – is a^k . The halting label l_h is introduced only in the last step of a computation in Π . Consequently, $L = Sz_\lambda(\Pi')$. \square

In the previous results we have imposed no restriction on the length of the symport and antiport rules; if such restrictions are considered, then a larger number of membranes is expected to be necessary.

The control words associated with transition P systems and with systems with active membranes remain to be investigated. In what follows we consider the case of SN P systems.

6 Control Words for SN P Systems

The fact that λ steps increase the power of systems is also confirmed for the control words associated with SN P systems, a case which is investigated in [33]. Let $SzSNP_m$, $Sz_\lambda SNP_m$ be the families of all languages $Sz(\Pi)$, $Sz_\lambda(\Pi)$, respectively, associated with SN P systems Π (with extended rules) with at most m neurons; if the number of neurons is not restricted, then we replace the subscript m by $*$. In [33] it is proved that $Sz_\lambda SNP_* = RE$, but $SzSNP_* \subset CS$, strict inclusion

(an example of a language not in $SzSNP_*$ is the linear language $\{xx^R \mid x \in V^*\}$, where V is an alphabet with at least two symbols and x^R is the reversal/mirror image of the string x). Moreover, a theorem is given in [33] stating that each regular language L is the λ -label restricted Szilard language of an SN P system Π – with the mentioning that the system Π uses extended rules of the form $E/a^c \rightarrow a^p$ without the restriction $p \leq c$ and it has arbitrarily many neurons. This result will be improved in the next theorem.

We give first an example, also improving a result from [33], where it is shown that $SzSNP_6$ contains non-context-free languages. We prove that four neurons suffice.

Consider the SN P system (with four neurons, $\sigma_1, \sigma_2, \sigma_3, \sigma_4$)

$$\begin{aligned} \Pi &= (\{a\}, \sigma_1, \sigma_2, \sigma_3, \sigma_4, syn), \text{ where:} \\ \sigma_1 &= \sigma_2 = (2, \{r_1 : a^2 \rightarrow a^2, r_2 : a^2 \rightarrow a\}), \\ \sigma_3 &= (1, \{r_2 : (a^4)^+ a/a \rightarrow a, r_3 : (a^4)^+ a^2/a^4 \rightarrow a\}), \\ \sigma_4 &= (1, \{r_2 : (a^4)^+ a/a \rightarrow a, r_4 : (a^4)^+ a^2/a^4 \rightarrow a\}), \\ syn &= \{(1, 2), (2, 1), (1, 3), (1, 4), (2, 3), (2, 4)\}. \end{aligned}$$

The system is given in a graphical form in Figure 1. Each neuron contains initially one or two spikes, but only σ_1 and σ_2 can fire. If the rules r_2 are used in σ_1 and σ_2 (not also in σ_3, σ_4 , because we do not have here enough spikes), then the computation halts. Let us assume that for a number n of steps we use the rule r_1 in σ_1 and σ_2 . Neurons 1 and 2 exchange spikes to each other and, together, they send four spikes to each of σ_3, σ_4 . These neurons cannot use the rules r_3, r_4 until getting inside an even number of spikes, and this means that the rules r_2 in σ_3, σ_4 were used. This however supposes that also σ_1, σ_2 use the rules r_2 (these rules are applicable, hence they must be applied), and this ends the work of these neurons. After using the rules r_2 , neurons 3 and 4 can fire nondeterministically, but not both at the same time: they have to use the rules r_3 and r_4 , which have different labels. After using the rules r_2 , each of σ_3 and σ_4 contains the same number of spikes, namely $4n + 2$, hence, besides the string r_2 , $Sz(\Pi)$ contains strings of

the form $r_1^n r_2 w$, with $w \in \{r_3, r_4\}^*$ containing the same number of r_3 and r_4 . This language is not context-free, hence $SzSNP_4 - CF \neq \emptyset$.

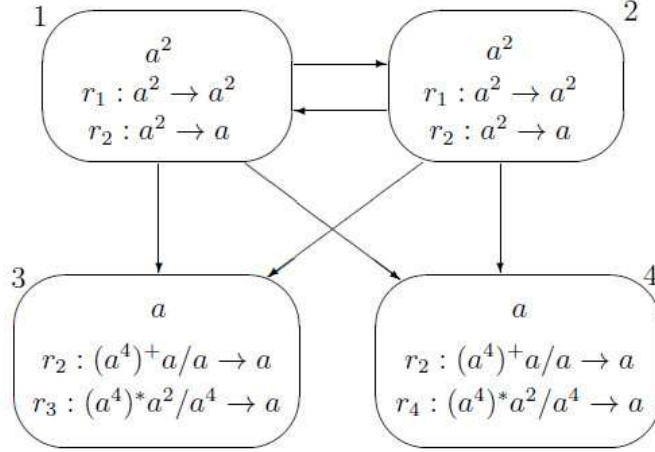


Figure 1. An SN P system whose Szilard language is not context-free.

We give now the improvement of the mentioned result from [33].

Theorem 6.1 $REG \subset SzSNP_4$.

Proof. In view of the previous example, it is enough to prove the inclusion $REG \subseteq SzSNP$. To this aim, let us consider a regular language L generated by a reduced regular grammar $G = (N, T, S, P)$ with $N = \{S = A_1, A_2, \dots, A_n\}$ and the rules in P of the forms $A_i \rightarrow bA_j$, $A_i \rightarrow b$, for some $A_i, A_j \in N$ and $b \in T$. Let us denote $J = \{1, 2, \dots, n\}$.

We construct the following SN P system of degree 4 (together with the rules we also specify their labels):

$$\begin{aligned} \Pi &= (\{a\}, (a^{2n+1}, R_{12}), (0, R_{12}), (a^{2n+1}, R_{34}), (0, R_{34}), syn), \\ R_{12} &= \{b : a^{2n+i} \rightarrow a^j \mid A_i \rightarrow bA_j \in R, i, j \in J\} \\ \cup &\{b : a^{2n+i} \rightarrow a^{2n} \mid A_i \rightarrow b \in R, i \in J\}, \end{aligned}$$

$$R_{34} = \{a^{2n+k} \rightarrow a^{2n} \mid k \in J\},$$

$$syn = \{(1, 2), (2, 1), (1, 4), (4, 1), (2, 3), (3, 2), (3, 4), (4, 3)\}.$$

The system is also given in a graphical form in Figure 2. Note that it is finite and uses no forgetting rule.

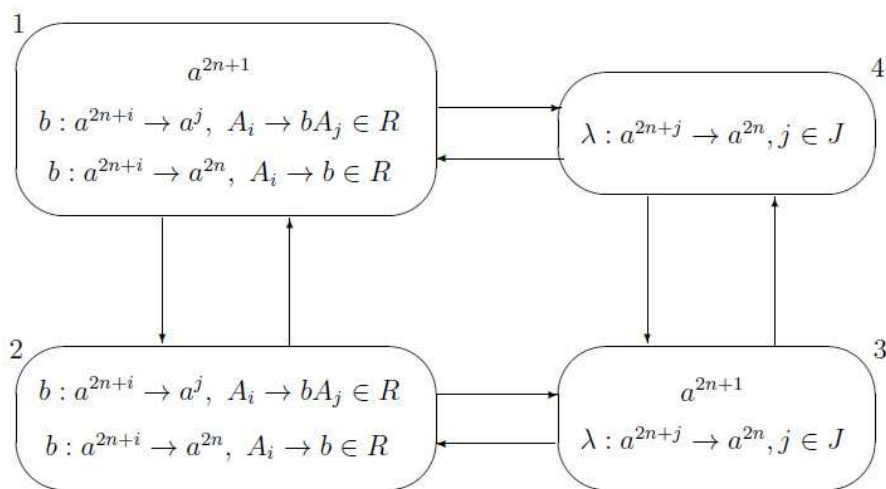


Figure 2. An SN P system whose control language is a given regular language

In the first step, neurons 1 and 3 can fire; in the next step, neurons 2 and 4 fire – and the computation proceeds in steps which alternate the previous pairs of neurons. When a pair of neurons fires, then no spike remains inside these neurons, but the other pair receives spikes. This means that in each step a rule with a label $b \in T$ and one with the label λ are used (hence the computation is λ -label restricted).

With each nonterminal $A_i, 1 \leq i \leq n$, we have associated $2n + i$ spikes; initially, we have in neurons 1 and 3 spikes which identify the nonterminal $S = A_1$.

Assume that either σ_1, σ_3 , or σ_2, σ_4 contain spikes, namely $2n + i$ in σ_1, σ_2 , for a rule $A_i \rightarrow bA_j \in R$, and $2n + k$ in σ_3, σ_4 , for some

$k \in J$. The rule $A_i \rightarrow bA_j$ is simulated by using the rule (with label b) $a^{2n+i} \rightarrow a^j$ in σ_1, σ_2 , simultaneously with using the rule (with label λ) $a^{2n+k} \rightarrow a^{2n}$ in σ_3, σ_4 . The symbol b is added to the control word, and the process is continued with the simulation of a rule $A_j \rightarrow u \in R, u \in T \cup TN$.

In the moment when a (terminal) rule $A_i \rightarrow b \in R$ is simulated, the active σ_1 or σ_2 introduces $2n$ spikes, at the same time with $2n$ spikes produced by the paired neuron σ_3, σ_4 . Two neurons are empty, the other two contain $4n$ spikes, hence no rule can be applied in any neuron. The computation halts, having as its control word the word generated by the derivation in G . Consequently, $Sz(\Pi) = L(G)$, which concludes the proof. \square

We do not know whether the number of neurons in the previous theorem can be decreased.

7 Controlled P Systems

In the previous sections, the control words were collected in order to have a new way of producing a language starting from a P system. The computations cannot proceed freely, but they should be label restricted or λ -label restricted. This restriction has an influence on the computing power of P systems, considered as number computing devices. Indeed, let us consider the following systems:

$$\begin{aligned} \Pi_1 &= (\{a, b\}, []_1, a, \{r_1 : a \rightarrow aa, r_2 : a \rightarrow b\}, 1), \\ \Pi_2 &= (\{a, b\}, []_1, a, \{a, b\}, \{r_1 : (a, out; aa, in), r_2 : (a, out; b, in)\}, 1). \end{aligned}$$

When only label restricted transitions are allowed, the two rules of each system cannot be used at the same time, hence we obtain $N_{lr}(\Pi_1) = N_{lr}(\Pi_2) = \{2^n \mid n \geq 0\}$ (we have added the subscript lr in order to indicate that only label restricted computations are allowed). This set of numbers cannot be generated by non-cooperative transition P systems, neither by symport-antiport P systems of this complexity (one membrane, two rules) with non-restricted computations.

A more general case is the one when a pair (Π, C) is considered, where Π is a P system of any type, with the rules labeled by elements of an alphabet H and $C \subseteq H^*$ is a given language. This language is used in order to restrict the computations in Π : only label restricted computations are allowed whose control words are in C . (This corresponds to controlled context-free grammars in regulated rewriting.)

The study of controlled P systems remains to be done (combining classes of P systems with types of control languages, as already done for Chomsky controlled grammars). It is expected that a control language provides a powerful way to “program” the work of a P system.

8 Final Remarks

Many research topics were mentioned in the previous sections, many others remain to be explored. For instance, we have said nothing about tissue-like P systems – is anything interesting in this case from the language computing point of view? How this case compares with the four types of P systems considered above?

Another direction of investigation concerns sets of infinite sequences (also called ω -languages). Some results were reported in [15] for symport-antiport P systems, and in [29] and [14] for SN P systems.

A related issue was considered in [35]: handling languages over infinite alphabets.

Besides the previous ways to associate a language with a P system, also other ideas were preliminarily explored. One of them is to encode a string in the membrane structure itself, and then handling the membrane structure means processing the string; see [5] for some details.

For all families of languages which are not equal to RE it makes sense to consider the classic problems investigated in formal language theory: closure properties, decidability, representation theorems, semi-linearity, and so on. Also, the membership complexity is of interest (an issue considered already in [2]). In view of possible applications in modeling aspects related to natural languages, it would be of interest to find ways to generate *mildly context-sensitive languages* (semi-

linear, parsable in polynomial time, powerful enough to cover some non-context-free constructions in natural languages).

A related research direction concerns the translation of languages. Some attempts were reported in [11] and [25].

We can conclude with the observation that many things were done in membrane computing in handling languages by means of P systems with symbol objects, but a lot of work still remains to be carried out.

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Self-Stabilization in Membrane Systems*

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Abstract

In this paper we study a notion of self-stabilization, inspired from biology and engineering. Multiple variants of formalization of this notion are considered, and we discuss how such properties affect the computational power of multiset rewriting systems.

1 Introduction

Membrane systems, also called P systems, are a framework for (bio-inspired) computational models, see [9], [10] and [14]. In this paper we consider a one-region rewriting model with symbol objects. In this case, membrane computing can be considered as (maximally parallel or sequential) multiset processing. In general, a computation is a sequence of transitions between configurations. Configurations are multisets, and the transitions are induced by rules, defined by reactants, products and control (additional applicability conditions, if any), viewed as formal computational systems (generating/accepting numeric/vector sets, or computing functions).

We will call a property dynamic if it depends on the behaviour of a system and cannot be easily derived from its description (as opposed to syntactic properties). Given any finite computation, we assume that the property is easily verifiable. The two usual sources of undecidability are a) that we do not always know whether we are dealing with finite

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or infinite computations, and b) that some properties are defined on infinite number of computations (due to non-determinism, to the initial input or to some other parameter). In the case of this paper, another source of potential undecidability is the finite set to be reached as given in the definitions below.

Since in this paper we will deal with reachability issues, we would also like to mention the connection with temporal logic [5].

Self-stabilization is a known concept in conventional distributed computing, introduced by E. Dijkstra in [4], as well as in systems biology, but not yet considered in the framework of membrane computing. Other works on self-stabilization are [12], [1], [7], [13], [6], [3], to name a few. It has been recalled by Jacob Beal during the Twelfth Conference in Membrane Computing, CMC12, and an attempt to formalize it in the membrane computing framework has been done in [2]. The underlying idea is the tolerance of natural and engineering systems to perturbations. The formulation from [15] says:

A system is self-stabilizing if and only if:

1. Starting from any state, it is guaranteed that the system will eventually reach a correct state (convergence).
2. Given that the system is in a correct state, it is guaranteed to stay in a correct state, provided that no fault happens (closure).

In case of inherently non-deterministic systems, “with probability 1” should be added. Based on this concept, we propose to consider a few formal properties, following the discussion below.

In this paper we consider fully cooperative multiset rewriting, possibly with promoters/inhibitors/priorities, operating either in the maximally parallel or the sequential mode. We consider a single working region only, for two reasons. First, the properties of interest are unaffected by flattening the static membrane structure. Second, we would currently like to avoid the discussion about reachability related to “arbitrary configurations” with dynamic membrane structure.

2 Definitions

We assume the reader to be familiar with the basics of formal language theory, e.g., we refer to [11].

An *alphabet* is a finite non-empty set V of abstract *symbols*. The free monoid generated by V under the operation of concatenation is denoted by V^* ; the *empty string* is denoted by λ , and $V^* \setminus \{\lambda\}$ is denoted by V^+ . The family of all finite (recursive, recursively enumerable) sets of positive integers is denoted by $NFIN$ ($NREC$, NRE , respectively).

2.1 Membrane systems

A one-region (rewriting) membrane system is a tuple

$$\Pi = (O, w, R),$$

where O is a finite alphabet, $w \in O^*$ is a string representing the initial multiset, and R is a set of rules of the form $r : u \rightarrow v$, $u \in O^+$, $v \in O^*$.

A configuration of the system is represented by a multiset of objects from O contained in the region, and a rule $r : u \rightarrow v$ is applicable if the current configuration contains the multiset specified by u . Furthermore, applicability may be controlled by promoters ($r : u \rightarrow v|_a$), inhibitors ($r : u \rightarrow v|_{-b}$), or priorities ($r' > r$). Throughout the paper, we will use the word *control* to mean that at least one of these three features is allowed. In such cases, in addition to the availability of u for a rule r to be applicable, the promoter a must be present in the current configuration, the inhibitor b has to be absent in the current configuration, and no rule r' with higher priority than r is allowed to be applicable, respectively.

A computation step in the sequential mode consists of the non-deterministic application of one applicable rule, replacing its left side with its right side. In the maximally parallel mode, multiple applicable rules have to be applied multiple times, to disjoint submultisets, in a non-deterministic way, possibly leaving some objects idle, under the condition that no further rule is applicable to them. The computation step is denoted by the binary relation \Rightarrow . A computation halts when no rule is applicable to the current configuration (halting configuration).

For a generating system, the result of a halting computation is the total number of objects in the system when it halts. The set of numbers generated by a P system is the set of results of its computations. An accepting system is described as (O, Σ, w, R) , where Σ is an input alphabet: instead of w , the computation starts with wx , $x \in \Sigma^*$, and its result is $|x|$ if it halts. The set of numbers accepted by a P system is the set of results of its computations for all $x \in \Sigma^*$.

2.2 Self-stabilization and related properties

We now resume the discussion started at the end of the Introduction.

Clearly, “a correct state” should be rephrased as “a configuration in the set of correct configurations”. Moreover, we would like to eliminate the set of correct states, let us denote it by S , as a parameter. We say that our property holds if there exists some finite set S of configurations satisfying the conditions 1 and 2 above. Since membrane systems are inherently non-deterministic, we additionally propose two weaker degrees of such a property: possible (there exists a computation satisfying the conditions), almost sure (the conditions are satisfied with probability 1 with respect to non-determinism). Finally, if condition 2 is not required, we call the corresponding property (finite) set-convergence instead of self-stabilization. We now give the formal definitions from [2].

Definition 1 *A P system Π is possibly converging to a finite set S of configurations iff for every configuration C of Π there exists a configuration $C' \in S$ such that $C \Rightarrow^* C'$.*

Definition 2 *A P system Π is (almost surely) converging to a finite set S of configurations iff for every configuration C of Π the computations starting in C reach some configuration in S (with probability 1, respectively).*

Definition 3 *A P system Π is possibly closed with respect to a finite set S iff for every non-halting configuration $C \in S$ there exists a configuration $C' \in S$ such that $C \Rightarrow C'$.*

Definition 4 *A P system Π is closed with respect to a finite set S iff for every non-halting configuration $C \in S$ $C \Rightarrow C'$ implies $C' \in S$.*

We say that a system is **(possibly, almost surely) set-converging** if it is (possibly, almost surely, respectively) converging to some finite set of configurations.

We say that a system is **possibly self-stabilizing** if it is possibly converging to some finite set S of configurations and if it is possibly closed with respect to S .

We say that a system is **(almost surely) self-stabilizing** if it is (almost surely, respectively) converging to some finite set S of configurations and if it is closed with respect to S .

The examination of computational aspects of these properties motivates us to add “weakly” to the properties proposed in [2] – *(possibly, almost surely) converging, (possibly) closed, (possibly, almost surely) set-converging, (possibly, almost surely) self-stabilizing* – if the corresponding conditions over configurations C only span the **reachable non-halting** ones.

Another comment we can make on “almost sure” is that such a property may depend on how exactly the transition probability is defined. The easiest way is to assign equal probabilities to all transitions from a given configuration. Alternatively, to a transition via a multiset of rules $r_1^{n_1} \cdots r_m^{n_m}$ we may assign the weight of a multinomial coefficient $\binom{n_1 + \cdots + n_m}{n_1, \dots, n_m} = \frac{(n_1 + \cdots + n_m)!}{n_1! \cdots n_m!}$, which will make the corner cases less probable than the average ones. There can be other ways to define transition probabilities, but we would like to discuss the properties of interest without fixing a specific way. We assume the transition probabilities in an independent subsystem are the same as if it were the entire system.

An important assumption we impose on the probability distribution is that *the probability of each transition is uniquely determined by the associated multiset of rules and by the set of all applicable multisets of rules*, yet it does not depend on the objects that cannot react, or by the previous history of the computation.

2.3 Register machines

In what follows we will need to simulate register machines; here we briefly recall their definition and some of their computational properties. A *register machine* is a tuple $M = (m, B, l_0, l_h, P)$, where m is the number of registers, P is the set of instructions bijectively labeled by elements of B , $l_0 \in B$ is the initial label, and $l_h \in B$ is the final label. The instructions of M can be of the following forms:

- $l_1 : (ADD(j), l_2, l_3)$, with $l_1 \in B \setminus \{l_h\}$, $l_2, l_3 \in B$, $1 \leq j \leq m$
Increase the value of register j by one, and non-deterministically jump to instruction l_2 or l_3 . This instruction is called *increment*.
- $l_1 : (SUB(j), l_2, l_3)$, with $l_1 \in B \setminus \{l_h\}$, $l_2, l_3 \in B$, $1 \leq j \leq m$
If the value of register j is zero then jump to instruction l_3 , otherwise decrease the value of register j by one and jump to instruction l_2 . The two cases of this instruction are called *zero-test* and *decrement*, respectively.
- $l_h : HALT$. Stop the execution of the register machine.

A register machine is *deterministic* if $l_2 = l_3$ in all its *ADD* instructions. A *configuration* of a register machine is described by the contents of each register and by the value of the program counter, which indicates the next instruction to be executed. Computations start by executing the first instruction of P (labelled with l_0), and terminate with reaching a *HALT*-instruction.

Register machines provide a simple universal computational model [8]. Register machines can be used as *accepting* or as *generating* as well as as decision devices. In accepting register machines, a vector of non-negative integers is accepted if and only if the register machine halts having it as input. Usually, without loss of generality, we may assume that the instruction $l_h : HALT$ always appears exactly once in P , with label l_h . In the generative case, we start with empty registers and take as results of all possible halting computations. Being used as decision devices, register machines may halt in an accepting state with label l_{yes} or in a rejecting state l_{no} , respectively. In the following,

we shall call a specific model of P systems *computationally complete* if and only if for any register machine M we can effectively construct an equivalent P system Π of that type simulating each step of M in a bounded number of steps and yielding the same results.

3 Results

3.1 Accepting systems

For the following theorem we consider any computationally complete model of P systems as defined above, e.g., a model with maximally parallel multiset rewriting or with controlled sequential multiset rewriting.

Theorem 1 *If a model of P systems yields a computationally complete class, then the weakly self-stabilizing subclass accepts exactly NREC.*

Proof. For any recursive number set there is a register machine M with one accepting state q_{yes} and one rejecting state q_{no} , deciding it. We modify the register machine in order to obtain a register machine M' which, once the decision is made, i.e., q_{yes} or q_{no} has been reached, erases the workspace and then enters q'_{yes} or q'_{no} respectively, thereby halting in q'_{yes} if and only if the input is accepted or performing an infinite loop with $q'_{no} : (SUB(1), q'_{no}, q'_{no})$ if and only if the input x is rejected. This register machine M' now can be simulated with a P system Π , which by construction starts with a configuration representing the input x and will either end with halting in a configuration representing the state q'_{yes} or else looping in a configuration representing the state q'_{no} , i.e., Π is weakly self-stabilizing.

Conversely, consider a self-stabilizing P system Π , i.e., for each input x , Π performs a computation that ends up in a configuration from a finite set S and then cannot reach any other configuration outside S . Now consider the derivation graph for all possible computations of Π on the input x , i.e., the nodes of this directed graph represent the configurations and the edges indicate the derivation steps from one configuration to the next one during one of these computations. As the number of configurations directly derivable from any configuration

in Π is finite, this derivation graph is a connected directed graph with finite degree (from each node, only a finite number of edges is leaving); moreover, this graph cannot have a simple path (a path visiting each node at most once) which is infinite, as every computation in Π has to reach a configuration (node) from S and then cannot leave the set of configurations S any more. Due to König's lemma¹, the total number of nodes (configurations) in the derivation graph must be finite. Hence, even without knowing the set S , the bruteforce algorithm computing all possible transitions from the initial configuration, but halting as soon as the system halts or a configuration already passed previously is reached, yields a decision procedure for the set accepted by Π . \square

Strengthening this result by removing “weakly” is problematic, even if more powerful P systems are used. Indeed, self-stabilization also from unreachable configurations would need to handle not only the configurations without any state or with multiple states (which could be handled with the joint power of maximal parallelism and priorities), but also configurations representing a situation with only one state which is not the initial state of the underlying register machine. We have to leave this question open.

Theorem 2 *If a model of P systems yields a computationally complete class, then the weakly almost surely self-stabilizing P systems of this class accept exactly NRE.*

Proof. We start with the construction from Theorem 1. We want to show that relaxing the property “weakly self-stabilizing” to “almost surely” leads from recursiveness to computational completeness. It suffices to handle the case when the system rejects the input by never halting. We modify the underlying register machine as follows: add a non-deterministic transition from every state $p \in Q$ to a new state e , from e erase the contents of all registers and then jump

¹König's lemma: Let G be a connected graph with finite degree. If G contains an infinite number of nodes, then it contains an infinite simple path.

back to e ; this will not affect the accepting power, but it will provide a self-stabilizing path from any reachable non-halting configuration. The transition from p to e can be done by $p : (ADD(j), e, e)$, since the registers then are emptied anyway. Furthermore, the basic model of register machines does not allow non-determinism other than $p : (ADD(j), q, r)$. The branching at ADD instructions may be done by assuming the original computation to be deterministic and replacing $p : (ADD(j), q, q)$ by $p : (ADD(j), q, e)$. The branching at a SUB instruction $p : (SUB(j), q, r)$ may be done by the sequence of rules $p : (ADD(j), e, p')$, $p' : (SUB(j), p'', p'')$, $p'' : (SUB(j), q, r)$.

The probability that the computation does not self-stabilize for more than k steps decreases exponentially with respect to k . Indeed, the simulation of a register machine by P system has bounded parallelism, each instruction is simulated in a bounded number of steps, and at least one path leads to self-stabilization. Moreover, there only exists a finite number of different sets of applicable multisets containing a branching from the simulation into the self-stabilization path, so the minimum probability for this self-stabilization path is strictly positive. These observations conclude the proof. \square

Theorem 3 *If a model of P systems yields a computationally complete class, then the class of all almost surely self-stabilizing maximally parallel/sequential P systems with priorities accepts exactly NRE.*

Proof. Given a set L from NRE , we first construct a P system Π simulating a register machine M accepting L and then extend Π to a P system Π' even fulfilling the condition of almost surely self-stabilizing.

Let $M = (m, B, l_0, l_h, P)$ a deterministic register machine accepting L . We now construct the P system $\Pi = (O, l_0, R, >)$ with priorities accepting L :

$$\begin{aligned}
 O &= B \cup \{a_i \mid 1 \leq i \leq m\}, \\
 R &= \{l_1 \rightarrow a_j l_2 \mid l_1 : (ADD(j), l_2) \in P\} \\
 &\quad \cup \{a_j l_1 \rightarrow l_2, l_1 \rightarrow l_3 \mid l_1 : (SUB(j), l_2, l_3) \in P\} \\
 > &= \{a_j l_1 \rightarrow l_2 > l_1 \rightarrow l_3 \mid l_1 : (SUB(j), l_2, l_3) \in P\}.
 \end{aligned}$$

The contents of a register i , $1 \leq i \leq m$, is represented by the number of symbols a_i in Π . The state l of the register machine is represented by the corresponding symbol l in Π , too. When M halts in l_h with all registers being empty, Π also halts with the configuration $\{l_h\}$. Obviously, Π accepts L , both in the sequential as well as in the maximally parallel mode.

To strengthen the result to even non-weak almost sure self-stabilization, we have to take into account the non-reachable configurations, too. The almost surely self-stabilizing P system $\Pi' = (O', l_0, R', >')$ with priorities accepting L is constructed as follows:

$$\begin{aligned}
 O' &= B \cup \{a_i \mid 1 \leq i \leq m\} \cup \{e\}, \\
 R' &= \{l_1 \rightarrow a_j l_2 \mid l_1 : (ADD(j), l_2) \in P\} \\
 &\cup \{a_j l_1 \rightarrow l_2, l_1 \rightarrow l_3 \mid l_1 : (SUB(j), l_2, l_3) \in P\} \\
 &\cup \{a_i \rightarrow e \mid 1 \leq i \leq m\} \cup \{ex \rightarrow e \mid x \in O'\} \cup \{e \rightarrow e\} \\
 &\cup \{l \rightarrow e \mid l \in B \setminus \{l_h\}\} \cup \{ll' \rightarrow e \mid l, l' \in B\}, \\
 >' &= \{a_j l_1 \rightarrow l_2 > l_1 \rightarrow l_3 \mid l_1 : (SUB(j), l_2, l_3) \in P\} \\
 &\cup \{ex \rightarrow e > r, ll' \rightarrow e > r \mid l, l' \in B, x \in O', r \in R\} \\
 &\cup \{l \rightarrow e > a_i \rightarrow e \mid l \in B \setminus \{l_h\}, 1 \leq i \leq m\} \\
 &\cup \{r > e \rightarrow e \mid r \in R' \setminus \{e \rightarrow e\}\}.
 \end{aligned}$$

In addition to the idea of the construction given in the proof of Theorem 2 using the exit e by applying a rule $l \rightarrow e$, $l \in B \setminus \{l_h\}$, it suffices to self-stabilize from the configurations with no state and from the configurations with multiple states of the register machine. Multiple states can be reduced by the rules $ll' \rightarrow e$, $l, l' \in B$. If no state symbol is present, then we may exit with one of the rules $a_i \rightarrow e$, $1 \leq i \leq m$. All remaining cases can be captured by the rules $ex \rightarrow e$, $x \in O'$. By construction, the self-stabilizing set S equals $\{\{l_h\}, \{e\}, \emptyset\}$. The whole construction again is valid for the sequential as well as the maximally parallel mode. \square

An open question is whether priorities in Theorem 3 can be replaced by promoters or inhibitors.

3.2 Generating systems

Theorem 4 *Any finite set M of numbers can be generated by some self-stabilizing membrane system without control.*

Proof. Consider a P system $\Pi = (\{s, a\}, s, R)$, where

$$R = \{s \rightarrow a^n \mid n \in M\} \cup \{a^{\max(M)+1} \rightarrow \lambda, ss \rightarrow s\}.$$

It is not difficult to see that Π generates M and (taking $S = \{a^n \mid n \leq \max(M)\} \cup \{s\}$) it is self-stabilizing. \square

Since self-stabilization implies set-convergence and closure, and relaxing either property (to possibly, almost surely and/or weakly) does not compromise the construction of the P system described in the proof of Theorem 4, the lower bound on the generative power of associated systems restricted to any property we have defined, is at least *NFIN*.

Lemma 1 *A possibly finite set-converging system only generates finite sets.*

Proof. By Definition 1, for a system possibly converging to a set S , S contains all halting configurations. Since S is finite, so is the set of all the halting configurations. Hence, at most *NFIN* is generated. \square

Theorem 5 *Any of the following classes of P systems $\mathbf{dpOP}^{\mathbf{m}}(\mathbf{c})$ generate exactly *NFIN*:*

- d** is possibly/almost surely/ -
- p** is self-stabilizing/finite set-converging
- m** is maximally parallel/sequential
- c** is uncontrolled/with promoters/with inhibitors/with priorities.

Proof. The claims directly follow from Theorems 4 and 5. \square

We now proceed to weak properties of generative systems.

Theorem 6 *Weakly almost surely self-stabilizing P systems generate exactly *NFIN*.*

Proof. The lower bound is shown by Theorem 4. Now take a weakly self-stabilizing P system Π , and its associated set S from the definition of the property. Consider an arbitrary halting computation of Π . Let C be the configuration of Π one step before the halting. Interpreting finite set-convergence for C implies that the halting configuration belongs to S . Since the halting computation has been arbitrarily chosen, the set of all halting configurations is a subset of S , and hence it is finite. Therefore, the set generated by Π is finite, too. \square

Theorem 7 *If a model of P system yields a computationally complete class, then weakly possibly self-stabilizing subclass generates NRE.*

Proof. Consider the construction from Theorem 2, but for a generative P system. The simulation of the underlying register machine is carried out until some point. Unless the P system has already halted, it always has a choice to self-stabilize and loop. \square

4 Conclusions

We have presented some results (some of them summarized in Table 1) concerning the notion of self-stabilization, recently proposed for membrane computing. Its essence is reachability and closure of a finite set.

Property	comput. complete	(sequ/maxpar) +pri	Thm
self stabilizing	acc. $?/F$		-/5
almost surely s.s.	acc. $?/F$	acc. NRE/F	3/5
possibly s.s.	acc. $?/F$	acc. NRE/F	3/5
weakly s.s.	acc. $NREC/F$		1/6
weakly almost surely s.s.	acc. NRE/F		2/6
weakly possibly s.s.	acc. $NRE/gen. NRE$		2/7

Table 1. Results (letter F stands for “generate exactly $NFIN$ ”).

One of the questions we proposed is whether priorities may be replaced by promoters or inhibitors in Theorem 2. Another open question is the power of accepting with unrestricted self-stabilization, even if maximal parallelism is combined with priorities (a comment after Theorem 1 and the first question mark in the table above). The other open questions are also marked with question marks in the table above. Any system in the corresponding classes must (besides doing the actual computation) converge (definitely, in probability or possibly) to some finite set from anywhere, without using the joint power of maximal parallelism and control.

We mention two topics that we did not deal with here. One is considering the finite set as a parameter, possibly leading to a discussion in model checking. The other one concerns reachability questions in dynamic membrane structures.

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Usability in Scientific Databases

Ana-Maria Suduc, Mihai Bîzoi, Florin Gheorghe Filip

Abstract

Usability, most often defined as the ease of use and acceptability of a system, affects the users' performance and their job satisfaction when working with a machine. Therefore, usability is a very important aspect which must be considered in the process of a system development. The paper presents several numerical data related to the history of the scientific research of the usability of information systems, as it is viewed in the information provided by three important scientific databases, Science Direct, ACM Digital Library and IEEE Xplore Digital Library, at different queries related to this field.

Keywords and phrases: usability, information systems, scientific databases

1 Introduction

Bragge et al. [1] show how the computer-supported research can facilitate the literature review and critical evaluation. Suduc et al. [2] noticed that many international scientific databases offer, on queries, a wide range of information (authors, publications, subjects, etc.), based on results of the query performed. These information are, usually, quite comprehensive to gain a "big picture" perspective on the research activity of that field. Suduc et al. [2] also noticed that this method of computer-aided research profiling substantially minimizes the data processing time comparing to the method used by [1] [3] [4] [5].

This paper aims at presenting and evaluating the information provided by three scientific databases, namely ACM Digital Library, IEEE

Xplore Digital Library, and Science Direct, to various queries concerning the usability of information systems with a view to identifying the trends in the evolution in time of the interest for this research field.

2 Usability concept

According to ISO 9241-11 (1988) and ISO 9241-171 (2008), for a product to be usable and accessible users should be able to use it to achieve their goals in an acceptable amount of time, and be satisfied with the results [6]. The new draft standard ISO/IEC CD 25010.2 (2008) proposes a more comprehensive breakdown of quality in use into usability in use, flexibility in use, and safety.

Usability in use corresponds to the ISO 9241-11 definition of usability as effectiveness, efficiency, and satisfaction. The *effectiveness* is provided if the user can successfully and correctly fulfil his objectives. The assistance quality within the interface can have a great impact on the effectiveness. The interface should be as informative as possible [7]. *Efficiency* can be described as the speed (with accuracy) in which users can complete the tasks for which they use the product [8]. *Satisfaction* is composed of comfort (overall physiological or emotional responses to use of the system) and acceptability of use (overall attitude towards the system, or the user's perception of specific aspects) [9].

Flexibility in use is a measure of the extent to which the product is usable in all potential contexts of use, including accessibility. Safety is concerned with minimising undesirable consequences [6].

During the process of designing and implementing information systems, sequences of decisions should be made with respect to the choice of the most adequate alternatives concerning several critical aspects, such as system orientation, composition of the team, method to be adopted, IT&C tools to be utilized, resources to be allocated and so on [10]. During this process there should be made the design decision that determines the usability of the system [11]. Therefore, usability expertise and knowledge is crucial in the projects. In any software project, there should be considered five essential usability characteristics [12]: (1) *learnability* – rapidly begin working with the system; (2) *efficiency*

– user high level of productivity; (3) *memorability* – no necessity to relearn everything after a period of not using the system; (4) *low error rate* – fewer and easily rectifiable errors while using the system, and no catastrophic errors occur; and (5) *satisfaction* – a system pleasant to use.

Systems that are difficult to use lead to business costs and losses. As shown in [13] if the system is difficult to use, people either won't use it at all or if they will eventually use it they will do so to the less extent possible, or they will waste unnecessary time. In addition more technical support and/or more technical changes and adaptations would be necessary.

There are good reasons to evaluate the usability in the design process of a product such as (a) a deeper understanding of the user needs and (b) to set the stage for product improvement in order to provide a better user experience.

3 Usability evolution

Usability concern is part of human being, but “the field of usability research really came into being when the tools we used started to run up against our cognitive and physical limitations” [14]. The term usability started to be used around 1980s in order to replace the term “user friendly” which “had acquired a host of undesirably vague and subjective connotations” [15].

Usability has evolved from “representing a relatively simple utilitarian concern for task performance into a highly complex notion of a contextualised human experience, also including emotional and social aspects” [16].

According to [14], it was the aviation engineers who started to think about usability seriously in order to reduce human errors of aviators. M. Soegaard [17] identifies the origins of the concept of usability in the falling prices of computers in the 1980s, when for the first time in the human history, it was feasible for many employees to have their own personal computer and, therefore, usability became a key goal for the design of any interactive software that would not have been used by

trained technical computer specialists. According to [18], the usability profession can be associated with the work of John Whiteside at DEC (Digital Equipment Corporation) and John Bennett at IBM. During the late 1980s, they published a number of chapters and papers on the topic of “usability engineering”. With their work they stressed a quantitative but practical engineering approach to product design. They stressed the importance of the work context in creating usable and functional products to improve productivity. They stressed also that it is useful to integrate usability specialists in the design and implementation team who aims at obtaining the best solution for the allocated resources [10]. At present, the terms “usable” and “usability engineering” are used to describe well-designed products and the process by which they should be designed [18].

The current understanding of usability evolved from its meaning of the starting days of the “usability movement” in the 1980s and the researches have ever more focused on usage contexts. “Usage quality no longer appeared to be a simple issue of how inherently usable an interactive system was, but how well it fitted its context of use” [17].

4 Method and Results

In order to identify a trend of the evolution, in time, of the interest for the usability research field, a study has been conducted in May, 2012. The study consisted in several queries, related to the usability research filed, on three major scientific databases, ACM Digital Library, IEEE Xplore Digital Library and Science Direct. Therefore, first, there have been searched all the scientific materials which contained the “usability” term in title, then in abstract and at the end in keywords. Second, there have been searched all the scientific materials which contained the “usability” word and also one of the following terms: “information system” or “information systems” or software.

Table 1 presents the number of the scientific materials contained by the three analysed scientific databases at 25th of June 2010 [19] and at 9th of May 2012. Comparing the numbers of materials at almost two years distance, it can be noticed that the databases increased in

content with good percentages: ACM Digital Library with almost 24% (365,331 items), IEEE Xplore Digital Library with 20% (527,853 items) and Science Direct with 12% (1,183,521 items).

Table 1. The numbers of scientific materials contained by ACM Digital Library, IEEE Xplore Digital Library and Science Direct

Database	Scientific materials (25 th of June 2010)	Scientific materials (9 th of May 2012)
ACM Digital Library	1,529,482	1,894,813
IEEE Xplore Digital Library	2,651,920	3,179,773
Science Direct	10,236,351	11,419,872

Table 2 shows the results of the queries performed: the number of scientific materials, contained by each of the three databases, which has (a) “usability” or (b) “usability” and “information system” or “information systems” or “software”, in title, abstract and keywords. The results show that there are not too many scientific materials which contain “usability” and “information system” or “information systems” or “software” in title or abstract but there are much more which contain “usability” in abstract, title or keywords fields.

Table 2. The numbers of scientific materials which contains the specified terms in title, abstract or keywords, indexed by ACM Digital Library, IEEE Xplore Digital Library and Science Direct

Searched term Database	Title		Abstract		Keywords
	Usability	Usability AND (“information system” OR “information systems” OR “software”)	Usability	Usability AND (“information system” OR “information systems” OR “software”)	
ACM Digital Library	2810	203	9700	2118	3309
IEEE Xplore Digital Library	940	134	5367	3771	679
Science Direct	582	43	2471	430	553

Comparing to the total number of the items in the scientific databases, the materials which contain the searched terms represents only a small part. For example in ACM Digital Library 0.511% of the scientific materials contains usability in abstract, in IEEE Xplore Digital Library 0.168% and in Science Direct 0.021%.

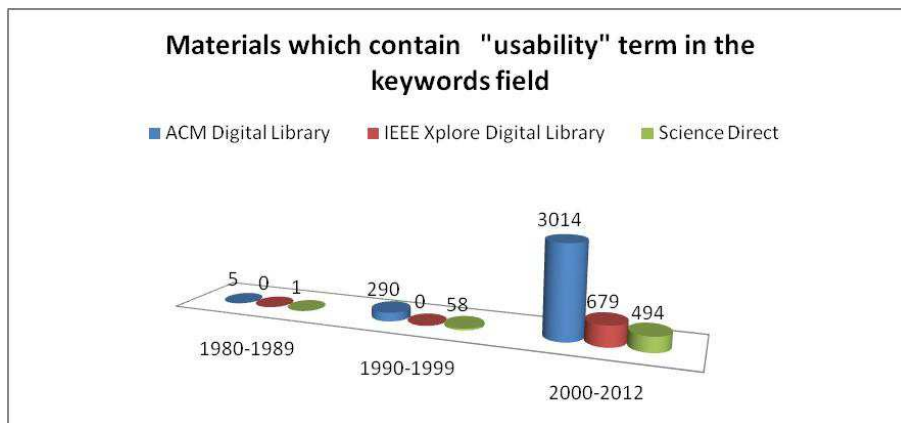


Figure 1. The number of scientific materials, per decades, included in ACM Digital Library, IEEE Xplore Digital Library and Science Direct, which contains "usability" term in the keywords field (on 9th of May 2012)

Because the keywords of a paper capture the main topics of the scientific material, there have been analysed the materials which contain usability as keyword. Therefore, Figure 1 presents the number of scientific materials in the usability research field in three periods of time: 1980-1989, 1990-1999 and 2000-2012. The results show clearly that this research area started in 80's, continued in 90's and increased a lot in the last twelve years.

Figures 2, 3 and 4 present the evolution in the last 12 years of the numbers of scientific materials, with "usability" as keyword, which are included in the three analysed scientific databases. The figures show an increasing interest for the usability research field.

Because the study was made in May 2012, it is obvious that the

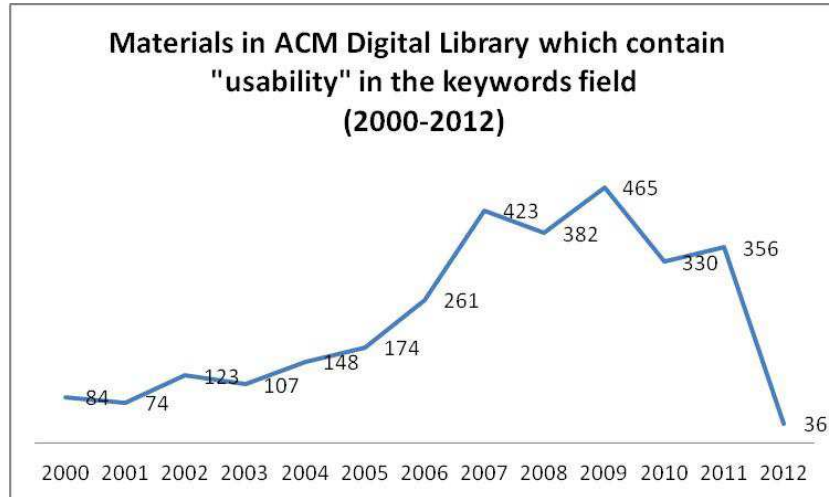


Figure 2. The number of scientific materials, published in the last 12 years and included in ACM Digital Library, which contains "usability" term in the keywords field (on 9th of May 2012)

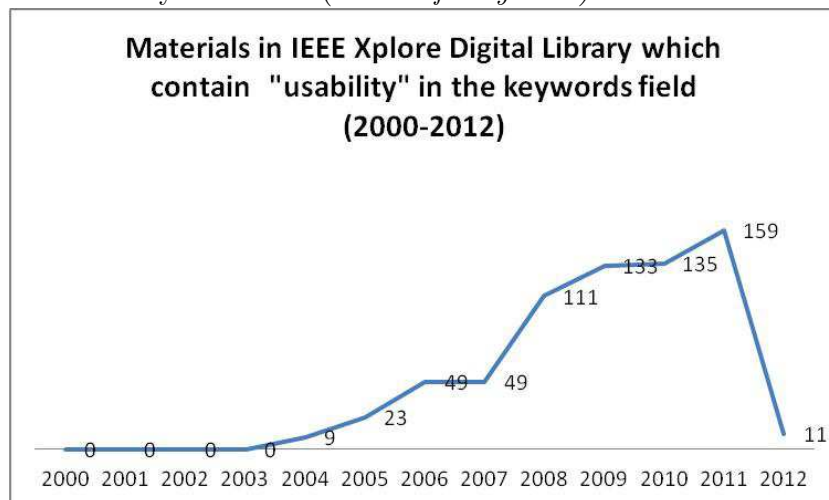


Figure 3. The number of scientific materials, published in the last 12 years and included in IEEE Xplore Digital Library, which contains "usability" term in the keywords field (on 9th of May 2012)

values for 2012 are only partially relevant. Also for 2011, the values might be influenced by the databases updating process for that year, which might be still ongoing.

ACM Digital Library and IEEE Xplore Digital Library, at any search, give the list of the authors of the scientific materials returned as results of the search. Science Direct does not offer such a list. Table 3 presents the top ten authors with the highest number of scientific materials in the usability research field included in ACM Digital Library and IEEE Xplore Digital Library.

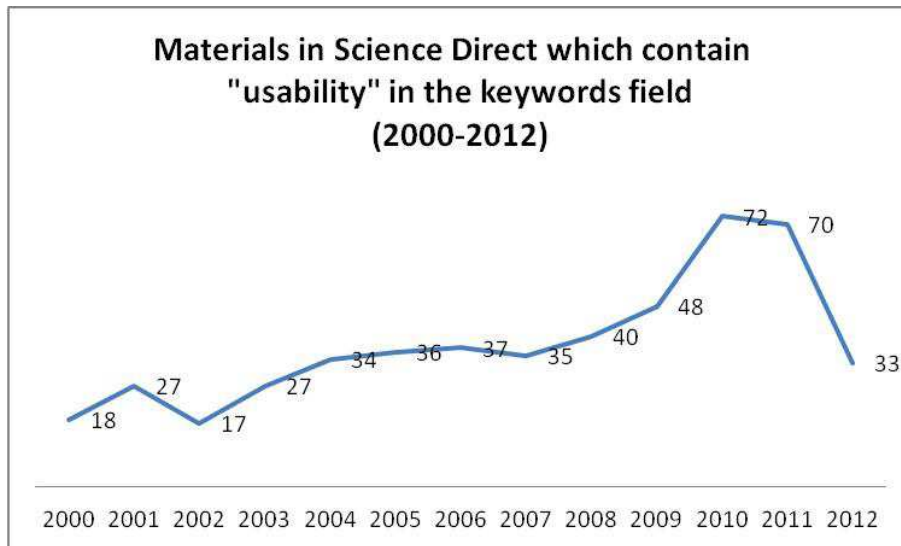


Figure 4. The number of scientific materials, published in the last 12 years and included in Science Direct, which contains "usability" term in the keywords field (on 9th of May 2012)

Table 3. The list of the first ten authors with the highest number of scientific materials published and included in ACM Digital Library and IEEE Xplore Digital Library, scientific materials which has “usability” term as keyword

ACM Digital Library		IEEE Xplore Digital Library	
Author	Number of scientific materials	Author	Number of scientific materials
Andreas Holzinger	29	Azizah Jaafar	8
Kasper Hornbaek	25	Suziah Sulaiman	7
Barbara Leporini	23	Cristian Rusu	6
Stephanie Rosenbaum	23	Silvana Roncagliolo	6
Marina Buzzi	21	John M. Carroll	5
Ann Blandford	17	Liang Lu	5
Bonnie E. John	17	Dimitrios Rigas	5
Jakob Nielsen	15	Bekim Fetaji	5
Jonathan Lazar	15	Majlinda Fetaji	5
Rolf Molich	14	Deng Xiaoling	5

All of these authors are researchers with wide experience and large number of scientific papers in human computer interaction area. For example Andreas Holzinger, the author with the highest number of scientific articles with “usability” as keyword in ACM Digital Library, in his online CV¹, presents himself as the author of more than 300 publications and as a researcher very involved in the HCI research area (e.g. he is chair of the Workgroup Human–Computer Interaction and Usability Engineering (HCI&UE) of the Austrian Computer Society (OCG) and founder and leader of the Special Interest Groups HCI4MED and HCI4EDU).

Therefore, a top of authors with the highest number of scientific articles which contain specific terms might be very useful for any researcher in order to identify people with similar research interests.

Table 4 presents the first ten publications (journals/proceedings) which contains articles in the usability research field. The publication with the highest number of papers in the usability field is *Interacting with Computers* (101 papers in Science Direct and 42 in ACM Digital Library), followed by *International Journal of Human-Computer Studies* (53 papers in Science Direct and 50 in ACM Digital Library) and *Proceedings of the SIGCHI conference on Human factors in computing systems* (52 papers in ACM Digital Library). Thus, a top of the publications with scientific articles which contain specific terms is also useful in order to identify the representative publications for a specific research filed.

¹<http://user.meduni-graz.at/andreas.holzinger/holzinger/>

Table 4. The list of the publication names with the highest number of scientific materials published and included in ACM Digital Library, IEEE Xplore Digital Library and Science Direct, scientific materials which has “usability” term as keyword

ACM Digital Library		IEEE Xplore Digital Library		Science Direct	
Publication name	Number of scientific materials	Publication name	Number of scientific materials	Publication name	Number of scientific materials
Proceedings of the SIGCHI conference on Human factors in computing systems	52	IEEE Transactions on Professional Communication	20	Interacting with Computers	101
International Journal of Human-Computer Studies	50	IEEE Security & Privacy	15	International Journal of Human-Computer Studies	53
CHI '04 extended abstracts on Human factors in computing systems	42	IEEE Software	10	International Journal of Medical Informatics	27
Interacting with Computers	42	Second International Conferences on Advances in Computer-Human Interactions, 2009. ACHI '09	10	Applied Ergonomics	26
CHI '06 extended abstracts on Human factors in computing systems	40	International Conference on User Science and Engineering (i-USEr), 2011	9	Computers in Human Behaviour	21

Continuation of Table 4

ACM Digital Library		IEEE Xplore Digital Library		Science Direct	
Publication name	N.of sc. mat.	Publication name	N.of sc. mat.	Publication name	N.of sc. mat.
Proceedings of the 2nd international conference on Usability and internationalization	40	IEEE Pervasive Computing	8	Journal of Biomedical Informatics	17
CHI '08 extended abstracts on Human factors in computing systems	35	9th International Conference on Computer-Aided Industrial Design and Conceptual Design, 2008. CAID/CD 2008	8	Journal of Systems and Software	17
Proceedings of the 12th international conference on Human-computer interaction: interaction design and usability	35	IEEE International Professional Communication Conference, 2009. IPCC 2009	8	Journal of Visual Languages & Computing	14
Universal Access in the Information Society	33	IEEE International Professional Communication Conference, 2006	7	Computers & Security	12
CHI '97 extended abstracts on Human factors in computing systems: looking to the future	32	IEEE 10th International Conference on Computer-Aided Industrial Design and Conceptual Design, 2009. CAID/CD 2009	7	Displays	11

5 Conclusions

The scientific databases, like Science Direct, ACM Digital Library and IEEE Xplore Digital Library, provide, on each search, besides the list of scientific papers which responds to the search criteria, useful information (e.g. representative publications and authors, etc.), which enable the researchers to better understand the research field and the deep meaning of what they can find in the database related to that field.

Although, research on usability has, since the late 2000s, been superseded by research on *user experience*, according to many authors, it has been and remains human computer interaction core concept. The results presented in this paper shows that the usability research area started in 80's, continued in 90's and increased a lot in the last twelve years. Also the results present the *Interacting with Computers* and *International Journal of Human-Computer Studies* as the most representative journals in the usability research area and authors such as Andreas Holzinger, Kasper Hornbaek and Barbara Leporini, the most prolific authors in this area, that are included in the analysed scientific databases.

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Yet Another Method for Image Segmentation based on Histograms and Heuristics *

Horia-Nicolai L. Teodorescu, Mariana Rusu

Abstract

We introduce a method for image segmentation that requires little computations, yet providing comparable results to other methods. While the proposed method resembles to the known ones based on histograms, it is still different in the use of the gray level distribution. When to the basic procedure we add several heuristic rules, the method produces results that, in some cases, may outperform the results produced by the known methods. The paper reports preliminary results. More details on the method, improvements, and results will be presented in a future paper.

Keywords: image processing, segmentation, mixed statistical-heuristic method, segmentation similarity index.

1 Introduction

Image segmentation is a recurrent subject in image processing journals and conferences. Although there is a huge number of segmentation methods proposed in the literature (see for example the reviews by Pal and Pal [1], by Cheng et al. [2], by Heimann and Meinzer [3], and by Mueller et al. [4]), none compares to the ability of human viewers to identify segments in images. This situation justifies the present proposal of segmentation procedure. In this section, we give

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the outline of the suggested segmentation method and its rationale. At our best knowledge, the procedure principle is new, although it has strong similarities with other well-known segmentation methods, see Zhang and Hu [5], Tobias and Seara [6], Khotanzad and Bouarfa, [7], and Kurugollu et al. [8].

Throughout this paper, we name segment a possibly disconnected subset of pixels of the image determined by a segmentation procedure. We name object any connected subset of a segment. With these terms, a segmented image is partitioned in a set of segments and every segment is partitioned in a set of objects. The purpose of the segmentation procedures is to determine such partitions that correspond to the elements of the image that are meaningful for a human observer. From this definition, we see that the segmentation problem is ill posed, because most segmentation procedures propose to perform segmentation based on geometrical and statistical properties of the image, while the result must be connected to information in the mind of the human observer, not in the image. Therefore, it is the opinion of the first author that any segmentation procedure must operate in two stages, the first one based on the geometrical and statistical properties of the image including some basic properties of connectedness, as in some graph-based approaches, while the second stage based on heuristic rules representing at least some elementary knowledge of the human viewer.

The paper deals with a novel way of using the global statistics of gray images for image segmentation. The statistics $p(G)$, where G is the gray level, is empirically represented by the histogram, $n(G)$. In the distribution function, instead of finding the ‘valleys’ or approximating it with a set of Gauss functions, as in other methods, we identify the intervals of almost constant probability, that is the intervals X_k satisfying one of the sets of conditions $\forall x_1, x_2 \in X_k \mid p(x_1) - p(x_2) \mid < \delta$ and $length(X_k) \geq \lambda \cdot G_{max}$, $0 \leq \lambda \leq 1$, with δ and λ predetermined parameters of the procedure, or $\forall X_k, STDV(X_k) < \delta$ and the second condition identical to the above. Once the intervals X_k are determined, the partition of the gray interval $[0, G_{max}]$ is completed with the remaining intervals. The segmentation of the image is performed according to the intervals X_k so determined. By varying the parameters δ and

λ , several segmentation results can be obtained. The method is further improved by automatically choosing the parameters such that the number of partition intervals is lower than a fixed number, for example $N = 5$. The obtained segments are labelled and further processed as explained in the final part of the paper.

The rationale of the method is as follows. A relatively constant value of the probability of occurrence of the gray levels in a quite large interval of gray levels may mean (that is, there is a great probability) that large patches of the image are uniform in gray level. Therefore, each of those regions should represent a significant object in the image and several such objects may occur in the image. Further, the intervals on the gray scale that are placed between the above determined intervals of almost-constant gray levels have large variations (larger than δ). These intervals correspond either to collections of small objects or to boundaries between larger objects. If they correspond to smaller objects, it is preferable to be retained as segments; when they represent boundaries that are segmented as different than the larger objects, they still can be merged with the larger objects in a subsequent phase using a dedicated procedure of merging. Thus, because at this stage we do not know if such lesser regions are objects or transition regions, they are preferably preserved as segments.

Notice that finding the intervals X_k is not trivial. These intervals are not necessarily unique. Explanations of the procedure used to determine a set of intervals X_k will be given in the next section. However, the proposed algorithm remains much simpler than other ones like those due to Kostas [9], Barret [10], or Udupa et al. [16].

2 Segmentation Algorithm

2.1 Basic algorithm – Preprocessing

The above principles need to be complemented with a set of techniques for preprocessing of the image as well as of the histogram. Image preprocessing is standard and comprises noise removal and weak smoothing of the gray level. For a 3×3 window, averaging filter is generally

enough. Even so, the histogram of the gray levels in the image is typically very irregular. The irregularity of the histogram hampers the application of the procedure, because either a large number of (false) intervals or no interval at all may be produced. To eliminate this drawback, the histogram is smoothed by twice applying to it a mixture of median and low pass filtering with windows with 5 to 11 samples (see Annex). We then apply the segmentation procedure on the smoothed histogram. This preliminary phase is illustrated in Fig. 1.

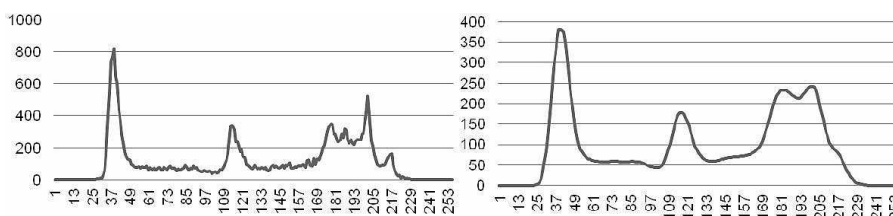


Figure 1. Example of preprocessing of the histogram

2.2 Basic algorithm: Segmentation

This sub-section follows [19]. The almost constant intervals were determined using an overlapping window of 24 samples considering the following rules:

1. $if \frac{V_{max} - V_{min}}{N_w} < 1.5$ then the interval is considered constant, where V_{max} and V_{min} are the maximum and minimum values of the window and N_w is the number of elements of the window. If two successive windows have this property we define the interval as being composed by both windows.
2. else the interval is considered not to be constant.

If we obtained several constant intervals, for the case with two thresholds we select the largest one, and its limits are considered thresholds. The segmentation is performed according to the example of pseudocode, where Th1 and Th2 are the limits of the largest quasi-constant

interval and $g(i, j)$ is the pixel value of the image:

```
if  $g(i, j) < Th1$  then  $g(i, j) \in \text{segment1}$   
if  $g(i, j) \geq Th1 \ \&\& \ g(i, j) \leq Th2$  then  $g(i, j) \in \text{segment2}$   
if  $g(i, j) > Th2$  then  $g(i, j) \in \text{segment3}$ 
```

If we use n thresholds, then there are $n + 1$ segments.

2.3 Post-processing – Removing the bright reflection spots

One of the almost omnipresent defects in the segmentation of images of scenes illuminated artificially – and for many natural scenes too – is the appearance of bright spots due to reflections. Surprisingly, while this deficiency is mentioned in many papers, we have not found in the literature any reference to a method to get rid of them. However, heuristically speaking, it is obvious that such spots are the brightest; and consequently we can easily remove them by applying a rule in the post-segmentation stage a rule as ‘Remove the brightest segment, whenever it has the characteristics of a spot of reflection, that is whenever its surface is much smaller (less than a given percentage) than the average surface of the objects in the image’. Notice that, to apply this rule in its full content, we need to compute beforehand the average dimension of the objects in the image.

3 Results

3.1 Segmentation results

We briefly illustrate the results obtained by our method and its variants and compare our segmentation results with several ones reported in the literature. We start with a simple case, of microscopic view of blood cells. The result is shown in Fig. 2 (original from [17]). The reader can visually compare our result with that in [6].

A typical test image used in the literature is the image of several

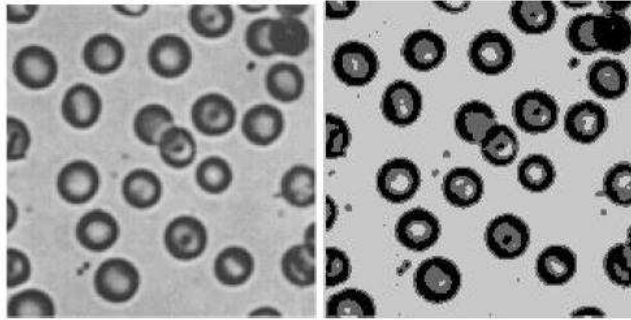


Figure 2. Simple segmentation case : blood red cells and nuclei. Left – original picture. Right: segmented, 2 thresholds. Compare to [6]

green sweet peppers [13]. The original image and two results obtained with our basic method, with the number of intervals X_k limited to 2, respectively 4, and correspondingly with 3, respectively 5 thresholds are shown in Fig. 3. These results compare well with those in the literature, see for example [14] and [18].



Figure 3. A typical test image: green sweet peppers. Left: original. Middle: segmentation with 2 thresholds. Right: 4 thresholds. Compare with [14]. Original picture from The USC-SIPI Image Database [13]

A difficult to segment case is a set of pictures recently published [12] and reproduced here with the kind permission of the author, Prof. Berkovitch. The ‘giraffe’ picture is however well segmented by the

proposed method, see Fig. 4. For the original and filtered histograms for the giraffes in Fig. 4, see Fig. 5.

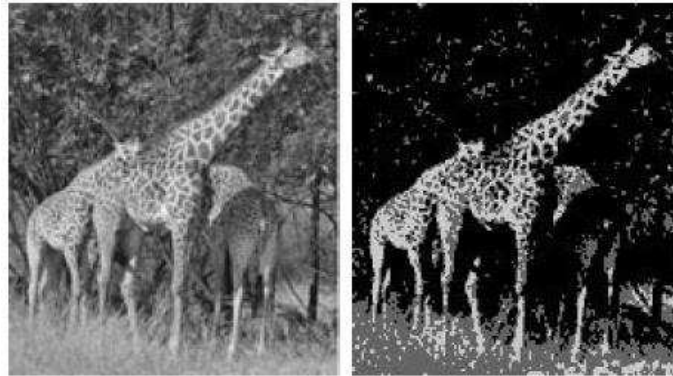


Figure 4. A difficult to segment pictures, with low contrast between the objects of interest (giraffes) and the background (savanna). For the original color and gray level picture, CopyRight 2012 by Berkovitch and [12].

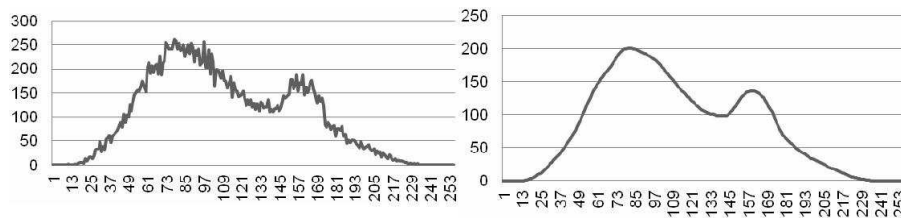


Figure 5. Original and smoothed histograms for the young giraffes picture

An example of result for the removing of bright reflectance spots is shown in Fig. 6, where the rule was applied without the condition on the area of the spots (direct application of the consequent of the rule whenever the object was bright.)

Notice that the procedure does not remove the gray contours of

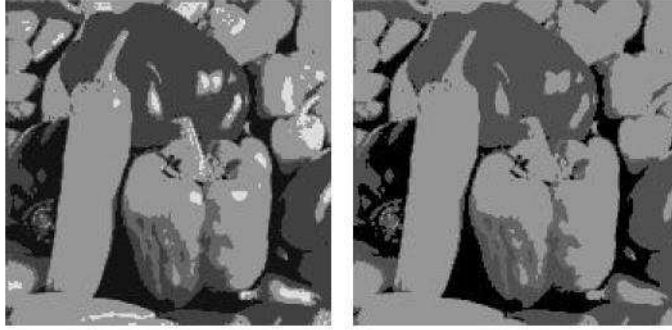


Figure 6. Removal of the reflection bright spot using the heuristic rule in the text

the bright spots. In another paper we will present a refinement of the procedure.

3.2 Indices of similarity

The visual comparison of the results produced by our method and by other method reported in the literature is time consuming and too subjective. There are several indices defined in the literature for assessing the results of segmentation [16], [15]. Most of these indices are based on counting the pixels that are common to the same segments in two segmented images (one of them being frequently segmented by a human operator), or on counting the number of pixels not in common to the corresponding segments. We defined a similar index as follows. To each object in an image, we associate the couple of values (S_k, O_j) , or equivalently (k, j) , where k is the number of the segment to which the object belongs, and j is the current number of the object in the segment S_k . For each object, we define the matrix $M_{k,j}^{[1,2]}$ with the same dimension as the image and with values 1 if the pixel belongs to the object, respectively 0 if it does not belong. For two segmentation results, we obtain the collection of matrices $A = \{M_{k,j}^{[1]}\}$ respectively $B = \{M_{k,j}^{[2]}\}$. First, assume that the number of segments is equal. We

count the absolute difference of the corresponding matrices for objects in the two sets, A, B . When an object occurs in one set, but not in the other, the missing object is represented by a null matrix. Next, we count the sum of the elements of the difference matrices for all the objects. Let us denote it by Δ . Then, the dissimilarity index of the two segmentations is defined as $D_1 = \Delta/N_{pixels}$, where N_{pixels} is the total number of pixels in the image. When $D_1 < 0.05$, the segmented images are very similar with respect to this criterion. A second index easy to define and compute in the same procedure is the number of non-corresponding objects. For every null matrix defined in the above procedure, we increment a counter for counting the total number of such objects. Denote this number by N_n . Also, we count the total number of objects in the images (that is, the total number of matrices in A and B , including the non-corresponding objects), N_o . The second dissimilarity index is defined as $D_2 = N_n/N_o$.

When the number of segments is different in the two images, we need a different approach for comparing the segmented images. We work directly with objects, not taking into account the segments. The procedure is as follows. From one image, we select the greatest object (with the largest number of pixels) and determine the object that best matches it in the second segmented picture. For the pair of objects so determined, we compute the number of non-matching pixels, N_{n1} . After removing the two objects, we iterate the same procedure until no objects remain unmatched. The sum of values N_{nk} is denoted by N_n . The dissimilarity is then computed as above.

Code for dissimilarity:

```

read A[N][M], B[N][M], i,j;
read long delta=0, k;
begin for i=0:N-1
    begin for j=0:M-1
        delta+=abs(A[i][j] - B[i][j]);
    end for
end for
D1=delta/(N×M);

```

if $D1 \leq 5/100$ **Images are similar**
else **Images are not similar**

We exemplify the results of comparison of segmented images for the images with green peppers. The results are not similar in several respects. Because we have applied a correction by removing the regions strongly reflecting light, these regions are no more obtained as segments, which is an improvement. In addition, some shades and some darker regions are not determined as segments by our method, which in some cases is good.

4 Discussion

In every sub-segment (object), we compute the average of the gray level, the median, and the standard deviation. Also, for full characterization of the objects, the histogram of gray levels of the objects is computed. This information is used in the comparison of the objects in the image and in detection of sub-classes of objects, taking into account that objects from the same segment may differ in their type. Two objects are classified as of the same type if their histograms are similar.

Because segmentation is prone to noise, we need an extra phase of cleaning the segments by removing noise pixels and small sets of pixels that represent 'segmentation noise'. Average filtering is not an option, because averaging would change the gray level inside the segment. Instead, median filtering with a small window (3×3) is useful in removing isolated noise pixels inside the segments. Yet, the median filter can not remove all noisy pixels. We tested the following simple procedures after the application of the median filter.

Segment compaction procedure #1 If in the initial segmented image, in a 3×3 window that is totally embedded in the segment (that is, all neighboring pixels belong to the segment) there are up to two pixels not belonging to the segment, then they are converted to the segment.

Segment compaction procedure #2 Any object of at most 5 pixels completely surrounded by pixels of another segment becomes the sur-

rounding segment.

Drawbacks of our methods are the need to pre-determine the procedure parameters δ and λ , or equivalently, δ and the number of segments. Also, the procedure of filtering the histogram is based on the first author experience and on experiments, namely the windows widths and the number of filtering stages being empirically chosen. The first drawback can be partly eliminated by imposing the number of segments and automatically adjusting the value of δ to obtain the number of segments. The second disadvantage can be eliminated by requiring a limited level of high frequency noise in the histogram and automatically tuning a filter to remove accordingly the noise. We will work out these improvements and show the results in another research.

5 Conclusions

We demonstrated a novel simple segmentation method based on a mixture of statistical and heuristic procedures. The method involves the selection of thresholds for the segments in a manner largely complementary to the well-known ‘valley’ method. In addition, the method uses a set of simple heuristic rules for further improving the segmentation. While the degree of novelty is limited to inverting the standard procedure based on the ‘valleys’ of the histogram and on adding a few features that improve the quality of the segmentation, the overall fabric of the algorithm undoubtedly brings novelty and improves results in case of some of the processed pictures.

The proposed segmentation procedure has the advantage of low computational requirements, making it suitable for small embedded systems and real-time applications. Further improvements regard the automation of the choice of the δ value and the filtering of the histogram.

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Authors' contributions. HNT proposed the topic, the method of solving the segmentation, the stages and main steps of the algorithms, some of the pictures for processing, interpreted most of the results and derived conclusions, wrote most of the paper, edited it (in LaTeX), and set in motion the writing of the code. MR wrote the code, performed simulations and experiments, contributed to the interpretation of the results, and contributed writing the paper.

Both authors agreed with the final form of the paper.

Annex

Histogram smoothing. The smoothing of the histogram is performed with the sequence of averaging and median (Med) filters:

$$n_1[k] = (1/11)Sum_{h=-5..+5}n_0[k + h]$$

$$n_2[k] = Med_{W_{h=-2..+2}}n_1[h + k]$$

For obtaining a smooth histogram we applied the average filter twice and then the median filter, using a window of 11 samples, respectively 5 samples (with centered pixel).

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Medical Image Registration by means of a Bio-Inspired Optimization Strategy

Hariton Costin, Silviu Bejinariu

Abstract

Medical imaging mainly treats and processes missing, ambiguous, complementary, redundant and distorted data. Biomedical image registration is the process of geometric overlaying or alignment of two or more 2D/3D images of the same scene, taken at different time slots, from different angles, and/or by different acquisition systems. In medical practice, it is becoming increasingly important in diagnosis, treatment planning, functional studies, computer-guided therapies, and in biomedical research. Technically, image registration implies a complex optimization of different parameters, performed at local or/and global levels. Local optimization methods frequently fail because functions of the involved metrics with respect to transformation parameters are generally nonconvex and irregular. Therefore, global methods are often required, at least at the beginning of the procedure. In this paper, a new evolutionary and bio-inspired approach – bacterial foraging optimization – is adapted for single-slice to 3-D PET and CT multimodal image registration. Preliminary results of optimizing the normalized mutual information similarity metric validated the efficacy of the proposed method by using a freely available medical image database.

Keywords: medical imaging, image registration, soft computing, evolutionary strategies, bacterial foraging algorithm, global optimization.

1 Introduction

Image registration (IR) is a fundamental task in computer vision used to find either a spatial *transformation* (e.g., rotation, translation, etc.)

or a correspondence (matching of similar image entities) among two (or more) images taken under different conditions (at different times, using different sensors, from different viewpoints, or a combination of them), with the aim of overlaying such images into a common one [Gon02], [Pra01], [Ran05]. Over the years, IR has been applied to a broad range of situations from remote sensing to medical images or artificial vision and CAD systems, and different techniques have been independently studied resulting in a large body of research.

IR methods can be classified in two groups according to the nature of images [Cor06]: *voxel*-based IR methods (also called *intensity*-based), where the whole image is considered for the registration process; and, on the other side, *feature*-based methods, which consider prominent information extracted from the images, being a reduced subset of them. The latter methods take advantage of the lesser amount of information managed in order to overcome the problems found in the former when the images present some inconsistencies to deal with, for example, regardless of changes in the geometry of the images, radiometric conditions, and appearance of noise and occlusion. These features correspond to *geometric primitives* (points, lines, surfaces, etc.) which are invariant to the transformation to be considered between the input images. Moreover, the latter methods perform faster than the former ones due to the reduced amount of data they take into account, at the expense of achieving *coarse* results.

Likewise, IR is the process of finding the optimal spatial transformation (e.g., rigid, similarity, affine, etc.) achieving the best overlaying between two (or more) different images named *scene and model* images (Figure 1). They both are related with the specific transformation, measured by a *similarity metric* function. Such transformation estimation is interpreted into an iterative optimization procedure in order to properly explore the search space. Two search approaches have been considered in the IR literature: *matching-based*, where the optimization problem is intended to look for a set of correspondences of pairs of those more similar image entities in both the scene and the model images, from which the registration transformation is derived; and the *transformation parameter-based*, where the strategy is to directly explore

inside each range of the transformation parameters. Both strategies can be used with either a voxel-based or a feature-based approach.

Specific aspects such as the presence of noise, image discretization, different amplitudes in the scale of the IR transformation parameters, the magnitude of the transformation to be estimated cause difficulties for traditional local optimizers (gradient- and nongradient-based) and they become prone to be trapped in local minima. As a consequence, global methods are preferred, at least at the beginning of the IR process.

Medical imaging modalities

Within the current clinical setting, medical imaging is a vital component of a large number of applications occurring throughout the clinical track of events, e.g. in clinical diagnostic, planning, consummation, and evaluation of surgical and radiotherapeutical procedures.

The imaging modalities can be divided into two global categories, i.e. *anatomical* and *functional*. Anatomical modalities include X-ray, CT (computed tomography), MRI (magnetic resonance imaging), US (ultrasound), and (video) sequences obtained by various catheter “scopes”.

Functional modalities depict primarily information on the metabolism of the specific anatomy. They include scintigraphy, SPECT (single photon emission computed tomography), PET (positron emission tomography), which all are *nuclear medicine* imaging modalities, then fMRI (functional MRI), pMRI (perfusion MRI), fCT (functional CT), EIT (electrical impedance tomography), and MRE (magnetic resonance elastography).

Since information gained from two images acquired in the clinical practice is usually of a complementary nature, proper *integration* of useful data obtained from the separate image modalities is often desired. A first step in this integration process is to bring the modalities involved into spatial alignment, a procedure referred to as *registration*. After registration, a *fusion* step may be required for the integrated display of the data involved.

2 The image registration problem

During the last decades, hundreds of papers were dedicated to image registration (IR) problem and different taxonomies have been established to classify the IR methods presented so far, considering different criteria: the image acquisition procedure, the search strategy, the type of transformation relating the images, and so forth [Mai98], [Zit03], [Zol03]. There is not a universal design for an IR method that could be applicable to all registration tasks, since various considerations on the particular application must be taken into account.

Yet, IR methods usually require the four following components (Figure 1): two input *Images*, named as Scene $Is = \{p_1, p_2, \dots, p_n\}$ and Model $Im = \{p_1, p_2, \dots, p_m\}$, with p_i and p_j being image points; a *registration transformation* f being a parametric function relating the two images; a *similarity metric function* F in order to measure a qualitative value of closeness or degree of fitting between the transformed scene image, denoted by $f'(Is)$, and the model image; and an *optimizer* which looks for the optimal transformation f inside the defined solution search space. Hence, the key idea of the IR process is focused on determining the unknown parametric *transformation* that relates both images, by placing them in a common coordinate system bringing the points as close as possible. Of course, the global optimum is obtained at the best registration transformation. Because of the uncertainty underlying such transformation, the IR task arises as a *nonlinear problem* that cannot be solved by a direct method (e.g., resolution of a simple system of linear equations). It should be solved by means of an iterative procedure searching for the *optimal estimation* of f , following a specific search space optimization scheme aiming at minimizing the error of a given *similarity metric* of resemblance. Classical local optimizers can be used for this task although their main drawback is that they usually get trapped in a local minima solution. The main reasons for such behavior are related to both the nature of the problem to be tackled and the greedy/local search features of these methods. So, the interest on the application of soft-computing and Artificial Intelligence in general to the IR optimization process has increased in the last decade due to

their global optimization nature.

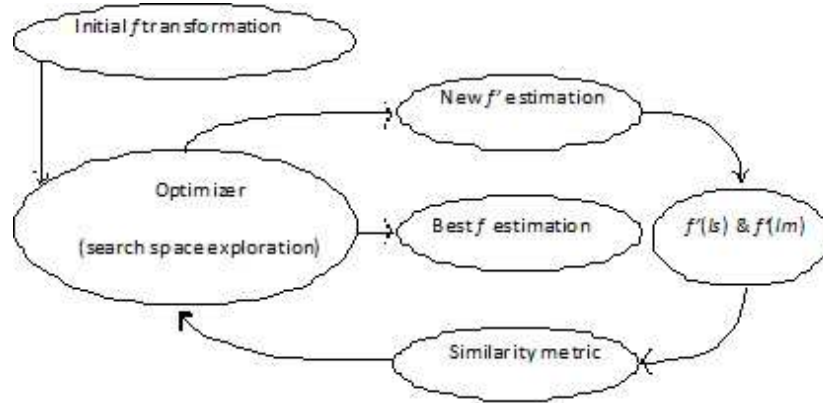


Figure 1. Image registration as an optimization process

According to the nature of images, IR methods can be classified as *voxel*-based (or *intensity*-based) and *feature*-based. The former directly operate with the whole raw images. The latter approach introduces a step before the application of the registration process: a reduced subset of the most relevant features is extracted from the images. One important drawback of voxel-based methods is that they can not reliably approach the variable contrast obtained during the acquisition of different images. In that case, the similarity metric offers unreliable measurements and often induces the optimization process to be trapped in local minima. The feature-based methods of IR are based on the extraction of salient *features* (e.g. geometric primitives) from the images. The feature detector has to accurately extract invariant features, i.e. regardless of changes in the geometry and contrast of the images and appearance of noise.

2.1 Transformations

The IR methods can be classified according to the registration transformation used to relate both the scene and the model images. The

first category of transformation models includes *linear transformations*, which preserves the operations of vector addition and scalar multiplication, being a combination of translation, rotation, global scaling, and shear components. The most common linear transformations are rigid, similarity, affine, projective, and curved. Linear transformations are global in nature, thus not being able to model local deformations. The second category of transformation models includes “*elastic*” or “*non-rigid*” transformations, which allow local warping of image features, thus providing support for local deformations.

2.2 Similarity metric

The similarity metric is a function F that measures the goodness of a given registration solution, that is, of a registration transformation f . The final performance of any IR method strongly depends on its accurate estimation. Each solution is evaluated by F applying such transformation f on one of the two images, usually to the scene image ($f(I_s)$). Next, the degree of closeness or fitting between the transformed scene and the model images, $\Psi(\cdot)$ must be determined,

$$F(I_s, I_m, f) = \Psi(f(I_s), I_m). \quad (1)$$

The main approaches trying to estimate the function $\Psi(\cdot)$ depend on the dimensionality (2D or 3D) and the nature of the considered images. There are: (a) voxel-based approach: sum of squared differences, normalized cross-correlation (i.e., correlation coefficient or phase correlation), and mutual information; (b) feature-based approach: feature values-based metrics (i.e., registration based on the curvature) and distance between corresponding geometric primitives.

Unfortunately, the F function is affected by both the discretization of images and the presence of noise, yielding worse estimations and favoring the IR to get trapped in local minima.

2.3 Search space strategies

The IR process performs an iterative exploration to obtain that optimal transformation f (introduced in Figure 1). So, the closer f to the unknown global optimum, the better the fitting (measured by the similarity metric F) between scene and model. The optimization process considered to obtain those solutions can be deterministic or stochastic (either a global or a local one).

Although the final registration problem solution consists of the right values for the parameters which determine f , we can distinguish two different strategies to solve the problem, each of them working in a different solution space:

- (i) the first searches in the *matching space* to obtain a set of correspondences of pairs of the most similar image entities in both the scene and the model images, from which the registration transformation is derived;
- (ii) the second directly makes a search in the space of the f parameters guided by the F function, called *transformation parameters space*.

The matching-based search space exploration usually consists of the two following stages: first, a set of correspondences with those more similar regions of pixels (voxel-based) or geometric primitives (feature-based) in both the scene and the model images must be computed; second, the transformation f is assessed by numerical methods considering the previous matching.

On the contrary, transformation parameters-based search space involves directly searching for the solution in the space of parameters of the transformation f . In this respect, each solution to the IR problem is encoded as a vector composed of the values for the parameters of f , and the IR method generates possible vectors of parameter values, that is, possible registration transformations. As a consequence, the search space exploration is guided by the similarity metric F . In this way, each solution vector is evaluated by the chosen metric, and the

IR problem becomes a parameter optimization procedure of finding the best values of f that maximize the similarity metric F .

Other classification divides search strategies in *local* and *global* ones. Local optimization techniques frequently fail because functions of these metrics with respect to transformation parameters are generally non-convex and irregular and, therefore, global methods – such as those based on evolutionary algorithms – are often required.

In recent years a lot of studies and papers were dedicated to medical IR [Alt06], [Coo03], [He02], [Hil94], [Lav04], [Lev08], [Mai96, 98], [Plu03], [Qin93], [Zib01], [Xua06]. Concerning the CT—PET images registration topic, some valuable attempts were made in the past. Thus, rigid 3D transformations were performed, e.g., by Alpert [Alp90] using the images principal axes and center of gravity, and by Pietrzyk [Pie94], who used a fully interactive method. Affine registration was obtained by Wahl [Wah93], employing user identified anatomical landmarks and external markers, and Maguire [Mag91], who optimized cross-correlation around such user identified anatomical landmarks and external markers. In [Lee06] a robust surface registration using a Gaussian-weighted distance map (GWDM) for PET-CT brain fusion was proposed. A similarity measure was evaluated repeatedly by weighted cross-correlation (WCC).

In recent years, the application of several well-known *evolutionary algorithms* (EAs) to the IR optimization process has introduced an outstanding interest in order to solve those problems due to their global optimization techniques nature. The first attempts to solve IR using evolutionary computation [Bac97] can be found in the early eighties, when Fitzpatrick et al. [Fit84] proposed such approach based on a genetic algorithm for the 2D case and applied it to angiographic images. Since then, several evolutionary approaches have been proposed to solve the IR problem, mainly in connection with the transformation parameters-based search space, as it is shown e.g. in [Cho04], [Cor06], [Cor07], [Eti00], [Rey06], [Rou00], [Wac04]. The main reason of using global optimization techniques, such as EAs-based algorithms for IR, is that they do not require an optimum solution to achieve high accuracy of registration.

3 Bacterial foraging algorithm

Introduced by Passino [Pas02], [Liu02], bacterial foraging paradigm is a bio-inspired optimization method based on the foraging model. This paradigm belongs to the broader class of distributed nongradient global optimization. A foraging animal takes actions to maximize the energy obtained per unit time spent for foraging, E/T , in the face of constraints presented by its own physiology (e.g., sensing and cognitive capabilities) and environment (e.g., density of prey, risks from predators, physical characteristics of the search area). In other words, these social animals, like *E. coli* – a bacterium, try to maximize their long-term average rate of energy intake.

Let us suppose that θ is the position of a bacterium and $J(\theta)$ represents the combined effects of attractants and repellants from the environment, with, for example, $J(\theta) < 0$, $J(\theta) = 0$, and $J(\theta) > 0$ representing that the bacterium at location θ is in nutrient-rich, neutral, and noxious environments, respectively. We want to find the minimum of $J(\theta)$, $\theta \in \mathbb{R}^p$, where we do not have measurements or an analytical description of the gradient $\nabla J(\theta)$. So, ideas from bacterial foraging are used to solve this nongradient optimization problem. Basically, *chemotaxis* is a foraging behavior that implements a type of optimization where bacteria try to climb up the nutrient concentration (find lower and lower values of $J(\theta)$), avoid noxious substances, and search for ways out of neutral media (avoid being at position θ where $J(\theta) \geq 0$). In this way, they implement a type of biased random walk.

The chemotactic actions of *E. coli* may be resumed as follows:

- (i) if in neutral medium, alternate tumbles and runs \Rightarrow search;
- (ii) if swimming up a nutrient gradient (or out of noxious substances), swim longer (climb up nutrient gradient or down noxious gradient) \Rightarrow seek increasingly favorable environments;
- (iii) if swimming down a nutrient gradient (or up noxious substance gradient), then search \Rightarrow avoid unfavorable environments.

3.1 Chemotaxis, swarming, reproduction, elimination, and dispersal

In [Pas02], [Pas05] a chemotactic step was defined to be a tumble followed by a tumble or a tumble followed by a run. Let j be the index for the chemotactic step. Let k be the index for the reproduction step. Let l be the index of the elimination-dispersal event. Let

$$P(j, k, l) = \{\theta^i(j, k, l) \mid i = 1, 2, \dots, S\} \quad (2)$$

represent the position of each member in the population of the S bacteria at the j th chemotactic step, k th reproduction step, and l th elimination-dispersal event. Here, let $J(i, j, k, l)$ denote the cost at the location of the i th bacterium $\theta^i(j, k, l) \in \mathbb{R}^p$ (sometimes we may refer to the i th bacterium position as θ^i). Note: we will interchangeably refer to J as being a “cost” (using terminology from optimization theory) and as being a nutrient surface (in reference to the biological connections). For actual bacterial populations, S can be very large (e.g., $S = 10^9$), but $p = 3$. In computer simulations, we may use much smaller population sizes and keep the population size fixed. Let N_c be the length of the lifetime of the bacteria as measured by the number of chemotactic steps they take during their life. Let $C(i) > 0$, $i = 1, 2, \dots, S$, denote a basic chemotactic step size that we will use to define the lengths of steps during runs.

To represent a tumble, a unit length random direction, say $\phi(j)$, is generated; this will be used to define the direction of movement after a tumble. In particular, we let

$$\theta^i(j + 1, k, l) = \theta^i(j, k, l) + C(i)\phi(j) \quad (3)$$

so that $C(i)$ is the size of the step taken in the random direction specified by the tumble. If at $\theta^i(j + 1, k, l)$ the cost $J(i, j + 1, k, l)$ is better (lower) than at $\theta^i(j, k, l)$, then another step of size $C(i)$ in this same direction will be taken. This swim is continued as long as it continues to reduce the cost, but only up to a maximum number of steps, N_s . This represents that the cell will tend to keep moving if it is headed in

the direction of increasingly favorable environments. The above discussion is for the case where no cell-released attractants are used to signal other cells that they should swarm together. The cell-to-cell signaling via an attractant is represented with $J_{cc}^i(\theta, \theta^i(j, k, l))$, $i = 1, 2, \dots, S$, for the i th bacterium.

Let $d_{attract}$ be the depth of the attractant released by the cell and $w_{attract}$ be a measure of the width of the attractant signal (a quantification of the diffusion rate of the chemical). The cell also repels a nearby cell in the sense that it consumes nearby nutrients and it is not physically possible to have two cells at the same location. To model this, we let

$$h_{repellant} = d_{attract}$$

be the height of the repellant effect and $w_{repellant}$ be a measure of the width of the repellant.

Let

$$\begin{aligned} J_{cc}(\theta, P(j, k, l)) &= \sum_{i=1}^S J_{cc}^i(\theta, \theta^i(j, k, l)) = & (4) \\ &= \sum_{i=1}^S \left[-d_{attract} \exp \left(-w_{attract} \sum_{m=1}^p (\theta_m - \theta_m^i)^2 \right) \right] \\ &+ \sum_{i=1}^S \left[h_{repellant} \exp \left(-w_{repellant} \sum_{m=1}^p (\theta_m - \theta_m^i)^2 \right) \right] \end{aligned}$$

denote the combined cell-to-cell attraction and repelling effects, where $\theta = [\theta_1, \dots, \theta_p]^T$ is a point on the optimization domain and θ_m^i is the m th component of the i th bacterium position θ^i . Note that as each cell moves, so does its $J_{cc}^i(\theta, \theta^i(j, k, l))$ function, and this represents that it will release chemicals as it moves. Due to the movements of all the cells, the $J_{cc}(\theta, P(j, k, l))$ function is time varying in that if many cells come close together there will be a high amount of attractant and hence an increasing likelihood that other cells will move toward the group. This produces the swarming effect, where the i th bacterium, $I = 1, 2, \dots, S$,

will hill-climb on $J(i, j, k, l) + J_{cc}(\theta, P)$ (rather than the $J(I, j, k, l)$ defined above) so that the cells will try to find nutrients, avoid noxious substances, and at the same time try to move toward other cells, but not too close to them. The $J_{cc}(\theta, P)$ function dynamically deforms the search landscape as the cells move to represent the desire to swarm, i.e., swarming is viewed as a minimization process.

After N_c chemotactic steps, a reproduction step is taken. Let N_{re} be the number of reproduction steps to be taken. For convenience, we assume that S is a positive even integer.

Let

$$S_r = S/2 \tag{5}$$

be the number of population members who have had sufficient nutrients so that they will reproduce (split in two) with no mutations. For reproduction, the population is sorted in order of ascending accumulated cost (higher accumulated cost represents that a bacterium did not get as many nutrients during its lifetime of foraging and hence is not as “healthy” and thus unlikely to reproduce); then the S_r least healthy bacteria die and the other S_r healthiest bacteria each split into two bacteria, which are placed at the same location. Other fractions or approaches could be used in place of (5); this method rewards bacteria that have encountered a lot of nutrients and allows us to keep a constant population size, which is convenient in coding the algorithm.

Let N_{ed} be the number of elimination-dispersal events, and for each elimination-dispersal event each bacterium in the population is subjected to elimination-dispersal with probability p_{ed} . We assume that the frequency of chemotactic steps is greater than the frequency of reproduction steps, which is in turn greater in frequency than elimination-dispersal events (e.g., a bacterium will take many chemotactic steps before reproduction, and several generations may take place before an elimination-dispersal event).

The Bacterial Foraging Optimization Algorithm (BFOA) is fully described in pseudo-code in paper [Pas02] and was used as it is during our experiments.

4 Mutual information based multimodal image registration

Multimodal images acquired at different time moments have variations due to the acquisition system, position of the subject, and different geometric deformations. To optimally register and then fuse multimodal images, we have to minimize the linear and non-linear differences between the two images. In our paper we propose the use of *normalized mutual information* as a similarity metric for registering PET and CT images. Mutual information, which measures statistical dependence between two images viewed as random variables, has been proved to be robust for multimodal registration, with respect to dynamic range and intensity resolution of the images. Mutual information represents a measure of the relative independence of two images, in the sense that high values indicate high dependence.

Registration of multimodal medical images may be described as follows. For instance, let P and C be the PET and CT images for registration, respectively. *Mutual information* between the two images can be represented as

$$M(P, C) = H(P) + H(C) - H(P, C). \quad (6)$$

$H(\cdot)$ is the entropy of the image and $H(P, C)$ is the joint entropy. Registering P with respect to C (in this manner, as CT image has much more geometric information) requires maximization of mutual information between P and C , thus maximizing the entropy $H(P)$ and $H(C)$, and minimizing the joint entropy $H(P, C)$. Because mutual information based registration methods are sensitive to changes that occur in the distributions as a result of difference in overlapping regions, *normalized mutual information* can be used:

$$NM(P, C) = \frac{H(P) + H(C)}{H(P, C)}. \quad (7)$$

Our study approaches the *rigid body image registration*, which initially determines global alignment, followed by local elastic registration. Let T denote the spatial transformation that maps features or

coordinates (spatial locations) from one image or coordinate space to another image or coordinate space. Let p_A and p_B denote coordinate points (pixel locations) in images A and B , respectively. The image registration problem is to determine T so that the mapping $T : p_A \rightarrow p_B \Leftrightarrow T(p_A) = p_B$ results in the “best” alignment of A and B . For 3-D rigid body registration, the mapping of coordinates $p = [x, y, z]^T$ into $p' = [x', y', z']^T$ can be formulated as a matrix multiplication in homogeneous coordinates, as shown in (8) in an explicit manner. That is, the goal of the optimization is to determine the parameters $t_x, t_y, t_z, \alpha, \beta,$ and γ in (8).

Usually, optimization in image registration means to maximize similarity. Similarity metric values, as functions of transformation parameters, refer to *the objective function*, denoted as $f(x)$. Alternatively, one may formulate the image registration as a minimization problem and, thus, the goal is to minimize $-f(x)$. Although there is yet no proof for its optimality, because of its robustness (usually it attains its maximum at correct alignment) and good results in previous works, normalized mutual information was selected as the similarity measure in our study. Moreover, it is still generally non-smooth and prone to local optima. For this reason, global optimization approaches are preferred.

$$\begin{bmatrix} p' \\ 1 \end{bmatrix} = \mathbf{T} \begin{bmatrix} p \\ 1 \end{bmatrix} \Leftrightarrow \begin{bmatrix} x' \\ y' \\ z' \\ 1 \end{bmatrix} = \begin{bmatrix} \cos \beta \cos \gamma & \cos \alpha \sin \gamma + \sin \alpha \sin \beta \cos \gamma & \sin \alpha \sin \gamma - \cos \alpha \sin \beta \cos \gamma & t_x \\ -\cos \beta \sin \gamma & \cos \alpha \cos \gamma - \sin \alpha \sin \beta \sin \gamma & \sin \alpha \cos \gamma - \cos \alpha \sin \beta \sin \gamma & t_y \\ \sin \beta & -\sin \alpha \cos \beta & \cos \alpha \cos \beta & t_z \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ z \\ 1 \end{bmatrix} \quad (8)$$

5 Biomedical image registration using bacterial foraging algorithm

In contrast to genetic algorithms and evolutionary strategies, which exploit the competitive characteristics of biological evolution (e.g., sur-

vival of the fittest), bacterial foraging (BF) exploits cooperative and social aspects of animal colonies (like *E. coli* bacterium) in their attempts to obtain nutrients that maximize energy intake per unit time spent for foraging.

As it is shown before, the registration of an image with another is seen as the minimization of the objective function of normalized mutual information (7). For a rigid body registration this means to find the transformation \mathbf{T} (that is, parameters $t_x, t_y, t_z, \alpha, \beta,$ and γ in (8)) that maps the pixel p into pixel p' .

We have chosen to register 2-D PET images into 3-D CT images, taken from www.medcyclopaedia.com, as depicted in Figure 6 and Figure 7 below. Normalized mutual information was computed using 60 histogram bins, which generally produces a smooth density approximation while retaining intensity features [Mae97]. Each 2-D image was oriented at $d_0 = 10, 15, 20, 25,$ and 30 voxels from ground truth translation (relative small distances), as expert knowledge of the correct orientation can greatly help the search process. For each distance, ten orientations were applied, ranging from 5° to 45° . For each 2-D image, distance, and orientation, eight trials were performed. After some trials, the population size was chosen to be $S = 150$.

Transform T that maps the pixel p in pixel p' is defined by 6 parameters: $t_x, t_y, t_z, \alpha, \beta, \gamma$. To find the optimal transform in terms of normalized mutual information, the bacterial foraging algorithm was used for optimization in space \mathbb{R}^6 . To have a uniform treatment of the parameters, the search space was scaled in interval $[0, 100]$ for all six parameters.

Within the bacterial foraging paradigm, the following chemotactic actions are defined:

- (i) search in a neutral medium;
- (ii) seek increasingly favorable environments;
- (iii) avoiding unfavorable environments.

Considering that a priori information about the transform parameters is unknown, only the search case can be used. Cells-released attractants

are used to signal other cells the favorable movement directions.

In the example above, we reduced the search space to \mathfrak{R}^2 and the following parameters were used: number of bacteria in the population $S = 150$, number of chemotactic steps before reproduction – 100, magnitude of secretion of attractant $d_{attract} = 0.1$ and chemical cohesion signal $w_{attract} = 0.2$.

In Figure 2, the bacteria trajectories for the first 4 generations are presented. After 4 generations an elimination / dispersal was applied and the trajectories for the next 4 generations are shown in Figure 3.

Next, the following parameters were varied: magnitude of secretion of attractant, $d_{attract} = 0.25$ and chemical cohesion signal, $w_{attract} = 0.1$ (Figures 4 and 5). The more the chemical cohesion signal value is smaller, so the attractant is more diffused.

The validity of the proposed method was checked by means of the following metrics [Wac04]:

- 1) *accuracy*, as measured by the ratio of correct registrations to all registrations. A registration is considered to be correct if the Euclidean distance from the ground truth translation ($[t_{x0}, t_{y0}, t_{z0}]$) and final translation ($[t'_{x0}, t'_{y0}, t'_{z0}]$) is less than 2 voxels, and if the maximum absolute value of the three rotation errors is less than 2. These values have been found to be good indicators of registration quality; we obtained accuracies between 0.6 and 0.8 for different images; as anticipated, the best accuracies were obtained for $d_0 = 10$ voxels from ground truth translation;
- 2) *efficiency*, as measured by the mean number of function evaluations for correct registrations for each 2-D image registered to a 3-D volume.

The mean run time varied among different trials, between tens of seconds and 130 sec.

Moreover, registered PET-CT images are less sensitive to *contrast changes* compared to the CT images alone. As anticipated, the registered images also provide more distinguishing information compared to the PET and CT images. These properties of the proposed method

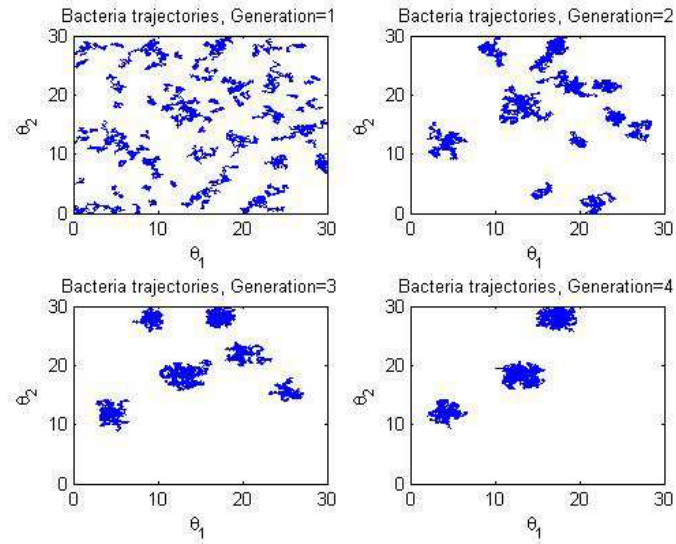


Figure 2. Bacteria trajectories for the first 4 generations $d_{attract} = 0.1$, $w_{attract} = 0.2$

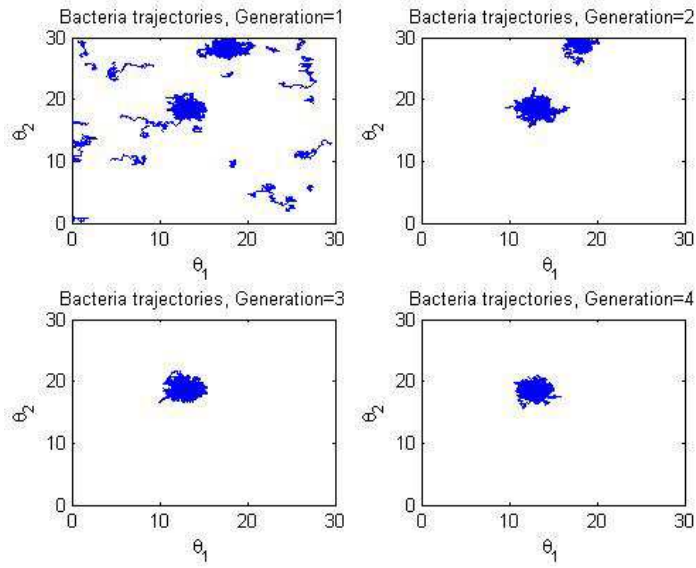


Figure 3. Bacteria trajectories for 4 generations after elimination dispersal, $d_{attract} = 0.1$, $w_{attract} = 0.2$

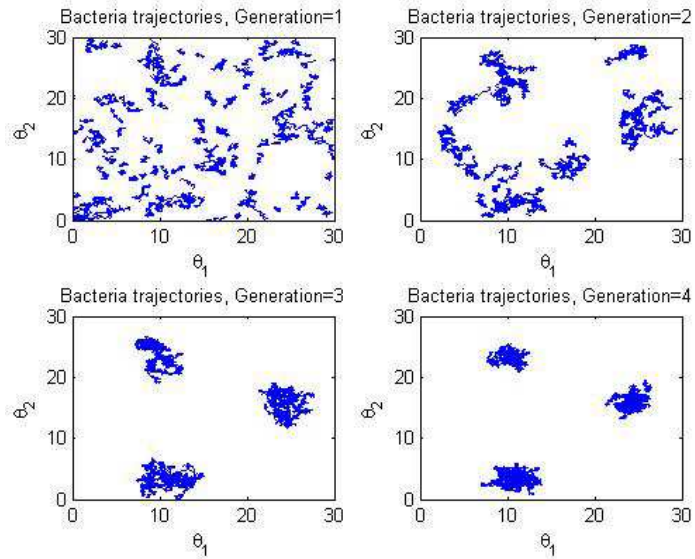


Figure 4. Bacteria trajectories for the first 4 generations $d_{attract} = 0.25$, $w_{attract} = 0.1$

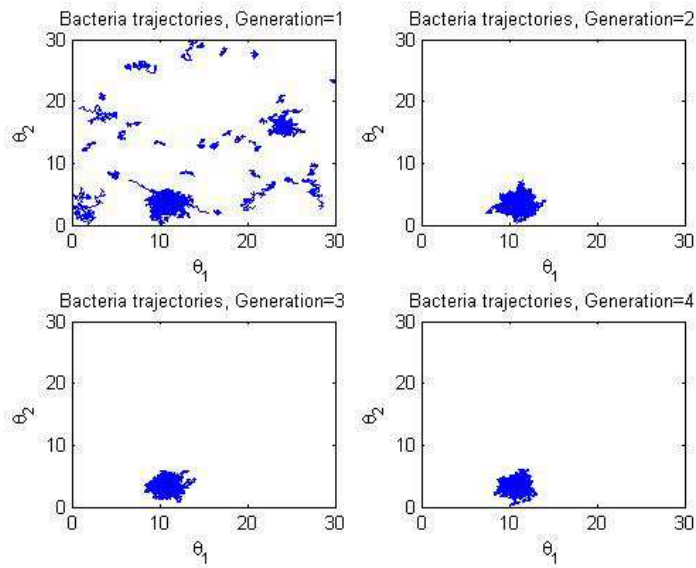


Figure 5. Bacteria trajectories for 4 generations after elimination dispersal, $d_{attract} = 0.25$, $w_{attract} = 0.1$

lead us to further continuing our study to improve the registration performance.

Figure 6 is an example of PET-CT image registration, with images taken from the portal www.medcyclopaedia.com. From medical point of view, it demonstrates the physiologic accumulation of fludeoxyglucose (FDG), a radiopharmaceutical, in the whiter regions of the body image.

In Figure 7, a coronal PET scan (b) presents an intense hypermetabolic activity shown by an arrow. This image may represent a tumor in the bowel or a mesenteric lymph node. This dilemma was later solved at biopsy, and a primary carcinoid tumor was found.

6 Conclusions

A new application of bacterial foraging optimization algorithm (BFOA), specifically used for biomedical image registration, was proposed in this paper. The preliminary results demonstrate the efficacy of using BF and stochastic global optimization for biomedical image registration. Moreover, like many evolutionary techniques, BFOA is intrinsically parallel, and execution times can be significantly improved by using distributed- or shared-memory computer architectures.

Concerning the actual application in medical imaging, it is already known that the primary advantage of PET-CT fusion technology is the ability to correlate findings from two complementary imaging modalities in a comprehensive way that synergetically combines anatomic information with functional and metabolic data. CT provides very fine anatomic details but does not yield functional information, whereas FDG PET lacks anatomic information but reveals aspects of different tumors and allows metabolic measurements. Yet, physiologic FDG uptake in non-malignant conditions limits the specificity of PET, particularly in the post-therapy setting. Hybrid PET-CT scanners allow PET and CT image fusion for differentiation of physiologic variants from juxtaposed or mimetic neoplastic lesions and more accurate tumor localization. However, software-based fusion of separately acquired PET and CT scans is more likely to lead to misregistration due to inde-

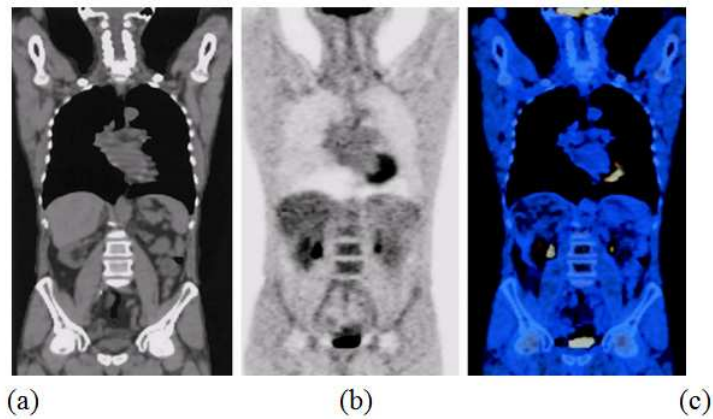


Figure 6. Coronal CT (a), PET (b), and PET-CT registered (c) images

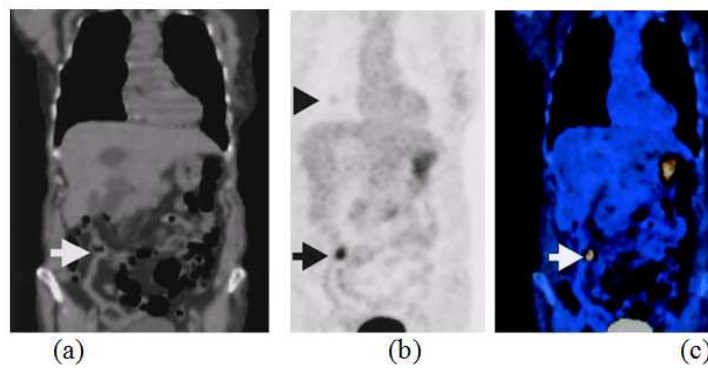


Figure 7. Primary carcinoid tumor of the bowel. CT image (a), PET image (b), and PET-CT image (c)

pendent parameters and differences in patient positioning. In addition, CT allows rapid acquisition of attenuation correction data for the PET scan.

This study shows that the accuracy obtained by image registration with BFOA is well suited for image-guided radiotherapy. Of course, we have to extend our work to annotated databases, both for PET-CT images, and for separately acquired PET and CT images.

Future work will be dedicated to combine bacterial foraging approach with other evolutionary techniques and local methods for image registration, as the need for hybrid approaches for difficult registration problems claims.

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Computation of Difference Gröbner Bases

Vladimir P. Gerdt, Daniel Robertz

Abstract

This paper is an updated and extended version of our note [1] (cf. also [2]). To compute difference Gröbner bases of ideals generated by linear polynomials we adopt to difference polynomial rings the involutive algorithm based on Janet-like division. The algorithm has been implemented in Maple in the form of the package LDA (Linear Difference Algebra) and we describe the main features of the package. Its applications are illustrated by generation of finite difference approximations to linear partial differential equations and by reduction of Feynman integrals. We also present the algorithm for an ideal generated by a finite set of nonlinear difference polynomials. If the algorithm terminates, then it constructs a Gröbner basis of the ideal.

1 Introduction

Being invented 47 years ago by Buchberger [3] for algorithmic solving of the membership problem in the theory of polynomial ideals, the Gröbner basis method has become a powerful universal algorithmic tool for solving various mathematical problems arising in science and engineering.

Though the overwhelming majority of Gröbner basis applications is still found in commutative polynomial algebra, over the last two decades a substantial progress has also been achieved in applications of Gröbner bases to noncommutative polynomial algebra, to algebra of differential operators and to linear partial differential equations (cf., for example, the book [4]). As to the difference algebra, i.e. algebra of difference polynomials [5], in spite of its conceptual algorithmic similarity to differential algebra, only a few efforts have been made to extend

the theory of Gröbner bases to difference algebra and to exploit their algorithmic power [5, 6, 7].

Recently, three promising applications of difference Gröbner bases were revealed:

- Generation of finite difference approximations to PDEs [8, 9].
- Consistency analysis of such approximations [10, 11].
- Reduction of multiloop Feynman integrals to the minimal set of basis integrals [12].

In this note we describe an algorithm (Section 4) for constructing Gröbner bases for linear difference systems that is an adaptation of the polynomial algorithm [13] to linear difference ideals. In so doing, we construct a Gröbner basis in its Janet-like form (Section 3), since this approach has shown its computational efficiency in the polynomial case [13, 14]. We briefly outline these efficiency issues in Section 5. The difference form of the algorithm exploits some basic notions and concepts of difference algebra (Section 2) as well as the definition of Janet-like Gröbner bases and Janet-like reductions together with the algorithmic characterization of Janet-like bases (Section 3). Extension of the notion of Gröbner basis to nonlinear difference polynomials, which has not been addressed in [1], [2], is briefly described in Section 6 where we also present the algorithm [11] for construction of such bases. In Section 7 we present our Maple package LDA for computing Gröbner bases of linear difference ideals, i.e. ideals generated by linear difference polynomials. The package is a modified version of our earlier package [17] oriented towards commutative and linear differential algebra and based on the involutive basis algorithm [14]. The modified version is specialized to linear difference ideals and uses both Janet and Janet-like divisions [13] adopted to linear difference polynomials [15]. In Sections 8 and 9 we illustrate LDA by simple examples of its application to the construction of finite difference approximations to linear systems of PDEs and to the reduction of Feynman integrals.

2 Elements of difference algebra

Let $\{y^1, \dots, y^m\}$ be the set of *indeterminates*, e.g., m functions of n variables x_1, \dots, x_n , and $\{\theta_1, \dots, \theta_n\}$ be the set of mutually commuting *difference operators (differences)*, i.e.,

$$(\theta_i \circ y^j)(x_1, \dots, x_n) = y^j(x_1, \dots, x_i + 1, \dots, x_n).$$

A *difference ring* R with differences $\theta_1, \dots, \theta_n$ is a commutative ring R such that for all $f, g \in R$, $1 \leq i, j \leq n$,

$$\begin{aligned} \theta_i \theta_j &= \theta_j \theta_i, & \theta_i \circ (f + g) &= \theta_i \circ f + \theta_i \circ g, \\ \theta_i \circ (fg) &= (\theta_i \circ f)(\theta_i \circ g). \end{aligned}$$

Similarly, one defines a *difference field*.

Let \mathcal{K} be a difference field, and $\mathcal{R} := \mathcal{K}\{y^1, \dots, y^m\}$ be the difference ring of polynomials over \mathcal{K} in variables

$$\{ \theta^\mu \circ y^k \mid \mu \in \mathbb{Z}_{\geq 0}^n, k = 1, \dots, m \}.$$

Hereafter, we denote by \mathcal{R}_L the set of linear polynomials in \mathcal{R} and use the notations:

$$\begin{aligned} \Theta &= \{ \theta^\mu \mid \mu \in \mathbb{Z}_{\geq 0}^n \}, & \deg_i(\theta^\mu \circ y^k) &= \mu_i, \\ \deg(\theta^\mu \circ y^k) &= |\mu| = \sum_{i=1}^n \mu_i. \end{aligned}$$

A *difference ideal* is an ideal $\mathcal{I} \subseteq \mathcal{R}$ closed under the action of any operator from Θ . For $F \subset \mathcal{R}$, the smallest difference ideal containing F will be denoted by $\text{Id}(F)$. If for an ideal \mathcal{I} there is $F \subset \mathcal{R}_L$ such that $\mathcal{I} = \text{Id}(F)$, then \mathcal{I} is a *linear difference ideal*.

A total ordering \succ on the set of $\theta^\mu \circ y^j$ is a *ranking* if for all i, j, k, μ, ν the following hold:

$$\begin{aligned} \theta_i \theta^\mu \circ y^j &\succ \theta^\mu \circ y^j, \\ \theta^\mu \circ y^j \succ \theta^\nu \circ y^k &\iff \theta_i \theta^\mu \circ y^j \succ \theta_i \theta^\nu \circ y^k. \end{aligned}$$

If $|\mu| > |\nu|$ implies $\theta^\mu \circ y^j \succ \theta^\nu \circ y^k$ for all j, k , then the ranking is *orderly*. If $j > k$ implies $\theta^\mu \circ y^j \succ \theta^\nu \circ y^k$ for all μ, ν , then the ranking is *elimination*.

Given a ranking \succ , a linear polynomial $f \in \mathcal{R}_L \setminus \{0\}$ has the *leading term* $a \vartheta \circ y^j$, $\vartheta \in \Theta$, $a \in \mathcal{K}$, where $\vartheta \circ y^j$ is maximal w.r.t. \succ among all $\theta^\mu \circ y^k$ which appear with nonzero coefficient in f . $\text{lc}(f) := a \in \mathcal{K} \setminus \{0\}$ is the *leading coefficient* and $\text{lm}(f) := \vartheta \circ y^j$ is the *leading monomial*.

A ranking acts in \mathcal{R}_L as a *monomial order*. If $F \subseteq \mathcal{R}_L \setminus \{0\}$, $\text{lm}(F)$ will denote the set of the leading monomials and $\text{lm}_j(F)$ will denote its subset for the indeterminate y^j . Thus,

$$\text{lm}(F) = \bigcup_{j=1}^m \text{lm}_j(F).$$

3 Janet-like Gröbner bases

Given a nonzero linear difference ideal $\mathcal{I} = \text{Id}(G)$ and a ranking \succ , the ideal generating set $G = \{g_1, \dots, g_s\} \subset \mathcal{R}_L$ is a *Gröbner basis* [4, 7] of \mathcal{I} if for all $f \in \mathcal{I} \cap \mathcal{R}_L \setminus \{0\}$:

$$\exists g \in G, \theta \in \Theta : \text{lm}(f) = \theta \circ \text{lm}(g). \quad (1)$$

It follows that $f \in \mathcal{I} \setminus \{0\}$ is *reducible modulo* G :

$$f \xrightarrow{g} f' := f - \text{lc}(f) \theta \circ (g / \text{lc}(g)), \quad f' \in \mathcal{I}.$$

If $f' \neq 0$, then it is again reducible modulo G , and, by repeating the reduction, in finitely many steps we obtain

$$f \xrightarrow{G} 0.$$

Similarly, a nonzero polynomial $h \in \mathcal{R}_L$, whose terms are reducible (if any) modulo a set $F \subset \mathcal{R}_L$, can be reduced to an irreducible polynomial \bar{h} , which is said to be in *normal form modulo* F (denotation: $\bar{h} = NF(h, F)$).

In our algorithmic construction of Gröbner bases we shall use a restricted set of reductions called *Janet-like* (cf. [13]) and defined as follows.

For a finite set $F \subseteq \mathcal{R}_L \setminus \{0\}$ and a ranking \succ , we partition every $\text{lm}_k(F)$ into subsets labeled by $d_0, \dots, d_i \in \mathbb{Z}_{\geq 0}$, ($0 \leq i \leq n$). Here $[0]_k := \text{lm}_k(F)$ and for $i > 0$ the subset $[d_0, \dots, d_i]_k$ is defined as

$$\{u \in \text{lm}_k(F) \mid d_0 = 0, d_j = \deg_j(u), 1 \leq j \leq i\}.$$

Denote by $h_i(u, \text{lm}_k(F))$ the nonnegative integer

$$\max\{\deg_i(v) \mid u, v \in [d_0, \dots, d_{i-1}]_k\} - \deg_i(u).$$

If $h_i(u, \text{lm}_k(F)) > 0$, then $\theta_i^{s_i}$ such that

$$s_i := \min\{\deg_i(v) - \deg_i(u) \mid u, v \in [d_0, \dots, d_{i-1}]_k, \deg_i(v) > \deg_i(u)\}$$

is called a *difference power* for $f \in F$ with $\text{lm}(f) = u$.

Let $DP(f, F)$ be the set of difference powers for $f \in F$, and $\mathcal{J}(f, F) := \Theta \setminus \bar{\Theta}$ be the subset of Θ with

$$\bar{\Theta} := \{\theta^\mu \mid \exists \theta^\nu \in DP(f, F) : \mu - \nu \in \mathbb{Z}_{\geq 0}^n\}.$$

A Gröbner basis G of $I = \text{Id}(G)$ is called *Janet-like* [13] if for all $f \in I \cap \mathcal{R}_L \setminus \{0\}$:

$$\exists g \in G, \vartheta \in \mathcal{J}(g, G) : \text{lm}(f) = \vartheta \circ \text{lm}(g). \quad (2)$$

This implies \mathcal{J} -reductions and the \mathcal{J} -normal form $NF_{\mathcal{J}}(f, F)$. It is clear that condition (2) implies condition (1). Note, however, that the converse is generally not true. Therefore, not every Gröbner basis is Janet-like.

The properties of a Janet-like basis are very similar to those of a Janet basis [14], but the former is generally more compact than the latter. More precisely, let GB be a reduced Gröbner basis [4], JB be a minimal Janet basis, and JLB be a minimal Janet-like basis of the same ideal for the same ranking. Then we have

$$\text{Card}(GB) \leq \text{Card}(JLB) \leq \text{Card}(JB), \quad (3)$$

where Card abbreviates *cardinality*, that is, the number of elements.

Whereas the algorithmic characterization of a Gröbner basis is zero redundancy of all its S -polynomials [3, 4], the algorithmic characterization of a Janet-like basis G is the following condition (cf. [13]):

$$\forall g \in G, \vartheta \in DP(g, G) : NF_{\mathcal{J}}(\vartheta \circ g, G) = 0. \quad (4)$$

This condition is at the root of the algorithmic construction of Janet-like bases as described in the next section.

4 Algorithm for Linear Difference Polynomials

The following algorithm is an adaptation of the polynomial version [13] to linear difference ideals.

Algorithm: Janet-like Gröbner Basis(F, \succ)

Input: $F \subseteq \mathcal{R}_L \setminus \{0\}$, a finite set; \succ , a ranking
Output: G , a Janet-like basis of $\text{Id}(F)$

- 1: **choose** $f \in F$ with the lowest $\text{lm}(f)$ w.r.t. \succ
- 2: $G := \{f\}$
- 3: $Q := F \setminus G$
- 4: **while** $Q \neq \emptyset$ **do**
- 5: $h := 0$
- 6: **while** $Q \neq \emptyset$ **and** $h = 0$ **do**
- 7: **choose** $p \in Q$ with the lowest $\text{lm}(p)$ w.r.t. \succ
- 8: $Q := Q \setminus \{p\}$
- 9: $h := \text{Normal Form}(p, G, \succ)$
- 10: **od**
- 11: **if** $h \neq 0$ **then**
- 12: **for all** $g \in G$ such that $\text{lm}(g) = \theta^\mu \circ \text{lm}(h)$, $|\mu| > 0$ **do**
- 13: $Q := Q \cup \{g\}$; $G := G \setminus \{g\}$
- 14: **od**
- 15: $G := G \cup \{h\}$
- 16: $Q := Q \cup \{\theta^\beta \circ g \mid g \in G, \theta^\beta \in DP(g, G)\}$
- 17: **fi**
- 18: **od**
- 19: **return** G

It outputs a minimal Janet-like Gröbner basis which (if monic, that is, normalized by division of each polynomial by its leading coefficient) is uniquely defined by the input set F and ranking \succ . Correctness and termination of the algorithm follow from the proof given in [13]; in so doing the displacement of some elements of the intermediate sets G into Q at step 13 provides minimality of the output basis. The algorithm terminates when the set Q becomes empty in accordance with (4).

The subalgorithm **Normal Form**(p, G, \succ) performs the Janet-like reductions (Section 3) of the input difference polynomial p modulo the set G and outputs the Janet-like normal form of p . As long as the intermediate difference polynomial h has a term Janet-like reducible modulo G , the elementary reduction of this term is done at step 4. As usually in the Gröbner bases techniques [4], the reduction terminates after finitely many steps due to the properties of the ranking (Section 2).

An improved version of the above algorithm can easily be derived from the one for the involutive algorithm [14] if one replaces the input involutive division by a Janet-like monomial division [13] and then translates the algorithm into linear difference algebra. In particular, the improved version includes Buchberger's criteria adjusted to Janet-like division and avoids the repeated prolongations $\theta^\beta \circ g$ at step 16 of the algorithm.

Algorithm: Normal Form(p, G, \succ)

Input: $p \in \mathcal{R}_L \setminus \{0\}$, a polynomial; $G \subset \mathcal{R}_L \setminus \{0\}$, a finite set; \succ , a ranking
Output: $h = NF_{\mathcal{J}}(p, G)$, the \mathcal{J} -normal form of p modulo G

- 1: $h := p$
- 2: **while** $h \neq 0$ **and** h has a monomial u with nonzero coefficient $b \in \mathcal{K}$ such that u is \mathcal{J} -reducible modulo G **do**
- 3: **take** $g \in G$ such that $u = \theta^\gamma \circ \text{lm}(g)$ with $\theta^\gamma \in \mathcal{J}(g, G)$
- 4: $h := h/b - \theta^\gamma \circ (g/\text{lc}(g))$
- 5: **od**
- 6: **return** h

5 Computational aspects

The polynomial version of algorithm *Janet-like Gröbner Basis* is implemented in its improved form in C++ [13] as a part of the specialized computer algebra system GINV [16]. It has disclosed its high computational efficiency for the standard set of benchmarks¹. If one compares this algorithm with the involutive one [14] specialized to Janet division, then all the computational merits of the latter algorithm are retained, namely:

- Automatic avoidance of some useless reductions.
- Weakened role of the criteria: even without applying any criteria the algorithm is reasonably fast. By contrast, Buchberger's algorithm without applying the criteria becomes unpractical even for rather small problems.
- Smooth growth of intermediate coefficients.
- Fast search of a polynomial reductor which provides an elementary Janet-like reduction of the given term. It should be noted that as well as in the involutive algorithm such a reductor, if it exists, is unique. The fast search is based on the special data structures called Janet trees [14].
- Natural and effective parallelism.

Though one needs intensive benchmarking for linear difference systems, we have solid grounds to believe that the above listed computational merits hold also for the difference case.

As this takes place, computation of a Janet-like basis is more efficient than computation of a Janet basis by the involutive algorithm [14]. The inequality (3) for monic bases is a consequence of the inclusion [13]:

$$GB \subseteq JLB \subseteq JB. \quad (5)$$

¹Cf. the web page <http://invo.jinr.ru>.

There are many systems for which the cardinality of a Janet-like basis is much closer to that of the reduced Gröbner basis than the cardinality of a Janet basis. Certain binomial ideals called toric form an important class of such problems. Toric ideals arise in a number of problems of algebraic geometry and closely related to integer programming. For this class of ideals the cardinality of Janet bases is typically much larger than that of reduced Gröbner bases [13]. For illustrative purposes consider a difference analogue of the simple toric ideal [13, 18] generated in the ring of difference operators by the following set:

$$\{ \theta_x^7 - \theta_y^2 \theta_z, \theta_x^4 \theta_w - \theta_y^3, \theta_x^3 \theta_y - \theta_z \theta_w \}.$$

The reduced Gröbner basis for the degree-reverse-lexicographic ranking with $\theta_x \succ \theta_y \succ \theta_z \succ \theta_w$ is given by

$$\{ \theta_x^7 - \theta_y^2 \theta_z, \theta_x^4 \theta_w - \theta_y^3, \theta_x^3 \theta_y - \theta_z \theta_w, \theta_y^4 - \theta_x \theta_z \theta_w^2 \}.$$

The Janet-like basis computed by the above algorithm contains one more element $\theta_x^4 \theta_w - \theta_y^3$ whereas the Janet basis adds another six elements to the Janet-like basis [13].

The presence of extra elements in a Janet basis in comparison with a Janet-like basis is obtained because of certain additional algebraic operations. That is why the computation of a Janet-like basis is more efficient than the computation of a Janet basis. Both bases, however, contain the reduced Gröbner basis as the internally fixed [14] subset of the output basis². Hence, having any of the bases computed, the reduced Gröbner basis is easily extracted without any extra computational costs.

6 Nonlinear Difference Polynomials

In this section we follow the paper [11] and define *difference standard bases* which generalize the concept of Gröbner bases to arbitrary ideals in the ring $\mathcal{R} = \mathcal{K}\{y^1, \dots, y^m\}$ of difference polynomials.

²In the improved versions of the algorithms.

A total ordering \succ on the set \mathcal{M} of *difference monomials*

$$\mathcal{M} := \{ (\theta_1 \circ y^1)^{i_1} \cdots (\theta_m \circ y^m)^{i_m} \mid \theta_j \in \Theta, i_j \in \mathbb{Z}_{\geq 0}, 1 \leq j \leq m \}$$

is *admissible* if it extends a ranking and satisfies

$$(\forall t \in \mathcal{M} \setminus \{1\}) [t \succ 1] \wedge (\forall \theta \in \Theta) (\forall t, v, w \in \mathcal{M}) \\ [v \succ w \iff t \cdot \theta \circ v \succ t \cdot \theta \circ w].$$

As an example of admissible monomial ordering we indicate the *lexicographical monomial ordering* compatible with a ranking.

Given an admissible ordering \succ , every nonzero difference polynomial f has the *leading monomial* $\text{lm}(f) \in \mathcal{M}$ with the *leading coefficient* $\text{lc}(f)$. In what follows, every nonzero difference polynomial is to be *normalized* (i.e., *monic*) by division of the polynomial by its leading coefficient.

If for $v, w \in \mathcal{M}$ the equality $w = t \cdot \theta \circ v$ holds with $\theta \in \Theta$ and $t \in \mathcal{M}$ we shall say that v *divides* w and write $v \mid w$. It is easy to see that this divisibility relation yields a *partial order*.

Given a difference ideal \mathcal{I} and an admissible monomial ordering \succ , a subset $G \subset \mathcal{I}$ is its (*difference*) *standard basis* if $\text{Id}(G) = \mathcal{I}$ and

$$(\forall f \in \mathcal{I})(\exists g \in G) [\text{lm}(g) \mid \text{lm}(f)]. \quad (6)$$

As in differential algebra [19], if a standard basis is finite it is called Gröbner basis.

A polynomial $p \in \mathcal{R} \setminus \{0\}$ is said to be *head reducible modulo* $q \in \mathcal{R} \setminus \{0\}$ to r if $r = p - m \cdot \theta \circ q$ and $m \in \mathcal{M}$, $\theta \in \Theta$ are such that $\text{lm}(p) = m \cdot \theta \circ \text{lm}(q)$. In this case the transformation from p to r is an *elementary reduction* and denoted by $p \xrightarrow[q]{} r$. Given a set $F \subset \mathcal{R} \setminus \{0\}$, p is *head reducible modulo* F (denotation: $p \xrightarrow[F]{} r$) if there is $f \in F$ such that p is head reducible modulo f . A polynomial p is *head reducible to* r *modulo* F if there is a chain of elementary reductions

$$p \xrightarrow[F]{} p_1 \xrightarrow[F]{} p_2 \xrightarrow[F]{} \cdots \xrightarrow[F]{} r. \quad (7)$$

Similarly, one can define *tail reduction*. If r in (7) and each of its monomials is neither head nor tail reducible modulo F , then we shall say that r is in *normal form modulo F* and write $r = \text{NF}(p, F)$. A polynomial set F with more than one element is *interreduced* if

$$(\forall f \in F) [f = \text{NF}(f, F \setminus \{f\})]. \quad (8)$$

Admissibility of \succ , as in commutative algebra, provides termination of chain (7) for any p and F . In doing so, $\text{NF}(p, F)$ can be computed by the difference version of a multivariate polynomial division algorithm [20, 21]. If G is a standard basis of $\text{Id}(G)$, then from the above definitions it follows

$$f \in \text{Id}(G) \iff \text{NF}(f, G) = 0.$$

Thus, if an ideal has a finite standard (Gröbner) basis, then its construction solves the ideal membership problem as well as in commutative [20, 21] and differential [19, 22] algebra. The algorithmic characterization of standard bases, and their construction in difference polynomial rings is done in terms of difference S -polynomials.

Given an admissible ordering, and monic difference polynomials p and q , the polynomial

$$S(p, q) := m_1 \cdot \theta_1 \circ p - m_2 \cdot \theta_2 \circ q$$

is called *S -polynomial* associated to p and q (for $p = q$ we shall say that the *S -polynomial* is associated with p) if

$$m_1 \cdot \theta_1 \circ \text{lm}(p) = m_2 \cdot \theta_2 \circ \text{lm}(q)$$

with coprime $m_1 \cdot \theta_1$ and $m_2 \cdot \theta_2$.

Algorithmic characterization of standard bases: Given a difference ideal $\mathcal{I} \subset \mathcal{R}$ and an admissible ordering \succ , a set of polynomials $G \subset \mathcal{I}$ is a standard basis of \mathcal{I} if and only if $\text{NF}(S(p, q), G) = 0$ for all S -polynomials, associated with polynomials in G . This result follows from the above definitions in line with the standard proof of the analogous characterization of Gröbner bases in commutative algebra [20, 21]

and with the proof of similar characterization of standard bases in differential algebra [19].

Let $\mathcal{I} = \text{Id}(F)$ be a difference ideal generated by a finite set $F \subset \mathcal{R}$ of difference polynomials. Then for a fixed admissible monomial ordering the following algorithm **StandardBasis**, if it terminates, returns a standard basis G of \mathcal{I} . The subalgorithm **Interreduce** invoked in step 11 performs mutual interreduction of the elements in \tilde{H} and returns a set satisfying (8).

Algorithm **StandardBasis** is a difference analogue of the simplest version of Buchberger's algorithm (cf. [19, 20, 21]). Its correctness is provided by the above formulated algorithmic characterization of standard bases. The algorithm always terminates when the input polynomials are linear. If this is not the case, the algorithm may not terminate. This means that the **do while**-loop (steps 2–10) may be infinite as in the differential case [19, 22]. One can improve the algorithm by taking into account Buchberger's criteria to avoid some useless zero reductions in step 5. The difference criteria are similar to the differential ones [19].

Algorithm: StandardBasis (F, \succ)

Input: $F \subset \mathcal{R} \setminus \{0\}$, a finite set of nonzero polynomials;
 \succ , an admissible monomial ordering
Output: G , an interreduced standard basis of $\text{Id}(F)$

- 1: $G := F$
- 2: **do**
- 3: $\tilde{H} := G$
- 4: **for all** S -polynomials s associated with elements in \tilde{H} **do**
- 5: $g := \text{NF}(s, \tilde{H})$
- 6: **if** $g \neq 0$ **then**
- 7: $G := G \cup \{g\}$
- 8: **fi**
- 9: **od**
- 10: **od while** $G \neq \tilde{H}$
- 11: $G := \text{Interreduce}(G)$
- 12: **return** G

7 The Maple Package LDA

The package LDA (abbreviation for **L**inear **D**ifference **A**lgebra)³ implements the involutive basis algorithm [14] for linear systems of difference equations using Janet division. In addition, the package implements a modification of the algorithm oriented towards Janet-like division [13] and, thus, computes Janet-like Gröbner bases of linear difference ideals.

Table 1 collects the most important commands of LDA. Its main procedure `JanetBasis` converts a given set of difference polynomials into its Janet basis or Janet-like Gröbner basis form. More precisely, let \mathcal{R} be the difference ring (cf. Section 2) of polynomials in the variables $\theta^\mu \circ y^k$, $\mu \in \mathbb{Z}_{\geq 0}^n$, $k = 1, \dots, m$, with coefficients in a difference field \mathcal{K} containing \mathbb{Q} for which the field operations can be carried out constructively in Maple. We denote again by \mathcal{R}_L the set of linear polynomials in \mathcal{R} . Given a finite generating set $F \subset \mathcal{R}_L$ for a linear difference ideal \mathcal{I} in \mathcal{R} , `JanetBasis` computes the minimal Janet(-like Gröbner) basis J of \mathcal{I} w.r.t. a certain monomial order (ranking). The input for `JanetBasis` consists of the left hand sides of a linear system of difference equations in the dependent variables y^1, \dots, y^m , e.g., functions of x_1, \dots, x_n . The difference ring \mathcal{R} is specified by the lists of independent variables x_1, \dots, x_n and dependent variables given to `JanetBasis`. The output is a list containing the Janet(-like Gröbner) basis J and the lists of independent and dependent variables.

After J is computed, the involutive/ \mathcal{J} -normal form of any element of \mathcal{R}_L modulo J can be computed using `InvReduce`. Given $p \in \mathcal{R}_L$ representing a residue class \bar{p} of the difference residue class ring \mathcal{R}/\mathcal{I} , `InvReduce` returns the unique representative $q \in \mathcal{R}_L$ of \bar{p} which is not involutively/ \mathcal{J} -reducible modulo J . A \mathcal{K} -basis of the vector space $\mathcal{R}_L/(I \cap \mathcal{R}_L)$ is returned by `ResidueClassBasis` as a list if it is finite or is enumerated by a formal power series [25] in case it is infinite. For examples of how to apply these two commands, cf. Section 9.

Given an affine (i.e. inhomogeneous) linear system of difference equations, a call of `CompCond` after the application of `JanetBasis` re-

³The package LDA is downloadable from the web page <http://wwwb.math.rwth-aachen.de/Janet>

turns a generating set of compatibility conditions for the affine part of the system, i.e. necessary conditions for the right hand sides of the inhomogeneous system for solvability.

Moreover, combinatorial devices to compute the Hilbert series and polynomial and function etc. [17] are included in LDA.

For the application of LDA to the reduction of Feynman integrals, a couple of special commands were implemented to impose further relations on the master integrals: By means of `AddRelation` an infinite sequence of master integrals parametrized by indeterminates which are not contained in the list of independent variables is set to zero. Subsequent calls of `InvReduce` and `ResidueClassBasis` take these additional relations into account (cf. Section 9).

LDA provides several tools for dealing with difference operators. Difference operators represented by polynomials can be applied to (lists of) expressions containing y^1, \dots, y^m as functions of the independent variables. Conversely, the difference operators can be extracted from systems of difference equations. Leading terms of difference equations can be selected.

We consider difference rings containing shift operators which act in one direction only. If a linear system of difference equations is given containing functions shifted in both directions, then the system needs to be shifted by the maximal negative shift in order to obtain a difference system with shifts in one direction only. However, LDA allows to change the shift direction globally.

Unnecessary computations of involutive reductions to zero are avoided using the four involutive criteria described in [14, 23, 24]. Fine-tuning is possible by selecting the criteria individually.

The implemented monomial orders/rankings are the (block) degree-reverse-lexicographical and the lexicographical one. In the case of more than one dependent variable, priority of comparison can be either given to the difference operators (“term over position”) or to the dependent variables (“position over term”/elimination ranking).

The ranking is controlled via options given to each command separately. The other options described above can be set for the entire LDA session using the command `LDAOptions` which also allows to select

Table 1. Main commands of LDA

<code>JanetBasis</code>	Compute Janet(-like Gröbner) basis
<code>InvReduce</code>	Involutive / \mathcal{J} -reduction modulo Janet(-like Gröbner) basis
<code>CompCond</code>	Return compatibility conditions for inhomogeneous system
<code>HilbertSeries</code> etc.	Combinatorial devices
<code>Pol2Shift</code> , <code>Shift2Pol</code>	Conversion between shift operators and equations
Some interpretations of commands for the reduction of Feynman integrals:	
<code>ResidueClassBasis</code>	Enumeration of the master integrals
<code>AddRelation</code>	Definition of additional relations for master integrals
<code>ResidueClassRelations</code>	Return the relations defined for master integrals

Janet or Janet-like division.

8 Generation of finite difference schemes for PDEs

We consider the Laplace equation $u_{xx} + u_{yy} = 0$ and rewrite it as the conservation law

$$\oint_{\Gamma} -u_y dx + u_x dy = 0.$$

Adding the integral relations

$$\begin{aligned} \int_{x_j}^{x_{j+2}} u_x dx &= u(x_{j+2}, y) - u(x_j, y), \\ \int_{y_k}^{y_{k+2}} u_y dy &= u(x, y_{k+2}) - u(x, y_k) \end{aligned}$$

and using the midpoint integration method we obtain the following discrete system:

$$\begin{cases} -(\theta_x - \theta_x \theta_y^2) \circ u_y + (\theta_x^2 \theta_y - \theta_y) \circ u_x = 0, \\ 2\Delta h \theta_x \circ u_x - (\theta_x^2 - 1) \circ u = 0, \\ 2\Delta h \theta_y \circ u_y - (\theta_y^2 - 1) \circ u = 0, \end{cases} \quad (9)$$

where θ_x and θ_y represent the right-shift operators w.r.t. x and y , e.g., $(\theta_x \circ u_y)(x, y) = u_y(x + 1, y)$.

We show how to use LDA to find a finite difference scheme for the Laplace equation:

```
> with(LDA):
```

We enter the independent and the dependent variables for the problem ($ux > uy > u$):

```
> ivar:=[x,y]: dvar:=[ux,uy,u]:
```

Next, we translate (9) into the input format of `JanetBasis`. Note that one can in general use `AppShiftOp` to apply a difference operator given as a polynomial similar to the ones in (9) to a difference polynomial.

```
> L:=[2*h*ux(x+1,y)-u(x+2,y)+u(x,y),
> 2*h*uy(x,y+1)-u(x,y+2)+u(x,y),
> 2*h*(ux(x+2,y+1)-ux(x,y+1))+2*h*(uy(x+1,y+2)-
> uy(x+1,y))]:
```

Then we compute the minimal Janet basis of the linear difference ideal generated by L w.r.t. a ranking which compares the dependent variables prior to the corresponding difference monomials (“position over term” order; this ranking is chosen when using the option 2 as below). The least element of this Janet basis is by construction a difference polynomial which does not contain any monomial in ux and uy because $ux > uy > u$.

```
> JanetBasis(L,ivar,dvar,2)[1][1];
```

$$\begin{aligned} & u(x + 4, y + 2) - 4u(x + 2, y + 2) + u(x, y + 2) + \\ & u(x + 2, y + 4) + u(x + 2, y) \end{aligned}$$

The computation takes less than one second of time on a Pentium III (1 GHz).

Dividing this difference polynomial by $4h^2$ we obtain the following finite difference scheme:

$$D_j^2(u_{jk}) + D_k^2(u_{jk}) = 0,$$

where

$$D_j^2(u_{jk}) = \frac{u_{j+2k} - 2u_{jk} + u_{j-2k}}{4h^2}$$

and

$$D_k^2(u_{jk}) = \frac{u_{jk+2} - 2u_{jk} + u_{jk-2}}{4h^2}$$

are discrete approximations of the second order partial derivatives occurring in Laplace's equation.

9 Reduction of Feynman integrals

In order to demonstrate how to use LDA for the reduction of Feynman integrals, we consider a simple one-loop propagator type scalar integral with one massive and another massless particle:

$$f(k, n) := I_{k,n} = \frac{1}{i\pi^{d/2}} \int \frac{d^d s}{P_{s-q,m}^k P_{s,0}^n}.$$

(Here k, n are the exponents of the propagators.)

The basis integrals for this example and the corresponding reduction formulae were found and studied by several authors (see, e.g., [26, 27]). Here we apply the Gröbner basis method, as implemented in LDA, directly to the recurrence relations which have the form:

$$\begin{cases} [d - 2k - n - 2m^2 k \mathbf{1}^+ - \\ n \mathbf{2}^+ (\mathbf{1}^- - q^2 + m^2)] f(k+1, n+1) = 0, \\ [n - k - k \mathbf{1}^+ (q^2 + m^2 - \mathbf{2}^-) - \\ n \mathbf{2}^+ (\mathbf{1}^- - q^2 + m^2)] f(k+1, n+1) = 0, \end{cases} \quad (10)$$

where

$$\mathbf{1}^\pm f(k, n) = f(k \pm 1, n), \quad \mathbf{2}^\pm f(k, n) = f(k, n \pm 1).$$

In addition, it is known that

$$f(k+i, n+j) = 0 \quad \forall i \leq 0 \quad \forall j \quad (11)$$

which we will take into account later.

```
> ivar:=[k,n]: dvar:=[f]:
```

We enter the recurrence relations (10):

```
> L:=[(d-2*k-n)*f(k+1,n+1)-2*m^2*k*f(k+2,n+1)-n*f(k,n+2)-
> n*(m^2-q^2)*f(k+1,n+2),
> (n-k)*f(k+1,n+1)-k*(q^2+m^2)*f(k+2,n+1)+
> k*f(k+2,n)-n*f(k,n+2)-n*(m^2-q^2)*f(k+1,n+2)]:
> JanetBasis(L,ivar,dvar):
```

Again, the computation time is less than one second. Now, the master integrals are given by:

```
> ResidueClassBasis(ivar,dvar);
```

$[f(k, n), f(k, n + 1), f(k + 1, n), f(k, n + 2), f(k + 1, n + 1), f(k + 2, n)]$

(11) implies additional relations on the master integrals. (Here, j is recognized as not being contained in `ivar` and thus serves as a parameter to define the additional relations.)

```
> AddRelation(f(k,n+j)=0,ivar,dvar):
```

The list of master integrals now becomes:

```
> ResidueClassBasis(ivar,dvar);
[f(k+1, n), f(k+1, n+1), f(k+2, n)]
```

Next, we recompute the Janet basis for $m = 0$:

```
> m:=0: J:=JanetBasis(L,ivar,dvar):
```

For the special case where $m = 0$, we impose the relation $f(k+i, n) = 0$ for all i :

```
> AddRelation(f(k+i,n)=0,ivar,dvar):
```

Now, we are left with one master integral:

```
> ResidueClassBasis(ivar,dvar);
      [f(k + 1, n + 1)]
```

We reduce $f(k+2, n+3)$ modulo J taking also the additionally imposed relations on the master integrals into account. (Here, the option “F” lets `InvReduce` return the result in factorized form.)

```
> InvReduce(f(k+2,n+3),J,"F");
      -((2n + 4 - d + 2k)(2n + 2 - d + 2k)(2k + n - d)(n + 3 - d + k)
      (n + 2 - d + k)f(k + 1, n + 1))/((n + 1)(2n - d + 4)nq^6k(d - 2k - 2))
```

Using `ResidueClassRelations` one can display the relations imposed on the master integrals:

```
> ResidueClassRelations(ivar,dvar,[i,j]);
      [f(k, n + j), f(k + i, n)]
```

The difference operators occurring in the last result can be extracted as polynomials in δ_k, δ_n :

```
> Shift2Pol(%,ivar,dvar,[delta[k],delta[n]]);
      [\delta_n^j, \delta_k^i]
```

10 Conclusion

The above presented algorithm *Janet-like Gröbner Basis* is implemented, in its improved form, in the Maple package LDA, and can be applied for generation of finite difference approximations to linear systems of PDEs, to the consistency analysis of such approximations [10], and to reduction of some loop Feynman integrals.

Alternatively, the Gröbner package in Maple in connection with the Ore algebra package [6] can be used to get the same results.

Two of these three applications were illustrated by rather simple examples. The first difference system (discrete Laplace equation and integral relations) contains two independent variables (x, y) and three

dependent variables (u, u_x, u_y) . The second system (recurrence relations for one-loop Feynman integral) also contains two independent variables/indices (k, n) , but the only dependent variable f . The second system, however, is computationally slightly harder than the first one because of explicit dependence of the recurrence relations on the indices and three parameters (d, m^2, q^2) involved in the dependence on indices.

Dependence on index variables and parameters is an attribute of recurrence relations for Feynman integrals. Similar dependence may occur in the generation of difference schemes for PDEs with variable coefficients containing parameters. Theoretically established exponential and superexponential (depends on the ideal and ordering) complexity of constructing polynomial Gröbner bases implies that construction of difference Gröbner bases is at least exponentially hard in the number of independent variables (indices). Besides, in the presence of parameters the volume of computation grows very rapidly as the number of parameters increases.

The reduction of loop Feynman integrals for more than 3 internal lines with masses is computationally hard for the current version of the package. One reason for this is that the Maple implementation does not support Janet trees since Maple does not provide efficient data structures for trees.

Another reason is that in the improved version of the algorithm there is still some freedom in the selection strategy for elements in Q to be reduced modulo G . Though our algorithms are much less sensitive to the selection strategy than Buchberger's algorithm, the running time still depends substantially on the selection strategy: mainly because of dependence of the intermediate coefficients growth on the selection strategy. To find a heuristically good selection strategy one needs to do intensive benchmarking with difference systems. In turn, this requires an extensive data base of various benchmarks that, unlike polynomial benchmarks, up to now is missing for difference systems.

For the problem of reduction of multiloop Feynman integrals recently some new reduction algorithms have been designed (cf. [28] and references therein) that exploit special structure of these integrals and by

this reason are computationally much more efficient than the universal Gröbner bases method.

The comparison of implementations of polynomial involutive algorithms for Janet bases in Maple and in C++ [17] shows that the C++ code is of two or three order faster than its Maple counterpart. Together with efficient parallelization of the algorithm this gives a real hope for its practical applicability to problems of current interest in reduction of loop integrals.

Thus, for successful application of the Gröbner basis technique to multiloop Feynman integrals with masses and to multidimensional PDEs with multiparametric variable coefficients one has not only to improve our Maple code but also to implement the algorithms for computing Janet and/or Janet-like difference bases in C++ as a special module of the GINV software [16] available on the web page <http://invo.jinr.ru>.

As to the algorithm *StandardBasis*, it has not been yet implemented. Another algorithmic development also aimed at computation of Gröbner bases for systems of nonlinear difference polynomials is described in recent paper [29].

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Finding Translation Examples for Under-Resourced Language Pairs or for Narrow Domains; the Case for Machine Translation

Dan Tufiş

Abstract

The cyberspace is populated with valuable information sources, expressed in about 1500 different languages and dialects. Yet, for the vast majority of WEB surfers this wealth of information is practically inaccessible or meaningless. Recent advancements in cross-lingual information retrieval, multilingual summarization, cross-lingual question answering and machine translation promise to narrow the linguistic gaps and lower the communication barriers between humans and/or software agents. Most of these language technologies are based on statistical machine learning techniques which require large volumes of cross lingual data. The most adequate type of cross-lingual data is represented by parallel corpora, collection of reciprocal translations. However, it is not easy to find enough parallel data for any language pair might be of interest. When required parallel data refers to specialized (narrow) domains, the scarcity of data becomes even more acute. Intelligent information extraction techniques from comparable corpora provide one of the possible answers to this lack of translation data.

Keywords: alignment, comparable corpora, document crawling, machine learning, multilingual corpora, parallel corpora, statistical machine translation

1 Introduction

According to the Ethnologue site <http://www.ethnologue.com/> there are 6909 languages in the world today. OLAC, the largest language

repository (The Open Language Archives Community) has linguistic data for 3930 languages. The Online Database of Interlinear text (ODIN) project (<http://www.csufresno.edu/odin/>) is a database of interlinear text “snippets” harvested mostly from scholarly documents posted on the Web (Lewis, 2006) and covers 1250 languages. Approximately 6% (389) of all extant languages are spoken by at least 1 million persons each, in total amounting for 94% of the Earth’s population. Recent estimations (indigenoustweets.blogspot.com/2011/12/) approximate to 1500 the number of languages for which, on the web, one could find “primary texts”: newspapers, blog posts, Wikipedia articles, Bible translations, etc. With such a linguistic diversity on the web, it is not surprising that the scientific and technological communities rank language technologies among the highest priorities. In a globalized information world, natural language communication mediated by computer is one of the most ambitious and difficult tasks. Cross-lingual information retrieval, natural question answering systems or machine translation are hot topics, substantially funded by international and national agencies. Large companies include these areas between their most promising research and development domains. Cross-lingual communication is not restricted to human use, but also it makes sense to conceive it among software agents, avatars of human users, in collaborative search for knowledge relevant to their masters’ informational needs. Machine translation, probably the oldest scientific endeavor in computer science, is frequently called the Queen of Artificial Intelligence as it incorporates the majority of methods and techniques developed in various fields of AI and language engineering. In spite of more than 60 years of huge world-wide research and computational efforts to solve the problem, Machine Translation and Natural Language Understanding are still far away from the performances ascribed by Science Fiction Literature to humanoid robots. However, the last 10-15 years or so have seen huge scientific and technological progress in the area of natural language processing: “...specialized efficient language processing algorithms, hardware with greater computing power and storage capacities, large volumes of digitized text and speech data and, most importantly, powerful new methods of statistical language

processing that could exploit the language data for learning hidden regularities governing our language use. Lately Google's web search, Autonomy's text analytics, Nuance's speech technology, Google's on-line translation, IBM Watson's question answering and Apple Siri's personal assistance have given us but a glimpse of the massive potential behind the evolving language technologies. Leading-edge industry has already reacted, but this time much more decisively. IBM, SAP, SDL, Apple, Google, Amazon, Nokia, Nuance, Facebook and others have started acquiring language technology enterprises, among them many small promising start-up companies"¹. Advanced technologies, enabled by natural language processors, such as those in automotive industry or, more recently in intelligent domotics, get us closer to the Science Fiction predictions, but only for very few languages. On-line machine translation services such as those offered by Google, Microsoft or Yahoo allow for assimilation of knowledge originally expressed in tens of languages unknown to the standard reader. Translations are available for many language pairs, but with very different quality. This is not arbitrary, but a direct consequence of the quantity and quality of the available linguistic resources.

2 Data hunger: better data is more data

With the great progress in data-driven machine learning methods and algorithms, to a large extent language independent, the focus of the natural language processing research shifted from individual language modelling to the more appealing multilingual statistical based approaches. The general lesson learnt from the latest research and development results is that the most urgent need is building an infrastructure to collect and distribute large quantities of multilingual data:

- a) monolingual lexicons, grammars, text and speech corpora for as many languages as possible;

¹Uszkoreit, H. (2012). Language Technology Before the Horizon. IT for Human Language, Understanding and Thought. Personal communication

- b) bi-lingual lexicons, grammars, text and speech corpora for as many language pairs as possible.

Currently, there are several large international initiatives such as CLARIN-ERIC or META-NET which complement and improve the services of older language resources associations such as ELRA/ELDA in Europe or LDC in USA. They were funded for creating appropriate technological infrastructures to support:

- a) collecting, organizing and disseminating information that gives an updated insight into the current status and the potential of language related activities, for each of the national and/or language communities represented in the project. This includes organizing and providing a description of: language usage and its economic dimensions; language technologies and resources, products and services; main actors in different areas, including research, industry, government and society in general; public policies and programmes; prevailing standards and practices; current level of development, main drivers and roadblocks; etc;
- b) assembling and preparing language resources for distribution. This includes collecting languages resources; documenting them and upgrading them to agreed standards and guidelines; linking and cross-lingual aligning them where appropriate.
- c) distributing the assembled language resources through exchange facilities that can be used by language researchers, developers and professionals. This includes collaborating with other projects and, where useful, with other relevant multi-national forums or activities. This includes also help in building and operating broad inter-connected repositories and exchange facilities;
- d) mobilising national and regional actors, public bodies and funding agencies by raising awareness with respect to the activities and results of the project, in particular, and of the whole area of language resources and technology, in general.

The web is the largest space from where such multilingual data can be collected, but there are several impediments in using this data:

- a) the web is highly unstructured and it requires significant effort to discover language data useful for technological developments;
- b) the IPR restrictions on many valuable resources (mono- and bilingual dictionaries, lexical ontologies, literature, etc) prevent the downloading and further use for building language and translation models;
- c) the IPR free resources are usually of low quality and need significant work to bring them to a usable quality; for instance, many texts in Romanian are written without diacritics, or with different character codes; user generated content is frequently affected by ungrammatical language, slang and coded abbreviations; additionally, the “google-isation” effect (posting on the web texts translated by Google) generates more and more poor quality language data. In spite of the data hunger of the statistical methods, the data source selection is of crucial importance in order to construct reliable language and translation models;
- d) Quantities of useful language data (both monolingual and multilingual) is highly unbalanced among the languages of the world.

The data-driven methods in machine translation among the language pairs for which large and good quality language resources exist (parallel corpora based on professional translations, bilingual electronic dictionaries, multilingual lexical ontologies, etc) demonstrated that the data issue is essential. Several experimental studies demonstrated that good quality automatic translations may be obtained in clearly delimited universes of discourse and for specific text registers, provided *enough* clean parallel text data is available. Typical examples are: formal language in juridical and legal area (e.g. the French-English parallel corpus based on The Hansards of the 36th Parliament of Canada; the 22 language parallel corpus of the Acquis Communautaire) or instructional language as in user manuals (e.g. Microsoft, UNIX, KDE

manuals, etc). What “*enough*” parallel data means is dependent on the universe of discourse and the linguistic registers used in the corpus, but most successful translation systems report at least one million of sentence pairs in the training/learning translation models and over one billion words in the monolingual corpora used for language modelling. To have a rough idea, a novel such as famous Orwell’s “1984” has about 6400 sentences per language (and about 110,000 words) in the Multext-East parallel corpus containing a dozen of different translations of the original.

On the Web there are almost 400 languages, each being spoken by more than 1,000,000 persons. It might sound as a reasonable objective to develop cross-lingual technological services for any pair of these languages. That is, almost 80,000 uni-directional language pairs! Theoretically, such an aim may be attained with the cutting edge technologies based on statistical methods and machine learning. The problem is that it is impossible to find on the Web parallel corpora for more than 200-300 of these language pairs. In fact, except maybe for less than a dozen of languages, the extant parallel corpora are very small, highly specialized or unavailable for research and development purposes.

Is this a dead-end? No, because following the lead of Munteanu and Marcu (2005), recent research (Rauf and Schwenk, 2009, 2011), (Ion et al, 2011a), (Skadiņa et al, 2010a,b; 2012), (Ştefănescu et al., 2012) etc., developed very promising methods to overcome this gap, by mining large bi-lingual collections of *comparable documents*. Unlike parallel data, comparable data can be found on the Web in much larger quantities (several orders of magnitude). Such collections are referred to *as comparable corpora*. A pair of documents is called comparable if they are about the same topic and use fragments of text that might be considered reciprocal translations. Based on this definition, depending on the quantity of overlapping translations, comparable corpora may be classified as *strongly comparable*, *medium comparable* and *weakly comparable*.

Comparable corpora for a language pair L1-L2 are usually built based on focused collection of monolingual data in L1 and L2 followed by a preliminary pairing of the cross-lingual most similar documents

in the two collections of documents. Afterwards, the document pairs with the similarity scores above a user-selected threshold are subject to an in-depth analysis to detect any parallel or almost parallel sentences. The major processing steps are suggested by the diagram in Figure 1 and will be briefly described in the following sections.

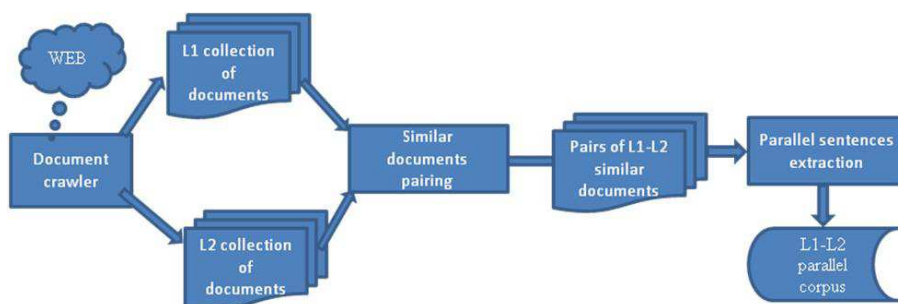


Figure 1. Processing flow for extraction of parallel data from comparable corpora

3 Collecting general and domain specific comparable corpora

The recently finished ACCURAT project² (2010-2012) developed several innovative methods and efficient algorithms to collect comparable data (Skadiņa et al, 2012). In principle, there are two types of comparable corpora one would be interested in collecting from the Web: general language corpora and domain specific corpora, containing more often than not specialized terminology.

Aker et al. (2012) describe the methodology and assumptions used to collect general language texts and assemble them into corpora. To do this, they make use of the current news articles and download huge amount of article titles using Google News Search and RSS News feeds. The downloaded titles are split into different bins based on their pub-

²European project no. 248347 (www accurat-project.eu).

lication dates. Each bin contains titles of the same week. Based on the motivation that news titles are a good indicator for the content of the news document (Edmundson, 1969, Lopez et al. 2011) the titles from each bin are taken as representatives of document contents and paired using different heuristics such as cosine similarity, title length difference, and publication date difference. Only contents of “good” article pairs are downloaded. This reduces costs measured in hard disk space and computational power, and also reduces noise in the pairing process by limiting search to one week time span. Following this strategy, for the languages of the project (Croatian, English, Estonian, German, Greek, Latvian, Lithuanian, Romanian and Slovene) the general crawler collected and preliminary classified as mentioned above tens of thousands of documents. The number of harvested and paired documents varied from 720 for Croatian-English to 29341 for German-English, with an average of 7366 documents per language pair. The document pairing based on the general heuristics (e.g. title cosine similarity, publication data) is extremely fast but inherently imprecise. However, the reduction of search space is significant, making room for more sophisticated and time-consuming algorithms to further filter out as much noise as possible.

For collecting domain-specific corpora from the web, a highly configurable Focused Monolingual Crawler (FMC) tool has been developed by our Greek partners from ILSP, based on the Bixo³ open-source web mining toolkit. Given a narrow domain (topic) and a language, the FMC tool requires two manually or semi-automatically produced input datasets: (i) a list of topic multi-word term expressions and (ii) a list of topic-related seed URLs (Skadiņa et al, 2012).

The user can then optionally configure FMC in a variety of ways, e.g. set file types to download, domain filtering options, self-terminating conditions, crawling politeness parameters, to name but a few. Crawling starts from the seed URLs and expands dynamically to other URLs, while a lightweight text classification is performed on the web pages being visited, so that to retrieve only those web documents that are relevant to the chosen topic. Operations such as boilerplate

³<http://bixo.101tec.com/>

removal, text normalization and cleaning, language identification, etc. are done during runtime, whereas some post-crawling processing steps (including removing duplicates, post-classification and filtering, etc.) are also implemented. The FMC output consists of the collected web documents in HTML and text format (UTF-8 encoding) as well as their metadata. Similarly to general language crawler, FMC achieves a preliminary pairing, removing from further consideration as many as possible unrelated documents. By using FMC, 28 comparable corpora have been constructed on 8 narrow domains⁴, in 6 language pairs⁵ amounting to a total of more than 148M tokens.

4 Pairing similar documents in comparable corpora

A metric for measuring comparability of pairs of documents in different languages performs two main functions: (1) *evaluates the quality* of the collected comparable corpora (2) *enhances* the corpora by ranking pairs of documents by their comparability, which indicates the likelihood of retrieving good-quality translation equivalents from the aligned document pairs. The consortium developed several programs to evaluate the comparability of the documents in the collected corpora.

Each of these programs generates pairs of documents associated with a comparability score. They differ both in accuracy but also in the running time necessary to complete the task. For instance, the EMACC (Expectation Maximization Alignment for Comparable Corpora) tool (Ion et al, 2011) although provided almost perfect pairings the algorithm is highly intensive and needs several days to finish pairing a relatively small comparable corpus of around 5000 documents per language.

On the other hand, the lexical based metric, DicMetric (Su et al., 2011) does not make categorical decisions and computes (very fast)

⁴Renewable Energy, Political News, Sports News, Technological News, Natural Disasters, Automotive Engineering, Assistive Technology, Software Localization

⁵EN-LV, EN-LT, EN-HR, EN-RO, EN-EL and EN-DE

similarity scores among various pairs of documents. It is based on bilingual dictionaries, and uses lexical, keyword, and named entity features which are weighted and compared as cosine similarity between the feature vectors. The weights were experimentally established so that the combination of these internal features could accurately predict externally defined comparability categories: parallel corpora, strongly comparable corpora and weakly comparable corpora. DicMetric produces a number in the range $[0, 1]$, with higher values corresponding to greater comparability. After the pairing analysis, the $[0, 1]$ interval was split into three intervals $[0.1, 0.2)$, $[0.2, 0.4)$, and $(0.4, 1]$ corresponding to the weakly comparable, strongly comparable and parallel documents as judged by the human assessors. The Spearman correlation among the automatic labeling and human annotation was very high, ranging from 0.883 to 0.999 with an average of 0.975.

5 Extraction of MT-related data from comparable corpora

By “MT-related data” extracted from comparable corpora we understand collections of translation equivalent chunks of text. Such a chunk may contain a pair of terminological expressions, a pair of named entities, a pair of regular phrases or even a pair of sentences or paragraphs. The ACCURAT project developed several tools for extracting this kind of translation equivalents. The general approach for less-resourced pairs of languages was to first extract monolingually lists of name entities and terms for each project language, and then to map crosslingually the extracted lists. All these tools are largely documented in one public deliverable of the project (Ion et al., 2011b) and can be downloaded from the project’s public site <http://www accurat-project.eu>. For name entities extraction the consortium partners either reused and adapted public language independent software which comes al-

ready trained for English (OpenNLP⁶, Stanford NER⁷ and MENER⁸), trained for some project languages (Latvian Lithuanian, Greek) or developed new tools, language dependent due to specific tokenization rules (NERA1 for English and Romanian, CroNerc for Croatian). The underlying processing models vary from Conditional Random Fields (Stanford NER), Maximum Entropy (OpenNLP, MENER, NERA1) to Rule-based (CroNerc). The monolingual terminological and named entities lists were cross-lingually mapped using GIZA++ dictionaries and various string-similarity measures (Stefănescu, 2012).

Identifying corresponding named entities in different languages works reasonably well (with precision better than 90%). However, this is not the case for mapping technical terms. We argue that one of the reasons is the lack of terminological and name-entity gold-standards and as such, the interpretations are highly subjective.

The extraction of chunks of parallel phrases and sentences from comparable corpora is a more difficult task than extraction and cross-lingual mapping of named entities and terms. The usual sentence alignment techniques applicable for parallel corpora rely on a fundamental property: the translation equivalent paragraphs (and to a large extent, sentences) have the same order in the two parts of the bitext. This property, which significantly reduces the alignment search space, is not valid anymore in comparable corpora.

LEXACC is a Lucene⁹-based phrase extraction algorithm from comparable corpora (Stefănescu et al., 2012) using cross-lingual information retrieval techniques. This program has been designed and implemented with the main emphasis on weakly comparable documents and, when available, it uses document pairing which could be explicitly specified (ex EMACC provided) or take into account all document pairs with a comparability score above a user specified threshold (as DicMetric generates). If document pairing is not available, it overcomes this lack

⁶<http://incubator.apache.org/opennlp/index.html>,

⁷<http://nlp.stanford.edu/software/CRF-NER.shtml>

⁸A highly modified version of the system developed by Chieu and Ng, the best-scoring system in the CoNLL-2003 shared task.

⁹<http://lucene.apache.org/core/>

on the expense of significant additional running time.

The collected documents in one of the languages of the comparable corpus (let's call it the target language) are multi-criterially indexed using the Lucene environment. The indexing phase requires a light pre-processing step¹⁰: each sentence of the target documents is stemmed (a list of endings in each language of interest is necessary) and all the functional words are removed (a list of functional words in each language of interest is required). Besides the stemmed content words, each target sentence is indexed by *its length class* (short, long and average) and the document pair in which it appears. The *length class* of an indexed sentence is computed based on average lengths of indexed sentences and standard deviation of the current sentence length from the average length. After the indexing phase, each sentence in the source language documents is turned into a Lucene Boolean query. This query generation follows the following steps (Ştefănescu et al., 2012):

- 1) the input sentence is stemmed and the functional words are purged;
- 2) the remaining stems are replaced by a disjunction of translation equivalents (a translation dictionary for the language pair of interest is necessary);
- 3) the query is conjunctively added the estimated length class of the parallel sentence (short, long and average);
- 4) if available, the document pair which the source sentence belongs to is added as a search constraint.

¹⁰Actually, LEXACC may take advantage of “heavier” resources (large bilingual lexicons) and processing tools: part of speech tagging, lemmatization, chunking. Indexing and retrieval of the information of interest is much more precise if such pre-processing is available. However, in the standard version we opted for relying on minimal pre-processing tools (stemmer) and resources (lists of typical endings for inflective languages, lists of functional words and seed bilingual lexicons) so that any pair of languages (especially for under-resourced ones) could be dealt with.

The translation dictionaries used in step 2) are automatically extracted using GIZA++ (Och and Ney, 2003) from whatever parallel corpora may be found for the considered language pair. The better translation dictionaries the better extraction results are.

The query built this way, is sent to Lucene search engine and the best matching N target sentences (implicitly 50) are returned. If the pairing information is available (item 4 above) the search will be restricted only in the target document of the pair. Otherwise, the search will consider all indexed sentences in the target language.

All the target sentences returned by Lucene search engine are similarity scored against the source sentence. LEXACC reuses the similarity measure of RACAI’s previous PEXACC system (Ion, 2011) which is a weighted sum of several *reifying* feature values (Tufiş et al., 2006). These features have been selected (Ştefănescu, et al. 2012), as indicative for the “parallelism” of two sentences: translation probabilities, relative position of the translation equivalents, final punctuation, etc. The weights are dependent on language pair and were optimized by a logistic regression classifier (trained on 10,000 parallel sentences as positive examples and 10,000 non-parallel sentences as negative examples. For a detailed presentation of LEXACC see (Ştefănescu et al., 2012). Besides full sentences, LEXACC may extract sub-sentential fragments as well. In this case the size of extracted data is significantly larger. Because manual validation is a very time consuming task, we restricted ourselves only to parallel sentence pair evaluation. Another motivation for preferring parallel sentences to sub-sentential chunks stems from the need to avoid as much as possible duplication. Identical sentence pair, although present in comparable corpora, are less numerous than sub-sentential word groups. All the sentence pairs that receive a similarity score above a user established confidence threshold, are retained and added to the parallel corpus under construction.

The quantity of (quasi-)parallel sentences extracted from the news corpora collected by the consortium for each language pair varies depending on the quantity of crawled documents and their comparability scores.

The Table 1 shows, for four language pairs, the results of manual

evaluation of the extraction process. As one can see, the extraction rate for English-Latvian comparable collected corpus is 1.44% with a precision of 84%. It means that 84% of extracted sentence pairs were correct and that for extracting 1 Mb of parallel text, 69.4 Mb of comparable corpus had to be collected. The table also shows, that when confidence threshold is increased (from 0.27 to 0.45) the precision of the extracted data also increased. As a matter of fact, we found that for a confidence threshold of 0.6 all the English-Romanian extracted sentence pairs were correct.

Table 1. Parallel sentences extracted by LEXACC from the ACCURAT News Comparable corpora

Lang. pair	Size of comparable corpora	# Extracted sentence pairs/size (MB)	Confidence threshold	Precision
en-lv	76.34 MB	3679 /1.1MB	0.27	84%
en-lt	74.80 MB	1583 /0.57MB	0.27	84%
en-et	34.78 MB	673 /0.2 MB	0.27	84%
en-ro	71 MB	2019 / 0.6MB	0.45	93%

This evaluation allows us to answer a possible question (at least with respect to the analyzed languages): what is the quantity of comparable corpora one has to collect in order to get *enough* data for a machine translation experiment? The answer depends on the language pair, the domain of the comparable corpora and what the purpose of the data is. If the data is meant for building a genuine new SMT, the answer is related to what we said in the section 2. If we want an English-Latvian SMT for the news domain, we would need to collect about 20.7 GB of comparable texts out of which we will presumably extract more than 1,000,000 of parallel sentences. If the extracted parallel data will be used in domain adaptation of an existing English-Latvian SMT, the size of the necessary comparable news corpora would

be around 0.8 GB¹¹. According to the current technology these figures are not scarring anymore. If such data is somewhere on the Web it may be put to good service for lesser resource languages. These estimations took into account some kind of worst-case scenario, because from the point of view of potential parallel sentences, the News corpora collected by the consortium with a general crawler may be characterized as weakly comparable corpora. For strongly comparable corpora, such as Wikipedia, the parallel sentence extraction rate is much higher (e.g. for Romanian-English this rate was about 70%, that is 80 times higher than for the News comparable corpora). In general, state of the art focused crawlers produce comparable corpora with much higher degree of comparability than the general crawlers, but on the other hand, they collect less data. The Table 2 and Table 3 exemplify the monolingual corpora collected in a narrow domain – renewable energy (Table 2) – from which LEXACC extracted the (quasi-)parallel sentences (Hunsicker and Chen, 2012) for various language pairs.

Table 2. Collected comparable monolingual corpora about renewable energy

LANGUAGE	SIZE (SENTENCES)
Croatian	19,742
Lithuanian	62,902
Latvian	23,893
Romanian	39,671
English	607,816

As one can see, the vast majority of the Latvian documents were translation of some English documents and to a large extent this was also the case for Romanian documents.

The extracted parallel data was used to adapt to the new domain (renewable energy) some general baseline SMT systems for the lan-

¹¹This estimation is based on experiments conducted by Sabine Hunsicker of DFKI within the ACCURAT project, which showed that good results in domain adaptation of a reliable SMT would require about 40,000 domain specific parallel sentences.

Table 3. Parallel data extracted from renewable energy comparable corpora

LANGUAGE PAIR	SIZE (SENTENCES)	EXTRACTION RATE (%)
Croatian-English	8,237	41.72
Lithuanian-English	16,743	26.61
Latvian-English	22,992	96.22
Romanian-English	26,939	67.90

guage pairs shown in Table 3. The improvements of the translation quality, measured in terms of BLEU scores (Hunsicker and Chen, 2012) were significant, ranging from 3.04 point for English-Romanian up to 31.84 points for English Lithuanian.

6 Conclusions

In this article we described a processing flow for exploiting comparable corpora in collecting parallel sentences meant for improving translation quality for under resourced languages and/or narrow domains. We presented tools and resources for collecting, evaluating and aligning of comparable texts for application in machine translation. MT-related data extracted from comparable corpora (parallel named entities pairs, parallel term pairs, parallel sub-sentential chunks and parallel sentences) can be reliably found even in weakly comparable corpora. Given that comparable corpora can be collected in large quantities (say GB), even a few percentages of extracted MT-related data can provide a significant help in building or adapting a SMT for which proper training parallel corpora cannot be easily found.

Tools and resources described in this paper are publicly available and largely described on ACCURAT project website: www accurat-project.eu.

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Comparison of indices of disproportionality in PR systems

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Abstract

Comparative analysis of 12 indices of disproportionality by such characteristics as: metric, definition domain, representation uniformity, invariance and utilization field, is done. As a result of comparison, the opportunity to use as index of disproportionality in elections the Average relative deviation one is argued. Graphic representation for the upper limit of optimal solutions' disproportionality, when using this index, is shown.

Keywords: collective decisions, elections, proportional representation, index of disproportionality, comparative analysis.

1 Introduction

When taking collective decisions, using voting systems with proportional representation (PR), to minimize the disproportion of deciders' will representation in the decision is required – disproportion caused by the character in integers of the number of deciders and that of alternative options. To estimate this disproportion, various indices were proposed, some of which are described in [1-8].

As it is shown in [9], minimizing the disproportionality, within the meaning of each of 11 such indices (Rae [3], Loosemore-Handby [1], Rose [5], Grofman [6], Lijphart [4], Gallagher [1], Square deviation [9], Sainte-Laguë [1], d'Hondt [9], Mean relative deviation [8] and Relative standard deviation [8]), is ensured, as appropriate, by one of three methods (votes-decision rules – VD): Hamilton [10], Sainte-Laguë [1] or d'Hondt [1]. But other methods are known, too, including that of

Huntington-Hill [10], Largest remainders with Droop quota [7], Largest remainders with Hagenbach-Bischoff quota [2], Largest remainders with Imperiali quota [2], etc.

In significant number of cases, solutions obtained with different methods do not coincide, which, in pursuing the same goals, shows possible reserves in the accuracy of used voting systems. To eliminate the uncertainty of applying different VD rules in specific cases, it is important to elucidate, first, the essence and mission of voting, then to select the appropriate index for assessing the disproportionality of deciders' will representation in the decision, further formulation of the respective optimization problem and, finally, defining the method for determining the expected optimal solution.

Thus, one of the important steps in implementing a voting system, adequate to voting mission in a particular case, is to select the relevant index of disproportionality. A successful selection requires as more complete as possible comparative analysis of known indices. Some such issues are addressed in [1, 4-6, 8]. In the following an attempt of comprehensive characterization of 12 indices of disproportionality is taken.

The most known practices with refer to the use of voting systems are, probably, the ones related to elections. Therefore, further, the addressed aspects of indices of disproportionality will be investigated, not harming the universality, through the party-lists (blocks, coalitions) PR elections – RPL. Also, it is considered that all voters have equal rights, i.e. all votes have the same weight. Results, obtained in such assumptions, can be, as a rule, relatively easy extended for elections with weighted votes. First, in Section 2 the general formulation of the problem of optimizing the distribution of seats between parties is given, later the essence of 12 indices of disproportionality (Section 3) is described and the criteria for the comparison of these indices (Section 4) are listed. Subsequently, in Sections 5-9, the concerned indices are characterized in accordance with the comparison criteria and, finally, in Section 10 the multidimensional comparison of the 12 investigated indices is performed.

2 The problem of distribution of seats in LPR elections

Identification of the place and elucidation of the role of indices of disproportionality in LPR elections can be made basing on formalizing the problem of seats distribution. Let $(i = \overline{1, n})$: M – total number of seats in the elective body; n – number of parties that have reached or exceeded the representation threshold; V – total valid votes cast for the n parties; V_i – total valid votes cast for party i ; x_i – number of seats to be allocated to party i .

If index I is used as disproportionality criterion, then the problem of optimizing the distribution of seats among n parties can be formulated as follows [8]. Let quantities (natural numbers) M ; n ; V_i , $i = \overline{1, n}$ are known and

$$\sum_{i=1}^n V_i = V. \quad (1)$$

It is required to determine the values of unknowns x_i ($i = \overline{1, n}$) – integers, which would ensure the extreme value for I (minimum or maximum, depending on the essence of I)

$$I = f(M; n; V_i, x_i, i = \overline{1, n}) \rightarrow \text{extremum} \quad (2)$$

in compliance with restrictions:

$$M = \sum_{i=1}^n x_i; \quad (3)$$

$$x_i \geq 1, \quad i = \overline{1, n}. \quad (4)$$

Sometimes, problem (2)-(4) is necessary to complete with monotonicity constraint, formalized in [11] as: to ensure the non-decreasing character of functions $x_i(D_i)$, $i = \overline{1, n}$, where [8]

$$D_i = dV_i = MV_i/V, \quad i = \overline{1, n} \quad (5)$$

are the party i rights in the elective body, delegated by the V_i votes of the electors (the summary value of the V_i votes), and $d = M/V$ is the value of one vote.

If, for example, in (2) the Sainte-Laguë index [1] is used as index I , then

$$I_{\text{S-L}} = \sum_{i=1}^n \frac{1}{v_i} (v_i - m_i)^2 = 100 \cdot V \sum_{i=1}^n \frac{1}{V_i} \left(\frac{V_i}{V} - \frac{x_i}{M} \right)^2 \rightarrow \min, \quad (6)$$

where $v_i = 100V_i/V$, $m_i = 100x_i/M$. It can be easily proved (using the Lagrange multipliers method) that, when quantities $x_i \geq 0$, $i = \overline{1, n}$ are real numbers, the problem {(2)-(3), (6)} solution is given by equalities

$$m_i = v_i, \quad i = \overline{1, n}. \quad (7)$$

This solution coincides with the proportional representation. But in practical cases, quantities x_i ($i = \overline{1, n}$) are integers, the problems (2)-(4) and (2)-(5) being of mathematical programming in integers.

In real elections, the probability to satisfy the equalities (7), at quantities x_i ($i = \overline{1, n}$) being integers, is very small. Thus, in real LPR elections there is a certain disproportion of seats distribution among parties. In such cases, it is important to assess the disproportionality in question. For this purpose, diverse criteria are used, called disproportionality indices, 12 of which are described in Section 3.

3 Indices of disproportionality

M. Gallagher highlights [1] two broad categories of measures of disproportionality in LPR elections: 1) measures based on the absolute difference between the party's seats and votes; 2) measures focused on the ratio between a party's seats and its votes. In both these categories, primary in assessing the disproportionality are parties. In reality, however, primary are voters; voters should be represented equally in the elective body or, if it is not possible, with a smallest possible disproportion. Therefore, at the base of the index of disproportionality the

value of each vote should stand – vote that reflects unequivocally the rights of each voter in the election. Namely, starting from the value of a vote $d = M/V$, in [8] for this purpose the index of Mean relative deviation is derived and proposed, which subsequently was converted to the form that plays parties representation.

Diverse indices of disproportionality are known and used. The essence of twelve of them is the following.

Rae index [3], noted here I_{Rae} , is proposed in 1967 and is determined as the mean absolute deviation of the percentage of votes from the percentage of seats per one party

$$I_{Rae} = \frac{1}{n} \sum_{i=1}^n |v_i - m_i|. \quad (8)$$

Loosemore-Handby index [1], noted here I_{L-H} , is proposed in 1971, can be interpreted as the total absolute deviation between m_i and v_i for parties with deficit of seats or the percentage of seats taken from some parties (parties that have become, under this operation, with deficit of seats – losing parties) and distributed to other parties (parties that have become, under this operation, with excess of seats – gaining parties) and is determined as

$$I_{L-H} = \frac{1}{2} \sum_{i=1}^n |v_i - m_i|. \quad (9)$$

Rose index of proportionality [5], noted here I_R , is proposed in 1998, being a normalized version of Loosemore-Handby index, in such a way that a value of 100% corresponds to proportional representation, and 0% – to the worst case, and is determined as

$$I_R = 100 - \frac{1}{2} \sum_{i=1}^n |v_i - m_i|. \quad (10)$$

Grofman index [6], noted here I_{Gr} , is proposed in 1985, differs from the Rae one only by the replacement of n by “effective number” of parties N , introduced by Laakso and Taagepera in [15].

$$I_{\text{Gr}} = \frac{1}{N} \sum_{i=1}^n |v_i - m_i|, \quad (11)$$

where $N = 10^4 / \sum_{i=1}^n v_i^2$. The value of N can be calculated from m_i [15], too, but, taking into account that when determining m_i , $i = \overline{1, n}$ primary are quantities v_i , $i = \overline{1, n}$ (and not vice versa) and quantities m_i , $i = \overline{1, n}$ can be with deviation from proportional representation, in this paper the already specified expression will be used.

Lijphart index [4], noted here I_{L} , is proposed in 1994 and represents the maximal absolute deviation between m_i and v_i

$$I_{\text{L}} = \max_{i=\overline{1, n}} |v_i - m_i|. \quad (12)$$

Gallagher index [1], noted here I_{Ga} , is proposed in 1991, differs from the Loosemore-Handby one by the representation of not absolute but of square total deviation between m_i and v_i for parties with deficit of seats, amplifying the weight of larger differences $|v_i - m_i|$ at the expense of weights of smaller differences $|v_i - m_i|$, and is determined as

$$I_{\text{Ga}} = \sqrt{\frac{1}{2} \sum_{i=1}^n (v_i - m_i)^2}. \quad (13)$$

It is easily seen that Gallagher index differs a little from the **Least square index**, noted here I_{LSM} , largely used in practice in diverse domains to assess discrepancies

$$I_{\text{LSM}} = \sqrt{\sum_{i=1}^n (v_i - m_i)^2}. \quad (14)$$

Sainte-Laguë index [2], noted here $I_{\text{S-L}}$, is determined as

$$I_{\text{S-L}} = \sum_{i=1}^n \frac{1}{v_i} (v_i - m_i)^2 = \sum_{i=1}^n v_i \left(1 - \frac{m_i}{v_i}\right)^2. \quad (15)$$

D'Hondt index [9], noted here I_H , represents the maximal ratio between v_i and m_i (in [2] in this purpose the maximal ratio between m_i and v_i) is proposed:

$$I_H = \min_{i=\overline{1,n}} \frac{v_i}{m_i}. \quad (16)$$

Mean relative deviation index [8], noted here I_d , specifies the average relative error (deviation) on election of the representation in the elective body of electors' rights $d_i = V_i/V$, $i = \overline{1,n}$ from the mean value $d = M/V$ and is determined as

$$I_d = \frac{\Delta d}{d} 100 = \sum_{i=1}^n |v_i - m_i|, \text{ where } \Delta d = \frac{1}{V} \sum_{i=1}^n V_i |d_i - d|. \quad (17)$$

Here $|d_i - d| = \Delta d_i$ specifies the absolute error of the representation in the x_i seats of the value d of rights of each elector that votes for party i , and Δd – the mean absolute error per election (totality of V voters) of the representation in the elective body of an elector rights of value d . The mean relative deviation $100 \cdot \Delta d/d$, measured in percent of Δd by d , is equivalent, as it is shown in [8], to the percent of seats by which the distribution $\{x_1, x_2, \dots, x_n\}$ differs from the distribution, which assures the equal representation in the elective body of electors' rights (of value d for each).

Relative standard deviation index [8], noted here I_σ , specifies the relative standard deviation of the representation in the elective body of electors' rights $d_i = x_i/V_i$ from the mean value $d = M/V$ and is determined as

$$I_\sigma = \frac{\sigma}{d} 100 = 10 \sqrt{\sum_{i=1}^n \frac{1}{v_i} (v_i - m_i)^2},$$

$$\text{where } \sigma = \sqrt{\frac{1}{V} \sum_{i=1}^n V_i (d_i - d)^2}. \quad (18)$$

Here σ is the standard deviation of the representation in the elective body of electors' rights d_i , $i = \overline{1, n}$ from the mean value d , by applying, for simplicity, the division to V and not to $V - 1$, the value of V being relatively large. In (18) I_σ is measured in percent of σ related to d .

Quasi invariant index [14], noted here I_{inv} , specifies the average number of seats to one party, by which the distribution $\{x_1, x_2, \dots, x_n\}$ differs from the proportional one and is determined as

$$I_{\text{inv}} = \frac{M}{100n} \sum_{i=1}^n |v_i - m_i|, \text{ seats/party.} \quad (19)$$

4 Criteria for the comparison of indices

The multitude of used indices of disproportionality is caused by the diversity of both, votes-seats (VS) rules applied in LPR elections and that of goals pursued in research. There is not yet a universally accepted index of disproportionality. M. Gallagher considers [1] that at theoretical level the soundest is, probably, the Sainte-Laguë index. One of the most used in the last years is the Gallagher index. Therefore, an important issue is to select or define such an index that will reflect as appropriate the essence of LPR election.

Of course, a comparative analysis of the respective indices would facilitate the successful selection of appropriate index in a certain situation. At the same time, a comparative analysis of various indices is difficult, because of their different meaning, in many cases; the value of already defined index is measured, as a rule, in different units. Hence, it follows the need to take into account, when comparing indices, diverse significant aspects, criteria. In the following, comparison will be made, where possible, by such characteristics as: metric, the definition domain, uniformity of representation, invariance and the usable field, including the comparative analysis.

5 Metric of indices

As it can be seen, the first five of indices listed in Section 3 – Rae (8), Loosemore-Handby (9), Rose (10), Grofman (11), Lijphart (12) and that of Mean relative deviation (17) are based on the absolute deviation of the percentage of seats m_i from the percentage of votes v_i ; the following four – Gallagher (13), Least square (14), Sainte-Laguë (15) and that of Relative standard deviation (18) are based on the square deviation of m_i from v_i , and that of D'Hondt (16) is based on the ratio between v_i and m_i . Regarding the measure unit of their value, this is for the index ($i = \overline{1, n}$):

- Rae – %/party, the percentage being in sense of the absolute summary deviation of m_i from v_i . Therefore, this can be interpreted as the average percentage to a party of seats, by which the distribution x_i , $i = \overline{1, n}$ differs from the proportional one, being measured in %seats/party;
- Loosemore-Handby – %, the percentage being in sense of the absolute summary deviation of $m_i/2$ from $v_i/2$. In other words, this can be interpreted as the summary percentage of seats taken from some parties (parties that have become, under this operation, with deficit of seats – losing parties) and distributed to other parties (parties that have become, under this operation, with excess of seats – gaining parties), being measured in %lost seats/party;
- Rose – %, the percentage being in sense of complementary to 100% of Loosemore-Handby index (index of proportionality), namely is measured in $100\% - \%$ lost seats;
- Grofman – %/effective party, the percentage being in sense of absolute summary deviation of m_i from v_i , namely is measured in %seats/effective party;
- Lijphart – %, the percentage being in sense of absolute maximum deviation of m_i from v_i , namely is measured in %seats;

- Mean relative deviation – %, the percentage being in sense of average relative error per election of the representation in the elective body of an elector rights or, that is the same, – in sense of summary absolute deviation of m_i from v_i , namely is measured in %seats;
- Sainte-Laguë – %, the percentage being in sense of the average, weighted by $1/v_i$, of squared deviation of m_i from v_i ;
- Gallagher – %, the percentage being in sense of square deviation of m_i from v_i , divided by $\sqrt{2}$, namely is measured in %seats/ $\sqrt{2}$;
- Least squares – %, the percentage being in sense of square deviation of m_i from v_i , namely is measured in %seats;
- Relative standard deviation – %, meaning the percentage represented by the standard deviation σ of an elector rights $d = M/V$;
- D’Hondt – non dimensional, what part of m_i constitutes v_i for the smallest such ratio. This index multiplied by 100 can be measured in %;
- Quasi invariant – seats/party, representing the average number of seats to a party, by which the distribution $x_i, i = \overline{1, n}$ differs from the proportional one.

Thus, for all twelve listed above indices the used metric differs. Even for indices measured in percent, the percentage has a different sense, being from different absolute quantities.

The following analytical relations among some of the 12 indices (see [9], and (17) and (19)) facilitate the comparative understanding of indices’ metric:

$$I_{L-H} = I_{Rae} \cdot n/2 = I_{Gr} \cdot N/2 = 100 - I_R = I_d/2 = 50nI_{inv}/M, \quad (20)$$

$$I_{Ga} = I_{LSM}/\sqrt{2}, \quad (21)$$

$$I_\sigma = 10\sqrt{I_{S-L}} \quad (22)$$

and $I_{\mathbf{d}} \leq I_{\sigma}$, the equality taking place only in cases when $|v_i - m_i| = \text{const}$, $i = \overline{1, n}$.

6 Definition domain of indices' values

The minimum value for Rae, Loosemore-Handby, Grofman, Lijphart, Gallagher, Least squares, Sainte-Laguë, Mean relative deviation, Relative standard deviation and the Quasi invariant indices is zero. The value zero is obtained if equalities (7) take place, and it corresponds to proportional representation. In contrast, the value of Rose index, in these conditions, is maximal and is equal to 100%. And the minimal one is 0 and corresponds to complete disproportion. The minimal value of d'Hondt index is equal to 0 and is obtained if at least one seat is assigned to a party, that has not acquired any vote – the representation is not proportional; if equalities (7) take place, then $I_{\mathbf{H}} = 1$, these being the $I_{\mathbf{H}}$ upper limit value and corresponding to proportional representation. It can be easily found, also, that if the threshold for party representation is 0, the indices' maximum limit value is: Loosemore-Handby, Lijphart and Gallagher – 100 %; Rae – $200/n$ %/party; Least squares – $100\sqrt{2}$ %; Grofman – 200% /party; Mean relative deviation – 200% ; Sainte-Laguë and Relative standard deviation – ∞ and Quasi invariant – $2M/n$. For example, the upper limit for I_{σ} index is obtained, according to (18) and taking into account that $d = M/V$, in case of upper limit of the standard deviation σ , so of upper limit of the quantity $d_i = x_i/V_i$, namely it is ∞ .

As noted in [13], the upper limit greater than 100%, for five indices of disproportionality (Grofman – 200% /party, Least squares – $100\sqrt{2}$, Sainte-Laguë – ∞ , Relative standard deviation – ∞ and Mean relative deviation – 200%), in case of their using in problems of minimizing the disproportionality, is less informative. For example, it cannot be considered real an election, in which seats will be distributed to a party that did not receive any vote. In such cases, it is reasonable to take into account the definition domain of index values for optimal solutions. For 12 such indices (indices (8)-(18), described in Section 3, and the General divisor index), the domain in question is given in [13] and,

partially, in Table 1, and for the Quasi invariant index [14] this is [0; 0,5] seats/party.

From Table 1 it can be seen that the definition domain for optimal solutions is considerably narrower than in the general case, the upper limit for disproportionality indices not exceeding 50% (Grofman and Mean relative deviation), and the lower one for indices of proportionality is not less than 50% (d'Hondt). In decreasing order, follows the upper limit for indices of disproportionality: Relative standard deviation – $100/\sqrt{3}\% \approx 57,7\%$; Least squares – $25\sqrt{2}\% \approx 35,4\%$, Sainte-Laguë – $100/3 \approx 33,3\%$, and the other (Rae, Loosemore-Handby, Lijphart and Gallagher) – 25%. The lower limit for Rose index of proportionality is 75%.

7 Uniformity of voters' will representation

In terms of uniformity of factors $|m_i - v_i|$ or v_i/m_i , $i = \overline{1, n}$ contribution to indices value, the twelve investigated indices can be grouped into two categories: 1) uniforms; 2) non uniforms. To uniforms the following indices relate: Rae, Loosemore-Handby, Rose, Grofman, Mean relative deviation and Quasi invariant, and to the non uniforms – indices: Sainte-Laguë, Gallagher, Least squares, Relative standard deviation, Lijphart and d'Hondt.

The non-uniformity of Sainte-Laguë, Gallagher, Least squares and Relative standard deviation indices is caused by the greater relative contribution to their value of greater deviations $|m_i - v_i|$ than that of smaller deviations $|m_i - v_i|$, because these deviations in indices are squared. Cause of the non-uniformity of Lijphart and d'Hondt indices is the contribution to their value of only one of the n factors (the largest absolute difference $|v_i - m_i|$ – in case of Lijphart index and the smallest ratio v_i/m_i – in case of d'Hondt index). By degree of uniformity, the non-uniform indices (of category 2) can be grouped into two subcategories: 2.1) partial uniforms – with a contribution other than 0 of all n factors (Sainte-Laguë, Gallagher, Least squares and Relative standard deviation); 2.2) non-uniforms – with the contribution of only one of the n factors (Lijphart and d'Hondt).

Table 1. Comparative characteristics of the 12 investigated indices

Index	Uniformity	Metric	Definition domain				Invariance to			Application field
			general case		optimal solution		M	n		
			min	max	min	max				
<i>Indices of disproportionality</i>										
Rae	uniform	%seats/party	0	100	0	25	no	yes	comparative analysis	
Loosemore-Handby	uniform	%lost seats	0	100	0	25	no	no	universal	
Grofman	uniform	%/ effective party	0	200	0	50	no	partial	comparative analysis	
Lijphart	non uniform	%seats	0	100	0	25	no	no	universal	
Gallagher	partial	%seats/ $\sqrt{2}$	0	100	0	25	no	no	universal	
Least squares	partial	%seats	0	$100\sqrt{2}$	0	$25\sqrt{2}$	no	no	universal	
Sainte-Laguë	partial	%	0	∞	0	$100/3$	no	no	universal	
Mean relative deviation	uniform	%seats	0	200	0	50	no	no	universal	
Relative standard deviation	partial	%	0	∞	0	$100/\sqrt{3}$	no	no	universal	
Quasi invariant	uniform	seats/party	0	$2M/n$	0	0,5	yes	yes	comparative analysis	
<i>Indices of proportionality</i>										
Rose	uniform	100%-% lost seats	0	100	75	100	no	no	universal	
D'Hondt	non uniform	%	0	100	50	100	no	no	universal	

It may be said, broadly, that the subcategory 2.2 indices are more non-uniform, than those of subcategory 2.1.

Thus, in order of decreasing degree of uniformity of factors $|v_i - m_i|$ or those of v_i/m_i contribution to the value of indices, follow: uniform indices (Rae, Loosemore-Handby, Rose, Grofman, Mean relative deviation and Quasi invariant), then the partial uniform (Sainte-Laguë, Gallagher, Least squares and Relative standard deviation) and, finally, the non-uniform ones (Lijphart and d'Hondt).

8 Invariance to M , V and n

In comparative analysis of various cases of collective decision making by voting, indices, invariant to some initial data, are useful. In LPR voting systems a part or all quantities M , V and n can serve as such initial data, depending on the purpose.

It can be proved that at $V \gg M \geq n$ all the 12 indices, described in Section 3, are, practically, invariant to the value of V . Also, Rae index (8) provides, to a considerable extent, invariance to the number n of parties, too, and the Grofman one (11) – to the effective number N of parties. Also, Quasi invariant index (19) ensures, to a considerable extent, both invariance to M and to n [14].

9 Application field

The appropriate field of using the 12 indices, described in Section 3, depends on their essence. At first analysis, one can conclude that the use of Rae (8), Grofman (11) and Quasi invariant (19) indices, for assessing the overall disproportionality of seats distribution in practical LPR elections, is not opportune. The first two of these three indices characterize the average disproportionality to a party (ordinary or “effective”), which is measured, respectively, in %seats/party and %seats/effective party. The third index also characterizes the average disproportionality to a party (ordinary), but is measured in seats/party. Therefore, these three indices is opportune to use in comparative anal-

ysis of disproportionality in diverse LPR elections, the Rae index assuring invariance to the number n of parties, the Grofman index – to the effective number N of parties, and the Quasi invariant index – both to n and to the overall number of seats M . At the same time, in such researches, the use of Rae index is preferable to that of Grofman index, the last weighting the n parties depending on values of quantities v_i , $i = \overline{1, n}$. The value of Grofman index increases with the increasing of dispersion of quantities v_i , $i = \overline{1, n}$.

The other nine indices, from the 12 described in Section 3, are designed to assess the overall disproportionality of seats distribution in LPR elections, although they may be used, in some cases with certain reservations, in comparative analysis, too. Since the Mean relative deviation index characterizes the error of elector's rights (vote) representation, this could be the most appropriate index for comparative analysis of various elections by the election overall disproportionality, too.

10 Multidimensional comparison of indices

The values of some comparison criteria for the 12 investigated indices are presented in Table 1. Preference for a particular index, based on these criteria, depends on the followed purpose. At such purposes may be referred: assessment of overall disproportionality per election; assessment of average disproportionality per election; assessment of maximal disproportionality per party; invariance to M , n and V , etc. In this section, only aspects referring to the assessment of overall disproportionality per election will be investigated, beginning with the correlation among the 12 investigated indices.

The correlation among indices, determined by relations (20)–(22), facilitates their comparative analysis. These relations cover 10 of the 12 investigated indices and define three groups of indices, strongly correlated with each other: a) I_{L-H} , I_{Rae} , I_{Gr} , I_R , I_d , I_{inv} ; b) I_{Ga} , I_{LSM} ; c) I_{S-L} , I_σ . Even if these indices differ by absolute value, all indices of each of these groups lead, in terms of minimizing the disproportionality, to the same solution: the fact of ensuring minimum of

disproportionality (within the meaning of problem (2)–(4)) for an election under one of them ensures minimum of disproportionality under each of the other indices of this group. So, in terms of minimizing the disproportionality, any of indices of that group can be used as optimization criterion (2).

Moreover, using the two indices of each of groups (b) and (c) in comparative analysis of elections, also lead to similar results – for example, when ordering elections in increasing order of disproportionality. This statement occurs for indices I_{L-H} , I_R and I_d of group (a), too, but not occurs for the other three indices of this group. Index I_{Rae} (8) is highly sensitive to the number of parties, representing, in fact, the average disproportionality by a party and not by the election as a whole, even if with the increasing number of parties the probability of greater disproportionality increases too. Index I_{Gr} (11) is also dependent on the number of parties; trying to bring elections with different numbers of parties to a common denominator, by weighting parties by the number of votes cast, this complicates and, also, makes less clear the essence of evaluated disproportionality.

From (21) it results that Gallagher index differs from the Least squares one only by the constant $1/\sqrt{2}$. Although, by normalization (dividing by $\sqrt{2}$), Gallagher index assures the definition domain $[0, 100]\%$, it becomes, at the same time, less clear the essence of the percentage of disproportionality. Moreover, the definition domain of optimal solutions, when using the Least squares index, is $[0; 25\sqrt{2}]\%$ (that for the general case is $[0; 100\sqrt{2}]\%$), the upper limit being much less than 100%. Therefore, from these two indices it would be preferable, however, the use of the Least squares index – a well-known and widely used in various fields index, the percentage being interpreted in the usual sense for this index.

In a similar mode, from (22) it results that using of both indices – Sainte-Laguë and Relative standard deviation one for assessing the disproportionality, is useless. The use of indices I_{S-L} and I_σ as optimization criterion (1) as well as in comparative analysis of LPR elections leads to similar results. For both these indices, the definition domain in general case is $[0; \infty]$, even in case of the optimal solutions

this is $[0; 100/3]$ for the Sainte-Laguë index and $[0; 100/\sqrt{3}]$ – for the Relative standard deviation index. However, the essence of index I_σ is easier to understand, the standard deviation being universally accepted and widely used in various fields, and the fact, that it is taking into account the relative standard deviation, do not worsen the situation. Thus, from these two indices it would be preferable, however, the application of Relative standard deviation index.

According to equalities (20), there exist similarities, with accuracy to constants, among indices Loosemore-Handby, Rose and the Mean relative deviation one. With refer to the other three indices from (20), namely Rae, Grofman and Quasi invariant ones, in their calculation the quantities n , N and M are also used, depending on the case.

The preliminary selection of an index for assessing the overall disproportionality per election. By uniformity, the uniform indices are preferable (with uniform contribution of factors $|m_i - v_i|$ or v_i/m_i , $i = \overline{1, n}$ to indices' value), the partially uniform ones being less preferred, and the non-uniform – non-preferred. In terms of metric, it would be preferable an index with a clear, successful interpretation of the measure unit in investigated purpose; it should adequately reflect the essence of LPR elections. Also, it would be better if the definition domain of the selected index is $[0, 100]\%$. Invariance, in examined case, does not matter, but preferably it should be an index with universal field of use. Obviously, you might not find an index that meets all these requirements. Then, it will be necessary to take into account the preferences of comparison criteria of greater importance.

In terms of uniformity of the representation of voters' will in the elective body, it would be preferable using, for this purpose, one of the uniform indices, namely: Rae, Loosemore-Handby, Grofman, Mean relative deviation, Quasi invariant or Rose ones. Indices Lijphart (12) and d'Hondt (16) are non-uniforms ones, not covering the entire set V of votes of the election, but only the votes of electors, supporters of the party with the highest deviation $|v_i - m_i|$ (Lijphart index) or, respectively, with the highest ratio v_i/m_i (d'Hondt index). Thus, these indices, being, of course, useful for specific research, less can be used to characterize the overall disproportionality of an LPR election. With

refer to indices of Least squares and the Relative standard deviation, they, like the Sainte-Laguë and Gallagher ones, are characterized by a higher relative contribution to their value of larger deviations $|m_i - v_i|$ comparatively to the relative contribution of smaller deviations $|m_i - v_i|$ (because these deviations in the index are squared); so, by definition, they cannot properly appreciate the proportional representation of voters' will of value d in the elective body. Therefore, their application, for investigated case of equality of electors' votes, is not so welcome. Their use may be indicated only in cases, when the application of uniform indices makes impossible the necessary research, the main drawback of assessing the disproportionality by absolute deviations $|v_i - m_i|$, as in indices (8) – (12), (17) and (19), consisting in that that the respective functions are not differentiable, which makes, in some cases, more difficult their apply in practice.

From the six indices, remaining to compare, the Rae, Grofman and Quasi invariant indices, according the invariance (and metric, too), are not appropriate, because they characterize the average disproportionality to a party and not that to the entire election. So we have to select one of the following three indices: Loosemore-Handby, Mean relative deviation and Rose ones. The Loosemore-Handby and Rose indices, in terms of using as index of disproportionality/proportionality across elections, are, as it is easily seen from their essence, mutually complementary and equivalent by efficiency. The difference is only in that that one (Loosemore-Handby) characterizes disproportionality, and the other (Rose) – “the degree of proportionality” of the representation in the elective body of electors' votes. Thus, for comparison with that of Mean relative deviation, one of these two indices is sufficient. However, with refer to the proportionality, it either exists (disproportionality is equal to 0) or does not exist (disproportionality is different from 0); so it is less successful to estimate “the degree of proportionality”. Thus, the comparison will be provided with Loosemore-Handby index.

The Loosemore-Handby and Mean relative deviation indices differ only by constant $1/2$. Their use both as optimization criterion (2), as well as in comparative analysis of LPR elections lead to similar results. Apparently, a slight advantage of the Loosemore-Handby index

could be in that that it is normalized, ensuring the definition domain $[0; 100]\%$, while that of the Mean relative deviation is $[0, 200]\%$ (see table 1). But, at a deeper analysis, this advantage becomes disputable, the normalization of Loosemore-Handby index leads to loss of essence in the content of the measure unit of disproportionality.

Indeed, with refer to the metric, from the 12 indices, including the Loosemore-Handby one, the clearest interpretation, in sense of conditions of proportionality (7), has the Mean relative deviation index. It measures the average relative error per election of the representation in the elective body of an elector rights of value $d = M/V$, equal to the summary percentage of seats, by which the distribution $x_i, i = \overline{1, n}$ differs from the proportional one. While, taking into account that the percentage of over represented votes is equal to that of under-represented votes in the elective body, the Loosemore-Handby index measures the percentage of additional seats allocated to votes (parties) over represented in the elective body or, equivalently, the percentage of more seats that should have to be allocated to votes (parties) under-represented in the elective body. Given the negative sense of disproportionality, the accent should be opportune to return to the second interpretation. However, if taken into account only this aspect, rendering of disproportionality would be not correct, because not only a part of votes is represented with lack of seats; the situation gets worse, in the same way, by that that another part of votes is represented with a surplus of seats. Thus, Loosemore-Handby index yields, with refer to the adequate reflecting of disproportionality, to that of Mean relative deviation.

Let's concretize this loss of essence basing on some examples. For this purpose, let's elucidate, first, the conditions, in which the Mean relative deviation index reaches 200% seats. This happens, for example, when, from two parties participating in elections, to party, which received all the votes, not to award any vote, although at proportional representation it should be allocated to it 100% of votes (deviation of 100% from the proportional distribution), and to party, which did not receive any vote to allocate all 100% of votes (deviation from the proportional distribution of another 100%). Thus, the error of 100%

distribution of seats is doubled.

Another example. Let it be two localities A and B , forming a territorial unit with a common budget, managed by a Council elected by vote. The two localities are represented in the Council by a number of councilors, respectively x_A and x_B , according to the number of inhabitants, respectively V_A and V_B (all inhabitants of the two localities have the right to vote and voted, arguing the locality representatives, and all ballots were valid). To organize the Christmas holidays, the Council decided to grant the two localities by one financial support F_A and F_B , proportional to the number of councilors x_A and x_B , i.e.: $F_A = (F_A + F_B)x_A/(x_A + x_B)$ and $F_B = (F_A + F_B)x_B/(x_A + x_B)$. One asks: Loosermore-Handby index or that of Mean relative deviation more adequately reflects disproportionality in providing the financial support in question?

Let: $V = V_A + V_B$, $F = F_A + F_B$ and $M = x_A + x_B$. Obviously, granting financial support is proportional, if to any individual citizen, regardless of locality, is returned the same financial support equal to $F/V = d_F$. But in fact to a resident of locality A a support equal to F_A/V_A is returned, and to a resident of locality B – a support equal to F_B/V_B .

Thus, the absolute difference between each of ratios F_A/V_A and F_B/V_B and the ratio F/V is the absolute disproportionality per capita in their localities, and the mean relative disproportionality I is

$$\begin{aligned} I &= \frac{1}{d_F V} \left[V_A \left| \frac{F_A}{V_A} - \frac{F}{V} \right| + V_B \left| \frac{F_B}{V_B} - \frac{F}{V} \right| \right] = \\ &= \frac{1}{F} \left[V_A \left| \frac{F x_A}{M V_A} - \frac{F}{V} \right| + V_B \left| \frac{F x_B}{M V_B} - \frac{F}{V} \right| \right] = \\ &= \left[\left| \frac{x_A}{M} - \frac{V_A}{V} \right| + \left| \frac{x_B}{M} - \frac{V_B}{V} \right| \right], \end{aligned}$$

which, multiplied by 100%, coincides with the Mean relative deviation index for this case. Thus, the Mean relative deviation index more appropriately reflects the disproportionality in providing the nominee financial support.

To note, also, that in practice there are other cases, too, when the used index has a definition domain exceeding 100%, for example, inflation and profitability. However, regarding the definition domain for optimal solutions, it, in case of Mean relative deviation index, is $[0, 50]\%$ (Table 1), the upper limit \widehat{I}_d^* , calculated according to the expression from [8], is achieved in rare cases and being at least two times less than 100% (Fig. 1).

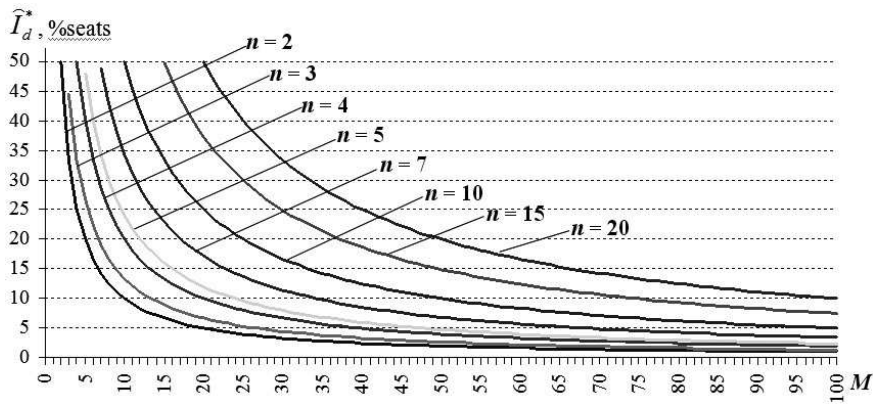


Figure 1. Graphics of the function $\widehat{I}_d^*(M, n)$

About some “shortcomings” of the Mean relative deviation index. The Mean relative deviation index is proposed recently in [8] and is therefore unknown. However, it is largely similar to the Loosemore-Handby one, well known and widely applied. The difference is only in constant $1/2$ and the content essence of the measure unit of disproportionality, discussed above. Therefore, the shortcomings of the Loosemore-Handby index, except that regarding the content essence in question, are reflected, almost equally, to the Mean relative deviation index, too.

On vulnerability of the Mean relative deviation index to “paradoxes”. A comparative analysis of six indices of disproportionality, basing on statistical data for 82 elections in 23 countries, is given in [1]. Regarding the Loosemore-Handby index, in [1], on the basis that

its application as criterion of minimizing the disproportionality leads to the use of Largest remainders method as VS rule, it is concluded that the vulnerability of the method in question to the Alabama, the Population and the New State paradoxes (see, for example, [1, 11]) implies the vulnerability to these paradoxes of the index itself. To note that, at such approach, in the same situation as the Loosemore-Handby index are the Rae, Rose, Grofman, Lijphart, Gallagher, Least squares and Mean relative deviation indices, the use of which as optimization criterion (2) implies [9] the solving of problem (2)-(3) also by the Largest remainders method.

In reality, these are two different aspects: one and the same criterion can be used in various problems, which, in their turn, may involve different optimization methods. In this particular case, if one wants that the optimal solutions not to be vulnerable to mentioned above paradoxes, it is sufficient to complete the optimization problem (2) – (3) with the constraint of ensuring a non-descending character of functions $x_i(D_i)$, $i = \overline{1, n}$, taking into account the relation (5). Such a problem, in which as optimization criterion (2) the Loosemore-Handby index is applied, already cannot be solved using the method of Largest remainders. Expected solution can be obtained according to monotone method described in [11], when using as divisor the expression $ca_i + 1$, where $a_i = \lceil dV_i \rceil$, $i = \overline{1, n}$, and c is the average of ratio $\Delta M/n$ for the given voting system. Here $\Delta M = M - (a_1 + a_2 + \dots + a_n)$. If ΔM has a symmetric distribution in the interval $[1; n - 1]$ from the middle of this interval, it takes place $c = 2$ [11].

About the sensitivity of the Mean relative deviation index to the number of parties. In [16], the Loosemore-Handby index is criticized as one “much too sensitive” to the number of parties. However, in [1], on the contrary, it is said that it is “much too insensitive” to the number of parties, basing on the following example. Let it be two elections, (a) and (b), with the following features:

1. $v_1 = 60\%$ votes, $m_1 = 64\%$ seats; $v_2 = 40\%$ votes, $m_1 = 36\%$ seats; $I_{L-H}^a = 4\%$; $I_{Rae}^a = 4\%$;
2. $v_1 = v_2 = v_3 = v_4 = 15\%$ votes, $m_1 = m_2 = m_3 = m_4 = 16\%$

seats; $v_5 = v_6 = v_7 = v_8 = 10\%$ votes, $m_5 = m_6 = m_7 = m_8 = 9\%$ seats; $I_{L-H}^b = 4\%$; $I_{Rae}^b = 1\%$.

According to Loosemore-Handby index, in both elections there is the same disproportionality of 4%, while under the Rae one the disproportionality in election (a) is 4%, and in (b) – 1%, i.e. in election (b) the disproportionality is considerably lower, than in the (a) one.

Which of these two indices assessed fairly, in reality, the disproportionality in these two elections? If to consider that the Loosemore-Handby index appreciates the overall disproportionality per election, and the Rae – the average disproportionality to a party, then there is no contradiction here, except the absolute value of these two indices. But if the Rae index also to apply for assessing the overall disproportionality per election, than more accurate is the assessment under the Loosemore-Handby index, showing that the disproportionality in the two elections is the same. Indeed, in both elections, the percentage of seats, taken by parties with seats deficiency and distributed to parties with seats in excess, is the same. And if to assess these elections, using the Mean relative deviation index, then the average relative error per election of the representation of an elector rights of value $d = M/V$ in the elective body is the same in both elections, being equal to 8%.

So, the Alabama, the Population and the New State paradoxes are not related to Loosemore-Handby index and, also, one cannot say that it is “much too sensitive” or “much too insensitive” to the number of parties. This statement equally refers to the Mean relative deviation index.

The general scheme of preference of investigated indices, for assessing the total vote disproportionality, is given in Figure 2. From the discussion above, one can conclude that the most suitable index, for assessing the total vote disproportionality, including the comparative analysis of various elections, is the Mean relative deviation index.

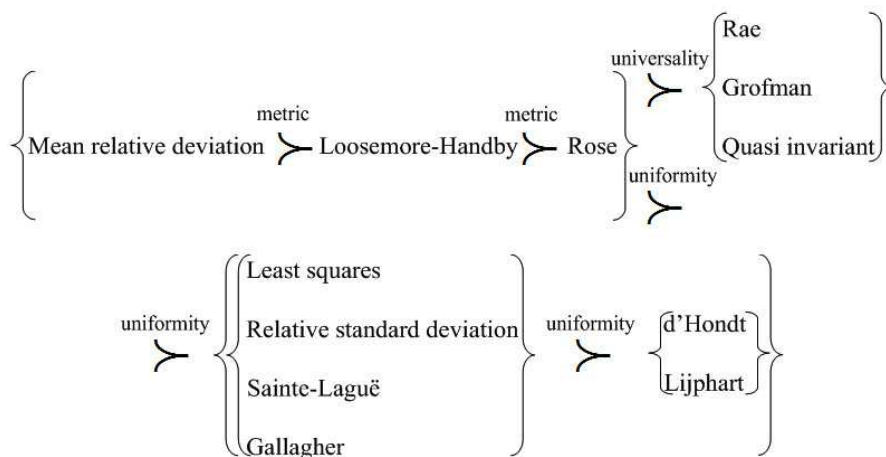


Figure 2. Scheme of preference of indices for assessing the total vote disproportionality

11 Conclusion

To identify the most appropriate index, for assessing the total vote disproportionality of the distribution of seats between parties in LPR systems, 12 indices are comparatively investigated. Comparison is made basing on the following features: metric, definition domain, uniformity of representation, invariance and field of use. Giving priority to the uniformity of voters' wills representation, and then, taking into account other characteristics, too, the set of candidate indices was reduced to three: Loosemore-Handby, Rose and the Mean relative deviation ones, then, finally, be argued the choice of the Mean relative deviation index. The last is uniform, with clear essence (the average relative error per election of the representation in the elective body of a voter's rights of value $d = M/V$), being measured in %seats, the definition domain for optimal solutions $[0, 50\%]$, dependent on M and n and can be used both for assessing of the total vote disproportionality and in comparative analysis of various elections. For a relatively large number of cases ($n \in [2; 20]$ and $M \in [2; 100]$), it is given the graphical representation of

the upper limit of disproportionality of optimal solutions, when using as optimization criterion the Mean relative deviation.

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