On a Possible Similarity between Gene and Semantic Networks

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Abstract

In several domains such as linguistics, molecular biology or social sciences, holistic effects are hardly well-defined by modeling with single units, but more and more studies tend to understand macro structures with the help of meaningful and useful associations in fields such as social networks, systems biology or semantic web. A stochastic multi-agent system offers both accurate theoretical framework and operational computing implementations to model large-scale associations, their dynamics and patterns extraction. We show that clustering around a target object in a set of associations of object prove some similarity in specific data and two case studies about gene-gene and term-term relationships leading to an idea of a common organizing principle of cognition with random and deterministic effects.

Keywords: stochastic multi-agent system, collective intelligence, aggregative model, gene networks, semantic networks, NetLogo, Brownian agent model

1 Introduction

Social insects can be viewed as powerful problem-solving systems with collective intelligence [4,16,3,19,2]. In this paper we describe a common framework to analyze evolution of gene networks or semantic networks and extract aggregates. Multiagent systems have been enriched since their origin for optimization of parallel process to nowadays framework [10]. We used

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NetLogo agent-modelling toolkit [22] to implement automatic extraction of aggregates. NetLogo is known in agent-based community and offer a script-language, available libraries to develop an *ad-hoc* model. There are two tasks about this data processing. Studies about knowledge and language focus on semantic networks by its own [9] [7], some studies try to associate biological constraints to phonemes formation [14]. High-throughput studies made possible reconstruction of gene networks and enhanced gene networks modeling [13]. But no analogy has been made between semantic network and gene network. We show in this paper that it is possible to settle a stochastic system with each relations defined explicitly and to observe how dynamics makes clusters of objects from the network represented by the set of relations.

Section 2 presents the stochastic multiagent framework. In Section 3 results show similarity between gene and semantic networks dynamics.

## 2 Agent-Based Modeling Framework

In this section, we present basics of the stochastic multi-agent model.

### 2.1 Previous studies

Agent-based systems become a new paradigm enabling an important step forward in empirical sciences, technology, and theory [10]. There is no strict or commonly accepted definition of an agent. However, some common attributes can be specified for particular agent concepts. In molecular biology, agents may represent different types of enzymes acting together in a regulatory network. In linguistics, agents may represent different kinds of concepts and terms acting together into a semantic network. A reactive agent is a minimalist agent, whereas a reflexive agent would certainly belong to a complex agent category. Between these two extreme we can find a Brownian agent approach of intermediate complexity. If interaction(s) govern(s) capabilities of an agent, an interaction in life science or cognition, can be asymmetrical, where an *agentA* is attracted by an *agentB*, but *agentB* is repelled from *agentA*.

In computational networking, the notion of an agent as a self-contained, concurrently executing software process, that encapsulates some state and is able to communicate with other agents via message passing, is seen as a natural development of the object-based concurrent programming paradigm [11].

Not all agents react at the same time, two possible architectures are the blackboard architecture defined by early AI community [12][1]. It resembles
a blackboard in the real-world, a data repository where agents can post and retrieve information. An alternative is the Flip-Tick architecture (FTA) based on distributd blackboards. Agents are functional units for processing data in a periodic operation called a cycle. Agents can be grouped into ensembles proceed in a synchronized way. After all agents of an ensemble have performed their cycles, a cylic counter of the ensemble representing its local time is incremented by one, as if a tick of a clock had occurred. After a tick, a new ensemble cycle occurs. Several agents may interact over many cycles by reading tags from tagborads, procesing them, and writing tags to tagboards. A tag is a data object. The communication via tagboards provides a very flexible mechanism for simulating interactions that evolve in time and/or space, as well as for parallel interactions on different spatial and temporal scales. Thus, distributed computer architectures which are based on cooperative/competitieve ensembles of small or medium-grained agents, such as FTA, may be much more suitable for coping with time-varying interaction tasks. Some complex relations involve evolution of interactions over time, because some structures could develops over time and influence interactions requiring adaptation.

[21], [20] and [8] investigates the agglomeration of active walkers on a two-dimensional surface, described by a potential $U(r,t)$, that determines the motion of walkers. Walkers are able to change $U(r,t)$ locally producing a component, that decreases $U(r,t)$ and which can diffuse and decompose. The approach is also viewed both as an agent-based framework and stochastic technique where agent moves with a random walk. Generally the technique tries to solve traditional equation of physics such as Langevin and Fokker-Planck, and spatio temoporal density distributions are analyzed across nonlinear aspects. [5] and [18] emphasized interest about dynamic aggregation using random walks.

### 2.2 Dynamic 2-Population Model

Let consider a map where area is divided into elementary patches (Figure 1).

**Definition 2.1** Patch

A Patch $q$ is an elementary 2-dimensional geometric area where an agent can move to. The space of movement can be settled by a vertical and horizontal number of patches. Lenght of area is defined by the amount $s$ of a patches; a specific is settle as a number of pixels.

We need to define what is a population of objects. An object can be a gene, a linguistic term or something else.
Definition 2.2  Population and Agent
A Population $P$ is defined by its size $N$ and the series of its objects $\{p_1, ..., p_N\}$. Let consider a grid of patches $\{q_1, ..., q_s\}$. Each object $p_i$ is called an agent and is assigned to a patch $q_j$.

Each agent is defined by some rules and a motility. This set of parameters constitutes the model of the multi-agent system. In our system a rule defines an interaction. Motility is a random orientation and a number of patches where agent is supposed to move.

Definition 2.3  Model
Let consider a set of $k$ populations $P_i$ with $i \in 1, ..., k$, the total number $N$ of agent is $N = \sum_{j=1}^{k} \#P_i$. Let consider an agent $a \in Pk$ and another agent $b \in Pm$ with $k \neq m$. $a$ and $b$ are defined by a same kind of motility $v_i$ defining a shift from current patch to another patch with a random orientation $g_i$; motility and orientation are states of an agent, called a Brownian agent. $a$ and $b$ are related by a link $I(a, b)$, so that $b$ modifies state of $a$.

If we assume that $N$ is constant:

$$P(r, g, t) = P(r_1, g_1, ..., r_N, g_N, t)$$  \hspace{1cm} (1)

$P(r, g, t)$ describes the probability density of finding $N$ Brownian agents with the distribution of internal parameters $g$ and positions $r$ considered. Considering both interaction (i.e. change of internal parameters $g_i$) and
movement of the agents, probability changes over time follow the Chapman-Kolmogorov equation:

$$\frac{\partial}{\partial t}P(r,g,t) = \sum_{r' \neq r} \{ w(r|r')P(r',g,t) - w(r'|r)P(r,g,t) \} + \sum_{g' \neq g} \{ w(g|g')P(r,g',t) - w(g'|g)P(r,g,t) \}$$

(2)

The first line of the right-hand side of Equation 3 describes the change in the probability due to the motion of the agents; the second line describes the "loss" and "gain" of agents with respect to changes in their internal parameter \( g \). The transition rates \( w(r|r') \) and \( w(g|g') \) refer to any possible transition within the distributions \( r' \) and \( g' \), respectively, which leads to the assumed distribution \( r \) and \( g \). In the limit of small jumps, the continuous part of Equation 2 can be derived into discrete version and be transformed into a second-order partial equation also called Fokker-Planck equation.

Internal parameter \( g \) can change over area (cell compartment in molecular biology, or document in electronic libraries). In first approximation we do not consider any internal parameter. So Equation 2 becomes:

$$\frac{\partial}{\partial t}P(r,t) = \sum_{r' \neq r} \{ w(r|r')P(r',t) - w(r'|r)P(r,t) \}$$

(3)

Discretization of space and time is revealed by polygons (i.e. patch) defining possible orientation how agents can move. Square lattice offers 8 possible orientations, let call \( d \) this number. It moves one step of constant length \( l \) per unit of time \( \Delta t \), i.e. the speed \( v_i = l/\Delta t \) remains constant. If \( r' \) is a nearest neighbour position, then possible positions are:

$$r' = r + \Delta r, \Delta r = l(\cos \tau g_x + \sin \tau g_y), \tau = \frac{n\pi}{3}, n = 1, ..., 8$$

(4)

For the transition rate with a jump of one per unit of time and a non-biased walker is:

$$w(r'|r) = \frac{1}{d}, w(r|r) = 0$$

(5)

For normalization \( \sum_{d} w(r'|r) = w = 1 \).

For a Brownian agent acting as a random walker with interaction, a potential
$h(r, t)$ on a landscape can symbolize an external force (i.e. interactions). The potential field influences movement through the gradient of the field, so transitions changes. Using the gradient:

$$\frac{\partial h(r, t)}{\partial r} = \frac{h(r + \Delta r, t) - h(r - \Delta r, t)}{|(r + \Delta r) - (r - \Delta r)|}. \quad (6)$$

Transition to $r'$ becomes with addition of a field and stochastic effects:

$$w(r + \Delta r|r) = \frac{1}{d} \left[ 1 + \beta \frac{h(r + \Delta r, t) - h(r - \Delta r, t)}{2 \Delta r} \right]. \quad (7)$$

$\beta$ acts as a dimensional constant. For a vanishing gradient $h(r + \Delta r, t) - h(r - \Delta r, t)$ and the random walker changes its position with equal probabilities for the possible directions.

Finally the master equation Equation 2 becomes for one agent and its associated density $p(r, g, t)$:

$$\frac{\partial}{\partial t} p(r, g, t) = -\frac{\partial}{\partial r} a_1(r) p(r, g, t) + \frac{1}{2} \frac{\partial^2}{\partial r^2} a_2(r) \quad (8)$$

With:

$$\left\{ \begin{array}{l}
    a_1(r) = \sum_{g'} (r' - r) \; w(r'|r), \\
    a_2(r) = \sum_{g} (r' - r)^2 \; w(r'|r).
\end{array} \right. \quad (9)$$

or

$$\left\{ \begin{array}{l}
    a_1(r) = w l \beta \frac{\partial h(r, t)}{\partial t}, \\
    a_2(r) = w l^2.
\end{array} \right. \quad (10)$$

We could derive such result with Langevin equation superposing deterministic and stochastic effects on Brownian particles. An adaptative landscape serves as an interaction medium for agents. This idea has similarity to communication via tagboards. Data read and written are considered as a structural information which is stored in a blackboard. Hence communication among agents can be seen as indirect communication. In a traditional stochastic multiagent system, field can be a quantity present around a given agent, and leave out by another agent in its neighbourhood. In our case the field is related by presence/absence of another agent in its close neighbourhood. So:
\[ h(r_i + \Delta r, t) = \sum_{j=1, i \neq j}^{k} \delta((r_i + \Delta r) - r_j)I(i, j) \tag{11} \]

It means that potential \( h(r', t) \) for a given agent \( a_i \) is the sum of interactions \( I(i, j) \) that takes values 1 if an agent \( a_j \) from population \( j \) is a neighbour of agent \( a_i \). Hence this interaction contributes to make agent to move from patch \( q(a(i)) \) to a patch \( q(a(j)) \).

We may defined some indices of homogeneity. First index is a critical density \( d_c \) for which all agents are equidistributed on the landscape and there free movement is frozen because of very near interactions. \( N_p \) is the number of patches on the landscape.

\[ N_p = A^2 \tag{12} \]

Where \( A \) is the size of the landscape (in unit of patches). Hence critical density is:

\[ d_c = \frac{n - \frac{3}{4}n}{N_p} \tag{13} \]

Where \( n \) is the number of agents of a given population, and \( a \) is size of an agent in term of a percent of the patch size. A patch having a size of 1 (area unit). For a high amount of agents, \( \frac{3}{4} \) is the amount of agents we lost as a direct nearest neighbours which will not move away but directly jump to a neighbour, in this way stochastic effect vanishes. Let suppose we lay out 8 agents as equidistribution on a landscape of 60 patches and separated at least by one patch each other, 45 patches are forbidden for layout to keep freedom of agents, hence 75% of patches.

Then for \( d_c = 1 \), critical number of agents \( n_c \) should be:

\[ n_c = \frac{N_p}{4} \tag{14} \]

A second indice is the equidistribution of all population \( P_k \mid k \in \{1, ..., N\} \) on the landscape leading to a complete frozen movement of agents if they have interaction because they can stay at their initial patch with other agents.
to which they interact with. For a given population $P_i$ we define set $S_i$ of its neighbourhood around a distance $d$ (in pixel unit).

$$S_i = \{ P_k \mid \exists a_j, a_j \in P_k \text{ and } |r_i - r_j| \leq d \}$$

In the case of equidistribution of all populations, we get $S_{i}^{eq}$:

$$S_{i}^{eq} = \{ P_k \mid k \in \{1, ..., N\} \}$$

2.3 Toy example

We used NetLogo tool to implement our model [22]. Lots of others tools are available to achieve multi agent systems [17]. Few of them propose a swarming modeling framework. Figure 2 shows an example of NetLogo agent language, in this case for population declaration and global variable; it is formerly a declarative programming language.

![Netlogo language](image)

Interactions are specified by a matrix specification (Figure 4) in a procedural way [15]. It is quite practical to define an interaction as a binary relation between two populations, set by an operator (Figure 3). Each operator is defined by primitives of Netlogo language. Interactions and matrix are written in separate files. A second interesting point is that no limit bounds interaction definition and in some context there is not only global interaction and some types of agents such as (electron, proton, neutron,
photon) in electromagnetism, or (big mass, small mass, vacuum) in gravitation. In molecular biology, social systems, or semantic analysis, several ten thousands different populations of agent may exist and interact, and so may be specified in an artificial system. So distinct definitions of specific interactions and relations between populations is of great interest.

| interaction walk
| actions random-walk deactivate-none
| end |

| interaction cooc
| actions follow-path deactivate-source
| end |

Figure 3: Interaction rules, here definition of walk and cooc.

| ; source-family interaction-name priority cardinality < target-family distance >
| particles walk 0 0
| walkers walk 0 0
| particles cooc 1 1 walkers 2 |

Figure 4: Matrix of interactions, here definition of interaction between particles and walkers populations.

The agents, called turtles in NetLogo, represent objects. They have physical properties such as localization (patch), color, form. Figure 5 shows a result obtain with the model presented in previous section settled with two populations (red and blue circles). As shown by previous figures about interaction population walkers is blue, population particles is in red. In practice interaction has been defined so that a walkers go to neighbourhood of particles agent. Figure 5 shows three configurations of population size (up: 200 particles and 800 walkers, centre: 500 walkers and particles, bottom: 800 walkers and 200 particles), and three configurations of time duration (t = 0, t = 3 and t = 10). Results show that independantly of size population, red population aggregates to blue population very fast (t = 3), and some fluctuation persists among red agents in any case at a long time (t = 10).
Figure 5: 200 blue 800 red (a, up), 500 blue 500 red (b, centre), 800 blue 200 red (c, bottom)

As $A = 51$, $N_p = 2,601$ patches, $n_c = 650$. In this toy example, the configuration (c) (Figure 5) having population under the critical density shows a result enough as good as other configuration.

3 Genetic and semantic networks

In this section, we present large-scale case studies.

3.1 Data collections

Gene lists

First data collection is associated to a specific molecular biological issue about trophoblast development. The trophoblast is an embryonic epithelium which combines three main processes among which proliferation and differenciation. Specificity of the bovine trophoblast is its exponential growth, which does not exist in rodents or primates. Conversely, the ruminant trophoblast does not seem to invade the uterus, when the trophoblast from rodents and primates do. The question we ask here is to mine the
literature concerning proliferation processes and differenciation processes. The first one is well documented in human cancer cells, the second is well studied in mouse embryos. Our aim was thus to study bovine, human and murine datasets for which respectively we get microarrays time series linked to bovine trophoblast, human cancer and mouse stem cells, even if the time series were different. In bovine species 1,975 genes are involed in this process. To solve the problem we try to extract relationship across species between each pair of genes in a collection of documents, called a corpus. It contains 29,000 documents. The gene names had been used to make a query and retrieve these document (except some of ones having big polysemy (set, via, p). The number of genes included in the corpus is 655 and between them we had extracted 2,752 uniques relationships based on cooccurrence in the corpus.

A second data collection is associated to a specific molecule: TOR. Target Of Rapamicyn - is a molecule playing a key role in cell development and its metabolism. TOR is present in all living organisms but interactome seems to vary from a species to another (i.e. sub-interactomes). About Arabidopsis Thaliana species, less knowledge are available. Knowledge extraction of a global interactome from scientific literature across species could ensure hypotheses concerning TOR sub-interactome in A.Thaliana. At least 53 components (certainly more) are known to regulate TOR or be regulated by TOR. A corpus of 14,000 documents about Tor has been defined.

**Terminological lists**

A corpus is the dataset and consists of 1,280 abstracts in the field of material chemistry. Some experts had defined 6,603 terms of the domain and their anchors in the documents with xml tags. Corpus has been defined as a reference for term recognition [6]. This is a sample of tagging:

```
<notice id="1"/>
  <variante refterme="5564" statut="novar" debut="12" fin="13"/>
</variante>
<texte>Xi is the dimensionless correlation length of the pair</texte>
  <ancre id="12">correlation function</ancre>
</notice>
```

In the previous example, abstract number 1 has been tagged with only one occurrence identified about term "correlation function". It occurs between tags <ancre id="12"> and <ancre id="13">. Identity of term is : 5,564. By cooccurrence analysis, we have found 9,591 relationships between pairs of terms occurring once (or more) in a same context.
3.2 Run configuration

Interactions operators are the same defined as seen in Section 2.3: walk and cooc. Section 3.3 shows a small set with more than only two populations. It involves ten populations. Section 3.4 reveals more large-scale relations, ranged from 37 to 515 populations, and 38 to 9,234 relations. These relations are extracted from validated facts in technical literature.

Display is made by \( A = 31 \) patches inline so \( N_p = 961 \) patches, and critical density is \( n_c = 240 \) agents. In experiments population size is 100. Figure 6 shows results at different timepoints from \( t = 0 \) to \( t = 1000 \).

![Figure 6: Display about 12 populations.](image)

Figure 7 shows init display with 515 populations from the terminological set.

![Figure 7: Display about terminological populations.](image)

3.3 Small set

The small set experiment, presented hereafter, do not gather all possible and real-world relations between components of an agent set. But contrary to the toy experiment in Section 2.3 complexity increases and becomes more realistic because of cross-relationships, as agent \( A \) interacts with agent \( B \), agent \( B \) interacts with agent \( C \) and agent \( C \) interacts with agent \( A \).
So question is: does agent dynamics converge to an interpretable neighbourhood?

Figure 8 shows the sets of relations between twelve populations. In this artificial experiment, such one in Section 2.3, our target population is walkers and the relations associated to this population is particles and ab initio calculations. Eleven other relationships are also defined to generate noise in the system. And all populations make a random walk.

| source-family interaction-name | priority | cardinality |
|-------------------------------|----------|-------------|
| particles walk 0 0            |          |             |
| walkers walk 0 0              |          |             |
| ab initio calculations walk 0 0 |          |             |
| abductor digiti minimi walk 0 0 |          |             |
| abductor pollicis brevis walk 0 0 |          |             |
| aberrant activation walk 0 0 |          |             |
| aberrant methylation walk 0 0 |          |             |
| aberrant regulation walk 0 0 |          |             |
| abnormal magnetic walk 0 0   |          |             |
| abnormal representation walk 0 0 |          |             |
| absolute expression walk 0 0 |          |             |
| abundance proteins walk 0 0  |          |             |
| abundant transcripts walk 0 0|          |             |
| particles cooc 1 1 walkers 2 |          |             |
| ab initio calculations cooc 1 1 walkers 2 | | |
| abductor digiti minimi cooc 1 1 abductor pollicis brevis 2 | | |
| abductor pollicis brevis cooc 1 1 aberrant activation 2 | | |
| aberrant activation cooc 1 1 aberrant methylation 2 | | |
| aberrant methylation cooc 1 1 aberrant regulation 2 | | |
| aberrant regulation cooc 1 1 abnormal magnetic 2 | | |
| abnormal magnetic cooc 1 1 abnormal representation 2 | | |
| abnormal representation cooc 1 1 absolute expression 2 | | |
| absolute expression cooc 1 1 abundance proteins 2 | | |
| abundance proteins cooc 1 1 abundant transcripts 2 | | |
| abundant transcripts cooc 1 1 abductor digiti minimi 2 | | |

Figure 8: Matrix of interactions.

Result, shown on Figure 9 is different over time. At beginning all populations are equidistributed around walkers agents but after 20 timepoints ab initio calculations and particles, are more present than other populations. It seems consistant with the kind of interactions defined with walkers population. But globally all populations surround walkers agents in average. In fact, frequency of the two close populations of walkers population
is twice more than the average agent frequency in the neighbourhood.

| population label                     | $t = 0$ | $t = 20$ | $t = 1000$ |
|--------------------------------------|---------|----------|------------|
| ab_initio_calculations               | 21      | 51       | 45         |
| abductor_digiti_minimi              | 23      | 31       | 19         |
| abductor_pollicis_brevis            | 29      | 29       | 28         |
| aberrant_activation                 | 31      | 26       | 27         |
| aberrant_methylation                | 26      | 30       | 21         |
| aberrant_regulation                 | 25      | 43       | 17         |
| abnormal_magnetic                   | 20      | 41       | 16         |
| abnormal_representation            | 23      | 35       | 15         |
| absolute_expression                 | 27      | 29       | 16         |
| abundance_proteins                  | 23      | 33       | 17         |
| abundant_transcripts                | 31      | 32       | 16         |
| particles                            | 23      | 61       | 55         |
| **< average >**                      | 27      | 34       | 21         |

Figure 9: $S_{walkers}$, set of neighbours of walkers population at different timepoints.

### 3.4 Real-world sets

Figure 10 shows parameters with three target populations: actb about embryo corpus, adsorption about material chemistry corpus, and tor about TOR molecule corpus. One achieved two experiments with each target population each one corresponding to two different initialization sets of relations. The first set is called "restricted" and is related to only relations of a target population with all populations with which it is linked. The other kind of experiment, called "extented", gathers all populations co-occurring with the target population, and populations linked to these co-occurring populations; the relations settled as init parameters are relations between these all populations.

| target agent label                  | #relations | #populations |
|-------------------------------------|------------|--------------|
| actb (extended)                     | 1511       | 474          |
| actb                                | 38         | 37           |
| adsorption (extended)               | 9234       | 515          |
| adsorption                          | 77         | 76           |
| tor (extended)                      | 3728       | 416          |
| tor                                 | 397        | 396          |

Figure 10: Target population label and the interaction/relation context.

We had extracted genes interactors from several databases:
Experiments on gene sets - focus on "Tor"

Rapamycin is a potent antibiotic produced by a strain of *Streptomyces Hygroscopicus* isolated from a soil sample collected in Rapa-Nui (Easter Island). The pharmaceutical potential of rapamycin was originally discovered in a screen for novel antifungal agents. Much later, rapamycin was found to exhibit immunosuppressive activity due to its capacity to block the growth and proliferation of T cells. More recently, rapamycin has been found to display anticancer properties. The atypical Ser/Thr kinase TOR (Target of Rapamycin) is a central controller of cell growth that is structurally and functionally conserved in all species. Four major inputs control mammalian TOR (mTOR): nutrients, such as amino acids; growth factors, such as insulin; cellular energy levels, such as the AMP:ATP ratio; and stress, such as hypoxia. mTOR controls cell growth by the positive and negative regulation of several anabolic and catabolic processes, respectively, that collectively determine cell size. These cellular processes include translation, ribosome biogenesis, nutrient transport, autophagy, and AGC kinase activation.

Figure 11 shows neighbourhood result of *tor*, in our multiagent modeling; the first 20 most frequent population of $S_{tor}$ for restricted and extended relations. Populations are different. Only population *cox2* is common.
### Figure 11: Display about tor population: restricted (left) and extended (right).

From databases we have identified 13 ortholog names, i.e. identical gene with different names in different species. And 49 variants names. It helped to extract candidate interactors stored in public databases, 414 has been found in possible interaction with TOR in any species. Running our model we find 45 populations having frequency over 2 times the average. After comparison with the set of interactor gene names we find 11 genes in common: `cdc25`, `map2`, `pho80`, `pkc1`, `plc1`, `rrn9`, `rsc9`, `sfp1`, `sik1`, `snf3`, `spr2`.

**Experiments on gene sets - focus on ”ActB”**

Beta actin is one of six different actin isoforms which have been identified. ACTB is one of the two nonmuscle cytoskeletal actins. Actins are highly conserved proteins that are involved in cell motility, structure and integrity. Actin is a ubiquitous protein involved in the formation of filaments that are major components of the cytoskeleton evolving in the cell cytoplasm. Figure 12 shows neighbourhood result of `actb`, in our multiagent modeling; the first 20 most frequent population of `S_{actb}` for restricted and extended relations. Populations are quite well different. Populations in common are: `arf1`, `ctsb`, `fau`, `gnb2l1`, `nebl`, `ppia`, `prpf8`, `rps23`, `tpi1`.

| population label | Neighbour Frequency | population label | Neighbour Frequency |
|------------------|---------------------|------------------|---------------------|
| sec14            | 6                   | bub2             | 12                  |
| ccc1             | 5                   | rce1             | 9                   |
| cdc42            | 5                   | shh22            | 9                   |
| lat1             | 5                   | pkl1             | 8                   |
| sap185           | 5                   | sec1             | 8                   |
| sip2             | 5                   | apg7             | 7                   |
| big1             | 4                   | bck2             | 7                   |
| cdc10            | 4                   | cox2             | 7                   |
| cox2             | 4                   | mak31            | 7                   |
| cyt1             | 4                   | mgm1             | 7                   |
| dal4             | 4                   | plc1             | 7                   |
| eap1             | 4                   | prs1             | 7                   |
| sapi             | 4                   | sec18            | 7                   |
| fh11             | 4                   | tad2             | 7                   |
| fol2             | 4                   | cdc37            | 6                   |
| grr1             | 4                   | hap4             | 6                   |
| gtri             | 4                   | hmo1             | 6                   |
| mhi1             | 4                   | maf1             | 6                   |
| pim1             | 4                   | mak3             | 6                   |
| pph21            | 4                   | pfk1             | 6                   |

<global average> 2.0 <global average> 2.6
From databases we have identified none ortholog names. And 2 variants names. We extracted 299 candidates interactors stored in public databases and in any species. Running our model we find 37 populations having frequency over 2 times the average frequency. After comparison with the set of interactor gene names we find 11 genes in common: \textit{anxa1}, \textit{anxa2}, \textit{arf1}, \textit{gnb2l1}, \textit{hspa9}, \textit{nebl}, \textit{rpl17}, \textit{rpl4}, \textit{rplp0}, \textit{rps23}, \textit{rps4}.

**Experiments on terminological sets - focus on ”adsorption”**

Adsorption is the process of attraction of atoms or molecules from an adjacent gas or liquid to an exposed solid surface. Such attraction forces (adhesion or cohesion) align the molecules into layers ("films") onto the existent surface.

Figure 13 shows neighbourhood result of \textit{adsorption}, in our multiagent modeling; the first 20 most frequent population of $S_{adsorption}$ for restricted and extended relations. Populations are quite well different. Populations in common are: \textit{ammonia}, \textit{benzene}, \textit{coadsorption}, \textit{electrode potential}.
Running our model we find 49 populations having frequency over 2 times the average frequency. We extracted 1006 singles words stored in Wikipedia page in English after removing stop words. After comparison with the set of Wikipedia words we find 11 phrases in common: acetic acid, growth mechanism, electrode potential, molecular beam, molecular mass, carbon monoxide, copper chloride, electromagnetic field, physisorption, sandwich structure, binding energy, electron microprobe analysis, heat of adsorption, phase diagram, skin effect, surface energy, surface reaction, surface temperature, electron energy loss. It means that one single word in these phrases occurs in the Wikipedia page. If we match only whole phrases in common: acetic acid, carbon monoxide and physisorption occur in the Wikipedia page.

### 4 Conclusion

A Brownian agent model defines a strong theoretical framework mixing stochastic and deterministic aspects of self-organization over time. Time, order and stochasticity are main parameters of real-world natural systems in which complexity is due to large number of components and can not be...
explained by traditional function modeling. This theoretical framework is also implicitly the core of a pragmatic implementation as a large-scale multi-agent system ensuring observation of dynamics and convergence of a specific required relational model. Model is itself defined by a set of rules and populations of agents. We adopt this framework to propose an aggregative model of gene sets dynamics (genetic net) and term set dynamics (semantic net). The set of rules are defined through a set of interactions primitives and a matrix of relations between populations. The knowledge of relations comes from large-scale literature mining. We show that choosing a target population, its neighbourhood is not random and consistent to reality either with a gene neighbourhood and a semantic neighbourhood, with a same way of self-organization (i.e. contextual aggregation). It should lead us to think in part that the way of aggregation between terms could be inspired from the way of genes organization. In this way, semantic nature of language is not fully deterministic but contains also a stochastic part not guided by intrinsic organization of biology. Such principle should not be so surprising since any language speaker is, initially, a biological entity.

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