

# AISB/IACAP World Congress 2012

Birmingham, UK, 2-6 July 2012

## UNDERSTANDING AND MODELLING COLLECTIVE PHENOMENA

Antony Galton and Zena Wood (Editors)



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## Foreword from the Congress Chairs

For the Turing year 2012, AISB (The Society for the Study of Artificial Intelligence and Simulation of Behaviour) and IACAP (The International Association for Computing and Philosophy) merged their annual symposia/conferences to form the AISB/IACAP World Congress. The congress took place 2–6 July 2012 at the University of Birmingham, UK.

The Congress was inspired by a desire to honour Alan Turing, and by the broad and deep significance of Turing’s work to AI, the philosophical ramifications of computing, and philosophy and computing more generally. The Congress was one of the events forming the Alan Turing Year.

The Congress consisted mainly of a number of colocated Symposia on specific research areas, together with six invited Plenary Talks. All papers other than the Plenaries were given within Symposia. This format is perfect for encouraging new dialogue and collaboration both within and between research areas.

This volume forms the proceedings of one of the component symposia. We are most grateful to the organizers of the Symposium for their hard work in creating it, attracting papers, doing the necessary reviewing, defining an exciting programme for the symposium, and compiling this volume. We also thank them for their flexibility and patience concerning the complex matter of fitting all the symposia and other events into the Congress week.

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# Understanding and Modelling Collective Phenomena

## (UMoCoP 2012)

By collective phenomena we understand phenomena which arise as a result of the combined actions of many individual entities and which exhibit some form of unity or coherence that goes beyond the sum of the individual actions, e.g., the behaviour of flocks, crowds, etc, traffic phenomena, and many social activities. An important subclass of collective phenomena are spatial collectives, in which the collective behaviour takes the form of some form of spatial coherence.

The aim of this Symposium is to explore a range of issues arising from the effort to understand and model collective phenomena, either from a philosophical standpoint or from a computational one. Of particular interest is the application of AI techniques (e.g., knowledge representation formalisms, algorithms for pattern recognition, machine learning methods) to the problems that they raise.

The call for papers listed the following topics as coming within the intended scope of the Symposium:

- Representation: how should collective phenomena be represented within some standard (or non-standard) knowledge representation formalism? What account should be given of the ontology of collectives?
- Analysis: By analysing real-world collective phenomena can we formulate a plausible set of principles for collective dynamics?
- Simulation: Can we use these principles to simulate collective phenomena in order to gain a controlled understanding of their dynamics?
- Recognition/Detection: Given data representing the movement patterns of many individuals, can we detect instances of collectivity through recognising various forms of spatial coherence within the data? Can we distinguish between different kinds of collective which owe their spatial coherence to different sources (e.g., internal causation, external causation, purpose, combinations of these)?

The five accepted papers (included in these proceedings) range widely over these and related areas, and it is hoped that by collecting them together here we will provide a stimulus to further research in this exciting and rapidly-developing field.

In addition, we are delighted to have Professor Peter Simons, from the Department of Philosophy, Trinity College Dublin, as our keynote speaker. He is well-known as the author of the pioneering and widely cited book *Parts: A Study in Ontology* (Oxford University Press, 1987), in which he already began to tackle problems related to the ontology of collectives (see §4.4), which forms the subject of his keynote talk in the Symposium.

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## KEYNOTE TALK

# The Ontology of Collectives

Peter SIMONS<sup>1</sup>

### Short Abstract

A collective is any entity which consists of more than one other entity, where “consists of” means the constituting entities are members rather than parts, so that a collective is in some way a plurality. Examples abound: families, forests, galaxies, clubs, teams, orchestras, ... the list goes on. Collectives come in many different kinds, and it is a job of ontology to propose the principles for their classification and for distinguishing them from other kinds of entity. We distinguish them here from individuals, masses, and institutions. In classifying them, two divisions cross. One is the division between extensional and non-extensional membership conditions. A collective is generally several entities such that —, where the blank is filled by some condition spelling out what is required to be one of the collective. If several entities are not such that —, they do not form a collective of the specific kind. If the same individuals fulfil more than one condition, they form distinct collectives, of different kinds. However if the condition is trivial or tautological, it is enough for the several entities in question simply to exist. In such a case the collective is nothing other than its several members, its identity conditions are extensional, and we call the collective a multitude. The other dimension of variation concerns whether a collective’s members are individuals or not. A collective all of whose members are individuals may be called first-order; one whose members are individuals or first-order collectives, and which has at least one first-order member, is second-order, and so on. Higher-order collectives may include associations of clubs and societies. Admission of higher-order multitudes, pluralities of pluralities, opens an interesting possibility: a nominalistically acceptable substitute for set theory in providing the semantics for first- and higher-order logic.

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# Collective bio-molecular processes: The hidden ontology of systems biology

Janna Hastings<sup>1</sup> and Colin Batchelor<sup>2</sup> and Stefan Schulz<sup>3</sup> and Ludger Jansen<sup>4</sup>

**Abstract.** Systems biology is concerned with the development of models for describing and predicting how molecular events such as biochemical reactions relate to physiological and pathological processes at the cellular or organismal level. Molecular events are often represented as interoperating networks where reactants and products are chained together through multiple reactions in an overall pathway models. Pathways form the units of meaningful knowledge into which many aspects of biological research are conducted, and representations of pathways are stored and exchanged between many biological databases. However, the ontological commitment of such pathways is usually not made clear. In this contribution, we will discuss the ontological nature of pathways, concluding that although pathway illustrations appear to represent chains of single biomolecular events, pathways are actually aggregate, or collective, processes. For examples to illustrate this discussion, we will draw on models described in the BioModels and Reactome databases. Furthermore, within systems biology, the features of the cellular or organismal processes can be described with quantitative methods and thereby used as input to simulation models. A prominent feature of many of these quantitative models are the so-called ‘rate equations’ that relate quantities of molecules to rates of processes. Understanding the rates of processes is crucial to adequate modelling, as fast processes can dominate a system even if the number of participating molecules in the process is small. We will further consider the ontological implications of these quantitative models and touch on the issue of reaction reversibility. Finally, we will identify dispositions at both the molecular level and the bulk level, and illustrate the relationship between the two.

## 1 INTRODUCTION

Systems biology is concerned with developing quantitative, predictive models for biological systems [16]. Models relate molecular events, such as biochemical reactions between individual molecules, to physiological and pathological processes at an organismal level, bridging basic molecular science and larger-scale organismal phenotypes. Models are encoded in computational formats and are used by simulation software to investigate complex perturbations of biological systems by varying parameters controlling the operation of the models. Depending on the model, both temporal and quantitative variance are taken into consideration. Developing such predictive modelling capability for a larger and more comprehensive set

of biological systems leads to better accuracy and range of *in silico* research to replace animal models and expensive trial and error in research into pressing biomedical challenges such as rare diseases and ageing [3].

Systems biology is a modelling approach that contributes to the understanding of biology from a systemic perspective [20]. It aims to represent the behaviour of the collective of interacting molecules in a system under actual cellular conditions, varying in different scenarios, using information about the individual elements and their relationships as constraints to models. Quantitative methods for relating individual elements of the system to the overarching collective behaviour include rate equations, which relate quantities of molecules to rates of processes. Understanding the rates of processes is crucial to adequate modelling, as fast processes can dominate a system even if the number of participating molecules in the process is small. In this work, we will focus on the rates of *collective processes* and describe the ways in which the rates of collective processes relate to the underlying molecular processes and the quantities of underlying molecular species.

Systems biology models are often annotated with terms from formal ontologies that describe the entities involved therein. Such annotations provide a context within which the entities referred to in the models can be linked to related biological knowledge [11], and in which the ontological relationships between the entities can be exploited for model searching and browsing [24].

Pathways form the units of meaningful knowledge into which many aspects of biological research are conducted, and representations of pathways are stored and exchanged between many biological databases. However, the ontological commitment of such pathways is usually not made clear, and as yet little has been said about the way in which the individual entities, and in particular the unitary reactions between individual entities that form the constituent building blocks of pathways, build up into the overall collective behaviour observed in biological systems.

In this paper, after a brief presentation of some relevant biochemical background material, we examine several questions surrounding this topic. Firstly, we discuss the ontological nature of pathways, concluding that although pathway illustrations appear to represent chains of single biomolecular events, pathways are actually aggregate, or collective, processes. For examples to illustrate this discussion, we will draw on models described in the BioModels and Reactome databases. Furthermore, within systems biology, the features of the cellular or organismal processes can be described with quantitative methods and thereby used as input to simulation models. A prominent feature of many of these quantitative models are the so-called ‘rate equations’ that relate quantities of molecules to rates of processes. Understanding the rates of processes is crucial to adequate

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modelling, as fast processes can dominate a system even if the number of participating molecules in the process is small. In the second part of the paper, we consider the ontological implications of these quantitative models and touch on the issue of reaction reversibility. Lastly, we turn to some questions surrounding dispositions and their realizations at the molecular and bulk levels of granularity.

## 2 BACKGROUND

### 2.1 Pathways and models

Many systems biology models are organised into units around what have been called pathways, that is, coherent chains of reactions organised around a biological objective, where the input of one reaction forms the output of another reaction. Such pathways are qualitatively described and visualised in pathway databases such as Reactome [18] and KEGG [15]. An example of a pathway is *Digestion of dietary carbohydrate* (REACT.9472.2). Reactome provides a schematic illustration for the pathway, illustrated in Figure 1, together with a breakdown of the reactions involved in the pathway. This diagram describes and relates all the elementary reactions involved in the digestion of carbohydrates. Complex pathways can be defined as aggregations of simpler pathways, which should at least consist of several reactions organised into a coherent whole by virtue of fulfilling some biological objective.

Figure 1 is merely a schematic illustration of the pathway intended for ease of human comprehension. In fact, much more detail is stored in Reactome for the pathway – a snapshot of a subsection of which is illustrated in Figure 2. In this more detailed pathway representation, specific types of proteins and small molecules are illustrated by labelled nodes with particular shapes – boxes with rounded edges for proteins, ellipses for small molecules – and these are linked together with lines via reactions that are catalyzed by enzymes. The cellular component as well as transport across membranes is explicitly illustrated.

While pathways allow the expression of interlinked networks of reactions with explicit locations, an additional mathematical layer is needed to represent the way in which the overall behaviour of a system changes as the conditions vary. Such quantitative predictive models are stored in the BioModels database [17]. An example of a quantitative model is the *Biochemical and genomic regulation of the trehalose cycle in yeast* (BIOMD0000000266). By varying the initial parameters passed to a mathematical simulation of the model, it is possible to predict the expression of genes in response to a heat shock in yeast, resulting in a substantial increase in the concentration of trehalose acting to protect the proteins and cellular membranes against the heat stress.

A key feature of such quantitative models is their inclusion of mathematical rules, such as those illustrated in Figure 3, that allow simulation of the quantitative aspects of the underlying biochemical pathways in such a fashion that a) allows predictions to be made that can be verified against experimental results; and b) if borne out by experiment, provide a much deeper explanation of underlying mechanisms than non-predictive descriptive models are able to. Pure phenotypic descriptions do not give sufficient information about underlying mechanisms in order to guide predictions. Systems biology aims to allow accurate predictions through integrating across levels of description, from underlying disturbances and mechanisms to the phenotypic layer, in models complex enough to allow simulations to be built up therefrom.

### 2.2 Semantic model annotations

It is increasingly common that each of the components of pathways and models such as those illustrated in the previous section are further annotated by ontology identifiers such as ChEBI [6] for small molecules and the Gene Ontology [26] for biological processes and cellular components.

For the exchange and computational representation of models such as pathways and quantitative predictive models a standardised language has been developed, the Systems Biology Markup Language (SBML) [13]. SBML allows the standardised representation of pathways, interactions and complex mathematical models that quantitatively relate components of the system to the overall behaviour. The actual mathematical expressions are embedded in MathML within the overall XML of the model representation. The descriptive potential of the model is greatly enhanced when each of the terms used in the model – representing, for example, the interacting molecular entities – are mapped back to the sorts of entities they are via such ontological annotations.

While SBML provides a standard format for exchange of models, unambiguous interpretation of models generated by different researchers requires annotation not only of the entities involved in the model (such as chemicals to ChEBI) but also annotation formalising the semantics of the model. The Systems Biology Ontology (SBO) [4] addresses this need. It provides a controlled vocabulary for annotating what the variables and the mathematical expressions of a model represent and how they were generated. SBO includes terms for participant roles such as *Catalyst*, modelling frameworks, mathematical expressions, and systems description parameters such as *Rate constant*. Where SBO terms include a mathematical expression, each symbol used within the expression is defined by another SBO term.

### 2.3 Ontological framework

Ontologies usually describe the relations between *types* of things, whereas our sensual perceptions and other empirical encounters always have particular things as their objects, which are instances of these types or classes.

Following the lead of upper level ontologies such as BFO [10] and DOLCE [9], we will distinguish between *continuant* (endurant) entities and *occurrent* (perdurant) entities. Continuants are those sorts of things that exist in full at any moment in which they exist, and continue to exist over an extended period of time, such as cells and molecules. Occurrents are those sorts of things that unfold over an extended period of time and do not exist in full until they have fully unfolded, such as the processes and reactions involved in cellular metabolism. According to BFO, continuants are further distinguished into those that are independent and those that are dependent. Independent continuants are those that do not depend on any other entities for their existence *per se* (although they may require other entities for their continued healthy existence, in the case of living material). Dependent continuants, by contrast, cannot exist without an independent continuant in which they inhere. Dependent continuants may themselves be subdivided into different types: qualities, such as colour and mass, are properties of their bearer at all times they exist; and dispositions, such as fragility, are properties of their bearers by virtue of what will happen if the bearer comes into certain circumstances. Previously, we have provided an analysis of the sorts of dispositions that inhere in molecular entities in biological contexts, including the sorts of mutual dispositions that are characteristically involved in reaction pairs, where the reaction happens because both

## CARBOHYDRATE DIGESTION

In intestinal lumen

starch  $\rightarrow$  limit dextrins + maltose

at enterocyte surface

lactose  $\rightarrow$  glucose + galactose

trehalose  $\rightarrow$  glucose

maltose  $\rightarrow$  glucose

limit dextrins  $\rightarrow$  glucose

sucrose  $\rightarrow$  glucose + fructose

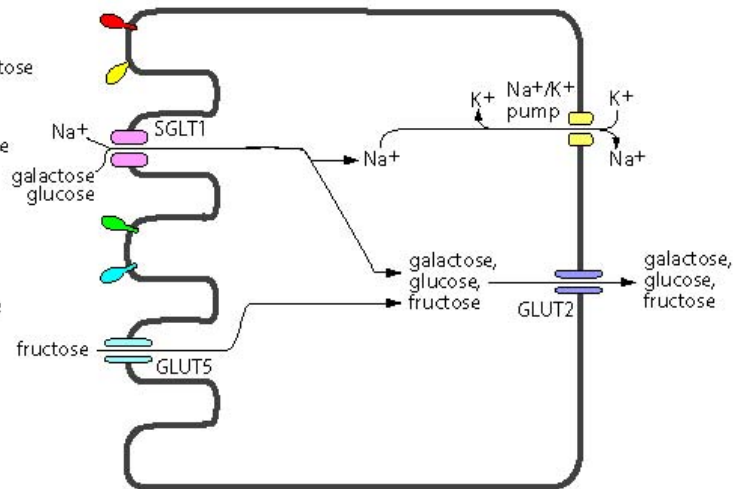
● lactase

● trehalase

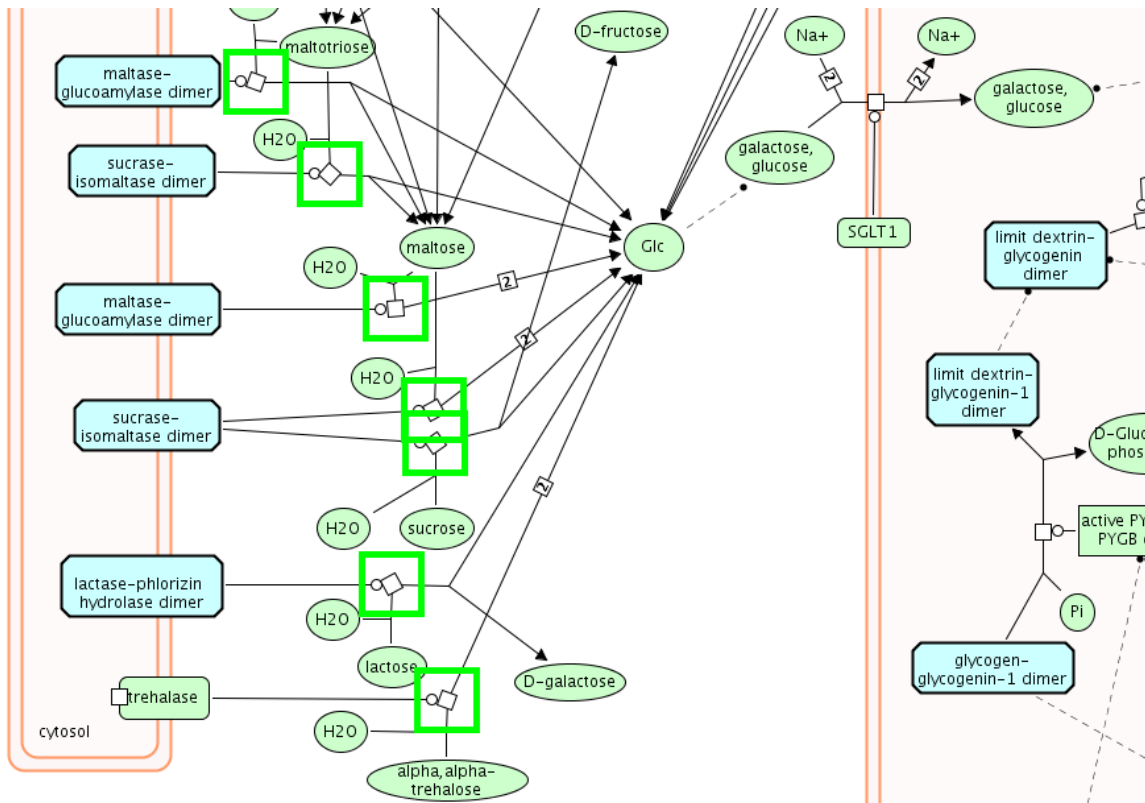
● maltase-glucoamylase

● sucrase-isomaltase

## HEXOSE UPTAKE



**Figure 1.** A schema for the digestion of carbohydrates in humans. Source: Reactome (REACT\_9472.2)



**Figure 2.** Pathway: the digestion of carbohydrates in humans. Source: Reactome (REACT\_9472.2)

Model	Overview	Math	Physical en
+ Assignment Rule <u>flux to glucose</u> = 31.912 * pow(X0, 0.968) * pow(X2, -0.194) * pow(X7, 0.00			
+ Assignment Rule <u>flux from glucose</u> = 89.935 * pow(X1, 0.75) * pow(X6, -0.4) * X9			
+ Rate Rule d [ <u>glucose</u> ] / d t = flux_X1_in - flux_X1_out			
+ Assignment Rule <u>flux to G6P</u> = 142.72 * pow(X1, 0.517) * pow(X2, -0.179) * pow(X3, 0.183) *			
+ Assignment Rule <u>flux from G6P</u> = 30.12 * pow(X1, -0.00333) * pow(X2, 0.575) * pow(X3, -0.1			
+ Rate Rule d [ <u>G6P</u> ] / d t = flux_X2_in - flux_X2_out			

Figure 3. Model: Biochemical regulation of the trehalose cycle. Source: Biomodels (BIOMD0000000266)

of the molecules involved in the reaction are disposed to so react with each other [1]. In what follows, we will extend these observations to the broader context of networks of interacting molecules in a cellular pathway context.

As in [1], we will distinguish between *molecular* granularity and *bulk* granularity. On the scale of molecular granularity single molecular entities such as particular proteins are being described, while descriptions on the scale of bulk granularity concern the behaviour of whole portions of substance, such as the collection of proteins within an entire cell or within a certain cellular compartment.

In the remainder of this document, ontology axioms will be illustrated in the Web Ontology Language, version 2 (OWL 2), Manchester Syntax [12]. OWL 2 is widely used in biomedical ontologies. It is based on Description Logics (DL) [21], a family of logic-based decidable fragments of first-order logic that have been optimised for classification knowledge representations tasks and algorithms.

Armed with these preliminaries, we will turn to the first question we have set ourselves.

### 3 WHAT ARE PATHWAYS AND MODELS?

#### 3.1 Pathway scope

On first glance, pathways appear to be grouping together interrelated chains of biochemical reactions. One interesting question is, what defines and delineates the scope of a pathway? Reactome, in their description of their data model, have this to say on the matter: “It is often convenient, if sometimes arbitrary, to group [...] sets of interlinked reactions into pathways”. On their own account, thus, their data model is frame-based, in the sense that frames may be arbitrarily chosen to group together reactions into pathways. However, the frames are not necessarily Davidsonian event frames [5]; although they do include events such as reactions, they also include physical entities (such as the small molecules and proteins as illustrated in Figure 2) and “catalyst activities”, each one of which “associates a specific PhysicalEntity with a specific GO MolecularFunction” [18].

The Reactome pathway REACT\_27232.1 describes trehalose biosynthesis in *Mycobacterium tuberculosis*. It gathers together five statements that unambiguously concern processes: (1) “Glucose is transferred from UDP-glucose onto glucose-6-phosphate”, (2) “Trehalose-6-phosphate is hydrolyzed to trehalose”, (3) “Maltose is converted to trehalose”, (4) “1,4-alpha-glucan is converted to glucanotrehalose”, and (5) “Glucanotrehalose is hydrolyzed to 1,4-alpha-glucan and trehalose”. Note that (3) is independent of the others, and that (1) and (2) are steps in a bigger process, as are (4) and (5). All of these processes are reversible, and given the presence of the right enzymes or small molecules, trehalose might be converted back into one of its precursors. This might be the reason why these processes are represented as one pathway rather than a group of process types that all have trehalose as their common product. That is, this pathway diagram describes connected units of biochemical operations, which, in this case, may all contribute to the synthesis of trehalose. Which of these biochemical reactions will in fact happen, may depend on environmental and contextual factors that can affect the outcome of each step in the process (such as the presence or absence of enzymes, or the surrounding cellular conditions).

This example might be seen as paradigmatic for a metabolic pathway, having something like a product and proceeding with a considerable transformation of energy. In contrast to this are signaling pathways, such as Reactome pathway REACT\_11044.2, which describes signalling by Rho GTPases in *Homo sapiens*. The Rho GTPase protein has two states, active and bound to guanine triphosphate (GTP) or inactive and bound to guanine diphosphate (GDP). The pathway describes five processes: (1) activation of the protein by swapping GDP for GTP, (2) inactivating the protein by hydrolysing GTP to GDP, (3) GDI proteins forming a complex with the protein and hence inactivating it, (4) such a complex falling apart and finally (5) the actual interaction of a GTP-bound Rho GTPase with an effector protein. Here the pathway has been identified as only those processes that involve a GTP-bound Rho GTPase. Signalling and transport pathways challenge an intuition that pathways might be essentially about the construction or synthesis of certain products

by biomolecular machinery.

### 3.2 Hidden space: Cellular compartments

In systems biology representations, cells are often divided into compartments, which is a way of representing the spatial extension of a cell, which is very large compared to the small molecules it contains. Although there is no necessity that the compartments defined by a cell model relate to any actual structures of the cell, compartments also help to capture the idea that cells have an internal structure and that molecules cannot necessarily move freely within this internal structure. They need help in the form of transporters, carriers or chaperones.

Some pathway databases (e.g. Reactome) and description languages (e.g. SBML) model, e.g., extracellular water molecules as being a different kind of thing from intracellular water molecules. This work-around helps to formally represent transport processes as those where (*water* and **has\_location** some *extracellular*) becomes (*water* and **has\_location** some *intracellular*). While this could be seen as a harmless *façon de parler*, it does blur the distinction between structural changes of molecules (represented as different molecular types on the input and output side of a reaction) and transport of molecules, in which the molecular type on either side is identical.

### 3.3 The ontological nature of pathways

Bearing these preliminaries in mind, we can consider several competing views for the ontological nature of pathways such as those represented in Reactome.

1. A pathway is a disposition that inheres in a certain physical ensemble (a cell, for example, or the intracellular environment, together with the presence of reactants, substrates and catalysts, at a certain temperature and concentration).
2. A pathway is a process that is the realization of (1).
3. A pathway is an information artefact, like a plan, which gets accomplished by (2).

There are challenges for each of these options.

In the case of (1), considering the pathway as a disposition, it is difficult to pinpoint the exact entity that the disposition inheres in, for two reasons. Firstly, many pathways describe intermediate products in reaction chains that then go on to form the input for further downstream reactions; these intermediaries may not exist at the time that the pathway begins its operation, thus, they cannot be bearers of the pathway disposition, nor can they be necessary parts of such bearers. Secondly, and more worryingly, pathways may describe multiple *possible* chains of reactions, where only one of the given chains is actually followed under a given set of circumstances. Thus, whole intermediaries nominated in the pathway model may be missed in reality while the pathway is still said to have been executed. A possible way to avoid these issues is to say that the pathway as a disposition inheres in the overall cell or organ or organism – whichever entity proves large enough to encompass all the possible participants of the pathway as it is realized. However, this seems to suffer from the problem of killing a mosquito with a hammer, since it then becomes impossible to pick out which parts of the cell or organ or organism bear the relevant parts of one pathway disposition as opposed to another, even if they actually have no reactions or participants in common but only overlap in terms of cellular location. We could differentiate them in terms of the processes that they are realized in rather than

the material entities in which they inhere, hence we still have to spell out the pathway processes as we would if we opted for case (2).

In the case of (2), we avoid the question in which physical entities the pathway process inheres; the relation between the pathway and the physical entities in this case is one of participation rather than inherence. However, we are still left with the problem of the multiple possibilities that are encoded in the pathway representation. The actual process that constitutes the pathway may differ from time to time as the conditions vary in the organism or cellular location. Indeed, this kind of variance points rather to the relation of realization than to the identity criteria for a particular process type. Moreover, if a pathway is a process, it should be possible to distinguish between types and instances of such pathway processes, and to say that a given instance happened at time  $t$ . But while there is no difficulty in saying when particular component reactions of a pathway take place, it sounds odd to ask when the pathway process as a whole takes place.

We may be tempted to throw our hands in the air and declare that both options (1) and (2) are incorrect, leading us to consider (3).

But there are problems with (3) as well. While it is clear that a pathway *diagram* is indeed an information artefact, as is the *representation* of a pathway in a computational model in SBML [13], it is counter-intuitive to specify that the pathway *itself* is an information artefact, since this would entail that the pathway was not something that could take place in living organisms, rather, that the pathway was a plan for the sorts of things that take place in living organisms. And the label “plan” here is certainly misleading, since the molecules and proteins would not themselves be following or enacting any plans when engaging in reactions, as they are of course not the sorts of cognitive entities that can follow plans. We could, however, stay on the safe side and refrain from speaking about pathways proper. We could then confine ourselves to talk about pathway diagrams only, such that the diagram as a whole does not refer to any pathway entity, while parts of the diagram like arrows and nodes can easily refer to types of reactions or molecules. This would, however, be a revisionary linguistic praxis, as life-scientists normally do talk as if pathways can be found in certain organisms or cells.

Hence we should not identify pathways with their diagrams, but consider them to be what pathway diagrams describe. What these diagrams describe are obviously *types* of entities: instances of the same pathway can occur in myriads of different cells, maybe even in different species. We argue now that these instances are not simple processes or dispositions for such, but process aggregates or aggregates of respective dispositions.

Pathway diagrams aggregate processes in at least three ways:

1. While it sounds odd to date a pathway as a whole, we could in principle easily date each of the single molecular reactions happening in its course. The pathway diagram itself, now, is about series of such single molecular reactions. We thus deal with a series of molecular processes.
2. Secondly, pathway diagrams may allow for branching, for parallel alternative ways, for reversible reactions and for cycles. A pathway type may thus be instantiated by an aggregation of several series of molecular reactions. Quite different series of reactions may thus relate to one and the same pathway type; pathway types could thus be seen as disjunctive classes of such reaction series. For example, a pathway P would allow the following variability in terms of subprocess sequence:  
P1: A - B - C - D  
P2: A - B - E - D  
P3: A - B - F - G - D

Hence P could be considered as a pathway type P as enclosing reaction series that follow P1 or P2 or P3 (without the need to exclude other possibilities).

3. Thirdly, the reactions depicted in a pathway diagram rarely (if ever) concern single molecules. In order to be triggered at all, a considerable amount of the reactants must be present in the cell, and many of them will undergo the reactions described in the diagram at the same time. What is represented in a pathway diagram is in some sense a whole collection of series of reactions.

Rather than being about simple processes, then, pathway diagrams are about collections of (a variety of) series of molecular reactions. For brevity's sake, we will refer to these as process aggregates. We need now to further inquire into the nature of these aggregates.

## 4 RATES OF PROCESS AGGREGATES

The hidden ontology of systems biology is thus that it describes overarching processes through representations of the individual constituents of these processes. However, as we shall demonstrate in this section, rates are a property of collections of reactions rather than individual molecular events.

### 4.1 Reactants, products and catalysts

Something that is essential but easily overlooked in considering the representation of the underlying biological reality in pathway models and in quantitative systems biology models is the implicit progression of time across the model. When two molecules react to form another molecule, the inputs are called the reactants and the output is called the product. The implicit arrow of time that underlies this story is that the reaction is a process; at the end of the reaction the input molecules *no longer exist* while the product molecule has *come into existence* (not out of nothing, of course, but through a rearrangement of the constituents of the input molecules). On this background, one could be inclined to say that a lengthy chain of interrelated reactions should therefore occupy a lengthy period of time, as each reaction's predecessor must take place before it can begin, with the output of earlier reactions forming the input to later reactions. On a more sophisticated account, however, the reactants are always present in the cell, only in differing concentrations. If this is the case, all of the reactions can happen at the very same time with different molecular participants.

It is also important to consider the ontological nature of the reaction roles such as “reactant” and “product”. While it is clear that calling something a reactant or a product only makes sense in the context of a given reaction, and that the terms “reactant” and “product” do not therefore denote natural kinds, it is important to remember that the same thing is true of catalysts. That something serves as a catalyst may only become clear by analysing all of the steps in a process. Some catalysts, such as a lump of palladium metal, are more or less unchanged throughout the processes they catalyse. In contrast, there are catalysts that undergo structural changes during catalysis, such as in the Cativa process, used in the industrialized production of acetic acid by carbonylation of methanol. The iridium catalyst molecule, while maintaining its diachronic identity, gains new parts in the form of first a methyl group and an iodine atom, then the iodine atom is displaced by a carbonyl group, then the molecule rearranges, losing an acetyl group in the process to reform a molecule with the same structure as the original molecule.

This brings us neatly to another problem in biochemical pathways and models, namely the depiction of *cycles* in such models. In fact,

cycles in the representation of pathways are quite common, with the output of a downstream reaction forming the input to a reaction upstream. However, actual instances of the pathway that is being represented do not “move backwards in time” to start over again at the beginning. Rather, several distinct instances of one and the same reaction sequence type happen one after another.

### 4.2 Reaction rates: from molecular to bulk granularity

The key property of processes such as biochemical reactions is *rate*. The speed of a moving object is the metaphor we use most often for talking about the rate of a process, hence we say that one process may be faster or slower than another. Sugar, for example, dissolves faster in hot coffee than in cold coffee. Finely-divided flour burns faster than the grain from which it has been milled. But what sort of thing is a rate?

A reaction rate is the rate of change of the amounts of relevant molecules [19]. In order to calculate rates, we use rate laws, which are written in terms of concentrations—that is to say, disguised amounts of molecule—and time. The total quantity of a given molecule at a given amount of time can be obtained mathematically by integrating the rate equations, but that is not the same as saying that aggregate of molecules depends ontologically on the rate. The molecules themselves have causal powers; it does not therefore necessarily follow that their amount has a causal power, nor indeed that the derivative of their amount has a causal power. As a derivative, a reaction rate is an instantaneous property and thus is unlike some other sorts of rate, for example a heart rate, which can only be defined over a length of time [2].

However, some further subtle refinements are needed: in most real systems, and certainly the systems that systems biologists are interested in, there are multiple competing reactions. This can make it harder to disentangle reaction rates. If in a large system, a cell, for example, we have two reactions, (1)  $A \rightarrow B$  and (2)  $C \rightarrow B$ , then we cannot simply identify the rate of reaction (1) with the rate of change of the concentration of B; we have to identify it with the rate of change of concentration of B that have been formed from A.

The phenomenon of dynamic equilibrium calls for another refinement. When a system reaches equilibrium, the concentrations of all of the species in the system become constant. However, it is not the case that all reactions stop. Rather the forward process and reverse process cancel each other out, as the product molecules are created by the forward reaction at exactly the same rate as they are destroyed by the reverse reaction. This is a typical phenomenon in living organisms, but is not restricted to these: a glass of water at room temperature may appear to be static, but is in fact the site of frantic activity as water molecules ( $H_2O$ ) ionize to produce protons ( $H^+$ ) and hydroxide ions ( $OH^-$ ), protons and hydroxide ions combine to form water molecules, protons are hydrated by water molecules to form hydronium ions ( $H_3O^+$ ), hydronium ions lose their protons, and so on.

### 4.3 Kinds of rate law

Reactions at the molecular level can be classified according to their *molecularity*, that is to say the number of participating molecules in the rate-determining step.

A molecular process may be unimolecular, such as a dissociation that only depends on the absorption of ultraviolet light and not the concentration of any species, or bimolecular, depending on

molecules of species A meeting species B. (Molecular processes that depend on a three-way collision are tremendously unlikely.) Some unimolecular reactions are most simply described as the manifestation of a one-sided disposition that has a triggering process such as the absorption of a photon or a collision with more or less anything; bimolecular reactions are the manifestation of the specific mutual dispositions of A to react with B and B with A.

At the bulk level, there are zero-order reactions which have a constant rate regardless of concentration, first-order reactions whose rate depends on the concentration of one of the participants, and second-order reactions, whose rate depends on the concentrations of both participants. The rate of radioactive decay is first-order because it is unimolecular. Similarly, bimolecular reactions, all other things being equal, can result in second-order rate laws at the bulk level. The reason for zero-order reactions is that competing reactions result in the bulk level kinetics not necessarily matching the molecular-level molecularity of the processes. Often finding out the molecularity of each process involves careful disentangling of complicating processes, and this is the job of chemical kinetics.

#### 4.4 Pathways as collective processes

As we have discussed, a straightforward ontological interpretation of pathways and the things that are described by systems biology models as the processes that realize reaction dispositions of the participants is not as easy as it may appear at first glance, due to the differing times at which the various reactions take place and the consequent appearance and disappearance of the reaction participants as the pathway instance progresses through time. We have seen that the only way to make sense of the time implication of a pathway illustration, particularly where cycles of reaction products are concerned, is to understand the diagram as representing a *process unit* of what is in fact always a *collective* process that is ongoing in an environment in which collectives of participants of the right sorts are available.

However, for ease of representation, pathway models are represented in the singular form, showing only singular participants in the reactions and other processes that constitute the pathway. Knowledge about the collective dynamics of such pathways, where it is available, is encoded in mathematical expressions that enable computational simulations of the collective behaviour of an overall system under specific conditions.

Clarity about the semantic commitment of computational representations, as for example between single molecules and collectives of molecules, enhances the predictive and descriptive value of these representations.

## 5 DISCUSSION

Our efforts to ontologically formalise the assumptions of models in systems biology are not without precedent. Indeed, one of the first pathway ‘ontologies’ developed in OWL is the BioPAX standard for the representation of pathway knowledge [7]. BioPAX is predominantly used in the exchange of encoded models between pathway databases. Unlike SBML, a pure data exchange and annotation format, BioPAX contains a data model that is itself formalised as an ontology and has built-in ontological commitments. It follows a foundational distinction between Entities and UtilityClasses.

Most of the UtilityClasses are for metadata, but clear exceptions to this are the classes DeltaG and KPrime, which express thermodynamic properties of the given solution at equilibrium.

As for the entities in BioPAX, these could be seen as straightforwardly material such as chemicals and proteins, but the documentation provided alludes to a broader interpretation. For example, the following extracts from the BioPAX documentation highlight differences between the BioPAX ontological commitment and that we have described above in our analysis of pathways and models:

- “Interactions as a formal concept is a continuant, it retains its identity regardless of time, or any differences in specific states or properties.”
- “Conceptually, physical entities are involved in interactions (or events) and the events are controlled or modified, not the physical entities themselves.”

Interactions by our ontology thus appear if they are meant to be processes. A notable type of Conversion is Transport, which BioPAX deems a conversion because molecules located in different parts of the cell are treated as different kinds of thing.

While the differences raised here are interesting, we leave aside a more detailed analysis of the discrepancies between our approach and that encoded in the BioPAX standard for future work.

Related to our discussion of reactants and products, earlier work by Dumontier and colleagues highlights the importance of reaction roles for reactants within a biochemical context [8]. The process relations underlying biochemical processes, including reaction relations such as those used to link inputs to outputs, have been formalised using the process specification language in [22]. Collective bio-molecular processes have also been further elucidated in [25] and [14]. Similar questions to those we have discussed for pathways also arise with regard to the ontological status of biochemical mechanisms [23]. The characterizations of these, too, switch between processes (i.e. occurrents) and molecules and their dispositions (i.e. continuants).

## 6 CONCLUSION

We have discussed some of the complexities regarding the ontological interpretation of pathways and systems biology models and identified the importance of dispositions, processes and information entities in the full ontological description of the models used in systems biology. Dispositions inhere in the underlying physical entities that participate in the processes, and are realized in the reactions that constitute bio-molecular events. Processes themselves take place both on the molecular granularity and on the collective scale. And representation of these underlying biological reality takes the form of information artefacts, both diagrammatic representations such as the standard biochemical pathway network diagram and the more sophisticated predictive representation found in the mathematical annotations to the SBML representation of models.

## ACKNOWLEDGEMENTS

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# Maintenance of Dot Pattern Footprints via Efficient Identification of Change

Maximillian Dupenois and Antony Galton<sup>1</sup>

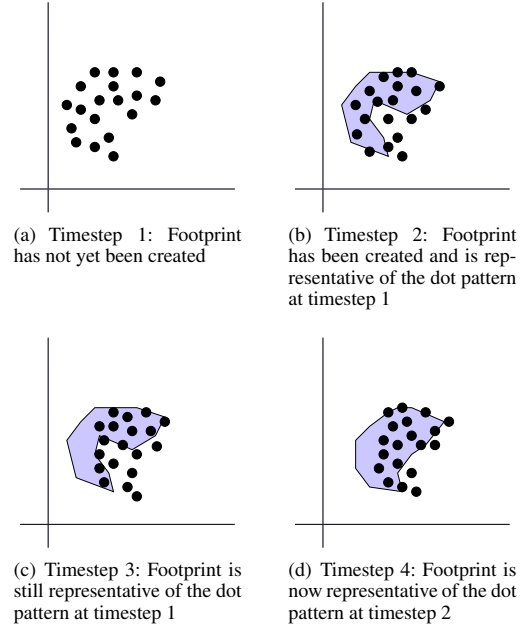
**Abstract.** Commonly, in the field of spatial knowledge representation, there is a need to assign to a group of individual entities, considered as an aggregate, a spatial location known as its ‘footprint’. For many practical applications, it is required to track the footprint of a ‘live’ dynamic system such as a crowd or flock. This paper looks at the problems involved in maintaining footprints over non-static dot patterns and how to negotiate the trade-offs between efficiency of computation and accuracy of result. The key notion is to use ‘change identifiers’ to determine when and how often the footprint of a moving aggregate should be updated.

## 1 Introduction

Many different applications make use of data that can be represented as a set of points. These sets of points, called *dot patterns*, appear in numerous fields including GIS gazetteers [1], parsing sensor data from distributed networks [15, 16] and the tracking of herds of animals [18, 5]. A commonly performed operation on these dot patterns is their reduction to a representative region; either for the associated reduction in memory, or so that queries can be performed on the region. Methods to produce these regions, called *footprints*, are the subject of much research with an impressive body of algorithms existing to create shapes that characterise a dot pattern (for example those given by [10, 7, 1, 4, 8], further examples and a discussion of their workings can be found in [9]). Despite the extent of this field it is, perhaps, surprising that little work has been done on comparison of the footprints produced, or on assessment of the quality of a footprint as a representative of a specific dot pattern. Notable exceptions that do perform such comparative analysis are [13, 12, 9]. One of the reasons for the large number of algorithms and the rarity of comparative analysis is that the quality of the footprint is difficult to assess as it tends to be context specific. There are some features which seem to be cognitively salient when deciding if a footprint is a good representation, for example Galton [12] shows that humans tend to favour footprints that fall on the Pareto front of minimising both area and perimeter, but in general the requirements of what makes a ‘good’ footprint are somewhat vague and relate to the requirements of the specific application for which their algorithms was created.

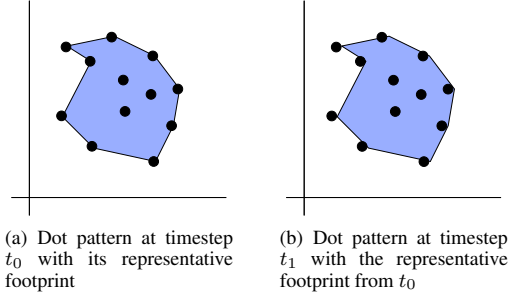
The extant footprint algorithms consider the pattern as static, but many of the phenomena underlying the patterns are dynamic, for example a flock of birds or a crowd of people moving through a shopping centre [2]. The algorithms also tend to be computationally slow, due mainly to the combination of an iterative process and multiple footprint validity checks. If the data is arriving more or less in time with the actual phenomenon, a ‘live’ system, then there is a strong

likelihood that updating the footprint for each change in the phenomenon will lead to the footprint being increasingly out of step with reality. Fig. 1 shows how this lag could appear if the patterns arrive at twice the speed that the footprint algorithm requires to compute the footprint. However, this lag can be controlled by not updating the footprint at every timestep. Earlier it was noted that the definition of a good footprint is somewhat vague, and this vagueness can be exploited when considering dynamic phenomena: If the footprint is a good representation of the dot pattern at timestep  $t_0$  it will likely also be an acceptable representation of the dot pattern at timestep  $t_1$  (see Fig. 2). To be able to reduce the number of required footprint updates we need to be able to identify when an update needs to occur in less time than it takes to compute the footprint. This paper presents a method to flag when change between timesteps is too great to ignore, using a suite of easily computed *change identifiers*. Recomputation is triggered when some aggregate value from the change identifiers exceeds a given threshold. Importantly the method this paper presents uses algorithms that are less computationally expensive than those used to generate the footprints.



**Figure 1.** Figure showing increasing lag in footprint representation

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**Figure 2.** Has the dot pattern at  $t_1$  changed sufficiently to require that the footprint be updated?

## 2 Terminology

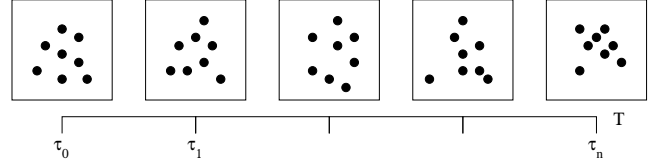
There are a number of terms used by this paper that require some justification, for example why use *dot* and not *point*? This section endeavours to make the distinctions clear.

**Dot:** A *dot* is described by an  $\langle \text{id, location} \rangle$  pair. It is a representative data point of any phenomenon that can be assigned a location within a space (whether real-world or abstract). The pairwise nature of a *dot* renders it very simple, since it is only when they are grouped and moving does complexity arise. The term *dot*, over the more common *point*, is used for two reasons. Firstly, a dot may have more data associated with it than just a location; for the definition used in this paper dots have an identifier. Secondly, to draw a distinction between the dot as a member of a dot pattern and a point within the dot pattern, for example the mean centre (centroid) of a pattern is a point that may not coincide with a dot. Note that the descriptors, and identifiers, presented in this paper do not make use of the identity attribute. This simplification allows us to use a less complex format for the expected dynamic dot pattern input files, thereby making the framework more generally applicable to a wide range of applications.

**Dot Pattern:** A set of dots is called a *dot pattern*. It is fully exhausted by these dots and is a mathematical abstraction. Its mathematical nature implies that it is incapable of change.

**Dynamic Dot Pattern:** As a dot pattern cannot undergo change we need a structure that uses dot patterns to represent the change of the underlying phenomenon. The *dynamic dot pattern* is a function mapping from time to dot pattern, as shown in Fig. 3. The function maps such that for each  $\tau \in T$  (where  $\tau$  is a timestep and  $T$  is a time domain),  $DP(\tau)$  is the dot pattern representative of the underlying phenomenon at time  $\tau$ . Rather than use  $DP(\tau)$  to refer to a dot pattern at a specific time we use the nomenclature *phase* (for which we borrow the wave notation of  $\phi$ ). For example the pattern in Fig. 3 at timestep  $\tau_0$  is the first phase ( $\phi_0$ ) of the dynamic dot pattern and the pattern at  $\tau_1$  is the second phase ( $\phi_1$ ).

The phenomenon that the dynamic dot pattern represents is likely to be changing in a continuous fashion. In our mathematical model, however, the phases are discrete steps. Thus the timesteps are used to provide a discretised time domain for the dynamic dot pattern to map from. There will almost certainly be change occurring between the timesteps, and therefore between the phases, but for the purposes of the work presented in this paper we can ignore the ‘in-between’ dot patterns as we are assuming that the *granularity* of the arriving data is



**Figure 3.** Time Domain ( $T$ )

appropriate to the application. For a further discussion on granularity of time domains see [20].

**Descriptor:** Dot patterns have various mathematical properties that arise from the cardinality and the locations of their member dots; for example the standard deviation from the mean centre. There is an incalculable number of these dot pattern *descriptors* but many will be measuring similar attributes of a pattern in different ways (e.g., bounding box area and standard deviation can both be said to be measures of the extent of the pattern).

**Change Identifier:** The entities that are represented by individual dots in a dot pattern can only change in three ways that concern us<sup>2</sup>: appearance, disappearance and translation (change in location) [21, 14]. In fact we can simplify further by considering translation as simply a function that combines a disappearance and an appearance. The dot pattern phases within a dynamic dot pattern can, therefore, only differ in the location and the cardinality of their members. The differences can be measured using the descriptors of the dot patterns, and comparison of the extent of these differences is a measure of the change undergone between the phases.

## 3 Describing Dot Patterns

There is a large amount of literature that examines spatio-temporal data. Generally this work focuses on identifying high-level movement patterns to ascertain the evolvments of the underlying collectives from a qualitative point of view. For example the herd evolvments of Huang *et al.* [14], the movement patterns of Laube *et al.* [18, 17] and the dynamic collective behaviours of Andrienko and Andrienko [3]. This paper presents a more quantitative approach, not dissimilar to that proposed by Thériault *et al.* [21], who note that the dots of a dynamic dot pattern<sup>3</sup> can only change in four simple ways: appearance, disappearance, translation and intensity change. From these simple changes they produce several low level components which, when combined, can be used as a description of the pattern at a given phase. The components they propose are:

- **Territorial Extent:** The extent of the space the pattern resides in that it encompasses.
- **Spatial Distribution:** This component contains several sub-properties, all but the last of which will re-appear in the set of descriptors we propose in this paper.
  - **Centre of Gravity:** The equilibrium point of the distribution. If the intensities of each dot are identical this is simply the mean average location.

<sup>2</sup> The entities could undergo many other types of change, ageing for example, but for our abstraction only the three given apply.

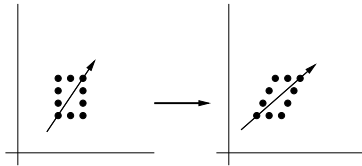
<sup>3</sup> In [21] these are referred to as sets of geographical entities or SGEs.

- **The Standard Distance:** The standard deviation from the centre of gravity.
- **The Orientation:** Thériault *et al.* use principal axis extraction to find the direction the pattern can be said to face.
- **Ellipse of Dispersion:** Using both of the vectors returned by the principal axis extraction<sup>4</sup> the maximum and minimum dispersion of the set are found. These extrema are used to define an ellipse centred on the centre of gravity.
- **Spatial Pattern:** Pattern in this instance refers to the degree of homogeneity across the dot pattern. In effect how clustered, random and regular the dot pattern is.
- **Spatial Autocorrelation:** The likelihood that dots in the pattern will be similar to their neighbours. If there is no intensity measure, or all intensities are identical, this equates to clustering analysis.

Unlike Thériault *et al.*, we do not consider intensity within this paper and so, as noted above, need only consider changes in membership (appearance and disappearance) and translation.

The core difference between the existing work and that presented within this paper is in the consideration of the dot pattern as a static entity. By looking at the measurable properties of a dot pattern at a specific timestep we can produce a description of its state at that phase. The change can then be given as the difference between the descriptor values of two phases. This method relies on the set of descriptors being broad enough to cover all the possible types of property that we might wish to be able to measure change in. However we must be wary not to measure the same property type multiple times; for example, as mentioned earlier, both the area of the isothetic minimum bounding box and the standard deviation can be said to be measures of the extent of the pattern. Should our change measure include descriptors for two extent measures then we are weighting extent as more important than other change types; which may be undesirable for the application. To avoid such weighting issues we propose several *classes* of descriptor that are general headings for types of information that can be retrieved from the pattern.

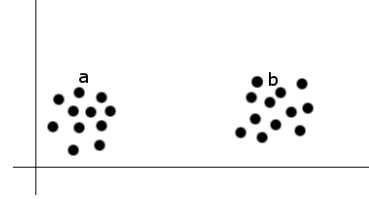
The affine transformations (translation, scaling rotation and shearing) provide a good starting point from which to discuss the choice of descriptor classes; the classes must allow us, at a minimum, to identify change in each of the affine transformations. Translation can be identified by a descriptor that measures the *location* of a pattern, scaling requires an *extent* measure, and rotation needs an *orientation* descriptor. Shearing can be ignored because any shearing the dynamic pattern undergoes will also change its orientation (see Fig. 4).



**Figure 4.** Dynamic dot pattern shearing. The arrow represents the pattern's orientation (as found by Ordinary Least Squares regression).

Further to the affine transformations we can also look at existing descriptions of regions to ascertain if any apply to dot patterns. Gal-

ton [11, ch. 4.7.3] provides a comprehensive overview of the possible attributes and relations of spatial regions; specifically: dimension, connectivity, location, orientation, size and shape. Of these attributes only dimension, connectivity and shape have not yet been discussed. For dimension we use Galton's notion of *apparent* dimension which is a product of the differing levels of granularity. A road is generally considered to be a 1-dimensional line on most maps, a 2-dimensional surface for most users and a 3-dimensional object for a road builder who has to be concerned with the depth as well as breadth and length. The *dimension* class, then, is concerned with the degree of dimension that a pattern exhibits; for example the collinearity of the dots. Connectivity is not a directly applicable term to dot patterns as the dots are, by their nature, disconnected. However, sometimes the dot patterns have areas that appear distinct from others. Fig. 5 shows a dot pattern in which part *a* is separated from part *b* by a distance that is substantial compared to the inter-dot differences within each part (we call each part a *component* of the dot pattern). Such dot patterns could be said to be disconnected and identifying such separations is intuitively important. The *connectivity* class is a way of assessing the number of components in the dot pattern. Shape does not apply to dot patterns per se, but all the shape properties would apply to footprints and may therefore be of use in classifying them.



**Figure 5.** A single dot pattern showing disconnected components.

The final class we introduce is *dispersion*. Dispersion acts as a miscellaneous class of descriptors that allows us to track properties such as homogeneity, global density and cardinality. This class bears a similarity to the spatial pattern attribute proposed by [21].

With classes in place we can look at some example descriptors. We note that the examples provided are by no means exhaustive but that they provide a good basis for both testing and discussion. Also we are only currently considering the case when the dots are in a planar space as this is the focus of much of the literature on footprint algorithms, however most of the calculations are directly extendable into other spaces.

**Position:** To compute a value for position requires a point or space relative to which we can measure it. Even with a clear origin or frame of reference there is a range of different units of measurement for position, either with numerical or with qualitative values; e.g., polar or Cartesian coordinates and compass positions respectively. It makes intuitive sense to use the frame of reference in which the dots themselves are positioned and to use the same unit.

- **Centroid** – The mean location of all the dots within the pattern.
- **Isothetic Bounding Box Centre** – The centre point of the axis-aligned (isothetic) minimum bounding box of the pattern.
- **Bounding Box Centre** – The centre point of the minimum bounding box of the pattern (non-axis aligned).
- **Minimum Disc Centre** – The centre point of the minimum bounding disc of the pattern.

<sup>4</sup> Principal axis extraction, or Principal Component Analysis (PCA), in 2-dimensions returns two perpendicular eigenvectors, the one with the highest eigenvalue is the principal axis.

It is apparent that there is a difference between the first and the last three given descriptors. The former descriptor treats the pattern as a set of points and the latter all apply a *surrogate* footprint to the pattern. Many of the classes have descriptors of each type. The minimum disc and the minimum bounding box (not axis aligned) are more computationally complex than the isothetic minimum bounding box and as a result may be unusable as change identifiers; it not being clear if they actually provide a sufficiently ‘better’ centre than any other measure for the greater computation time they take.

**Extent:** Unlike position, extent measures tend to be represented by a single value.

- **Variance from Centroid** – The variance from the centroid. We use variance so as to avoid the square roots required by the standard deviation.
- **Bounding Box Area** – The area of the isothetic minimum bounding box.
- **Diameter** – The greatest distance between any two dots.

The diameter of the pattern is found by locating all the external dots i.e., all the dots that are vertices on the convex hull of the pattern. This may make it too complex to be used when change identifiers are considered, despite its conceptual simplicity. However an approximation can be found by considering the mean between the lengths of the diagonal of the isothetic minimum bounding box<sup>5</sup> and the longest edge of the isothetic bounding box<sup>6</sup>. Alternatively a less accurate estimation can be attained using the greatest distance between the dots in the extremal axis aligned dimensions (for a planar pattern this would be the dots with the greatest and least  $x$  and  $y$  values). The bounding box of a pattern requires the extremal dots to be found before computing the vertices of its corners and will therefore take longer to compute than the less accurate estimation. This paper makes use of the axis-aligned extremal dots distance as its estimated diameter to provide a very computationally fast extent descriptor. To further increase its speed it uses the squared distance instead of the actual distance, avoiding the computationally difficult task of the square root. Of note is that all three measurements return a squared unit and this should be considered when comparing them to other descriptors.

**Orientation:** Orientation is the direction in which the pattern is facing. As the dots do not have an associated direction, unlike position, this cannot be an aggregate of individual values. In fact given the information inherent within the dot pattern a true orientation is impossible as even the ‘line of best fit’ will not tell you in which direction along the line the pattern points. From a change identifier point of view this is irrelevant, as all we need is a measure which will change as the orientation changes; the measure does not need to describe the orientation exactly, as long as it is linked to it.

- **Gradient of line of best fit** – There are multiple ways of measuring the line of best fit; however, the ordinary least squares (OLS) method is perhaps the least complex. OLS is a linear regression approach from the field of statistical analysis that minimises the squared vertical distances between the dots from the pattern and the line of best fit. As OLS is a statistical analysis technique it has some properties which do not apply directly to the use of spatial data. Within statistical analysis one of the variables would be expected to be an observed result dependent on another. For example when measuring the growth of children between the ages of 10 and 14, the height is observed data that is dependent on the age.

However, within a dot pattern all the variables<sup>7</sup> are independent.

- **Gradient of the Principal Component** – Found by principal component analysis (PCA). PCA finds the dimensions (components) with the highest variability within the pattern and is commonly used as a dimensionality reduction technique. Formally it transforms the coordinate system the data resides in so that, when the data is projected onto it, the distribution across the first coordinate has the greatest variance, the second coordinate has the second greatest, etc. To find the Principal Component we find the eigenvector corresponding to the largest eigenvalue of the covariance matrix of the data.

We note that the principal component is not always in the same direction as the line of best fit, as the OLS method minimises only the distance in the  $y$ -axis. Both PCA and the OLS linear regression technique are explained in more detail in [6].

**Connectedness:** Connectedness is actually a form of distribution measure as its measurements are performed by comparing inter-dot differences. It is, however, one that appears salient enough to warrant its own class. The patterns can often appear to split into separate groups and identifying the change in these groupings is similar to the behavioural evolvments of Huang [14] (herd splitting and joining). Connectedness in this fashion can be a discrete measure or a continuous value: the number of distinct groups and how connected the pattern is respectively. The continuous value approach, perhaps, fits better in the distribution class. Thus for the connectedness class we look only at the approach that provides an integer value for the number of clusters.

- **Greatest Jump Agglomerative Clustering** – This is an extension of the agglomerative clustering approach to give a possible value for the number of intuitively identifiable clusters. By running an agglomerative clustering method using Euclidean distance as its metric, a hierarchy of possible clusterings can be created. Agglomerative clustering iteratively concatenates the dots into clusters by finding the closest distance between any two clusters. We take note of the first unusually large jump in distance across the run of the clustering. If the jump is greater (by, for example, a factor of 2) than the average distance jump then the clustering preceding this jump is likely to contain a saliently identifiable set of clusters. This method is slow but effective at finding the parts of the pattern that we may identify as individual components.
- **K-Means Clustering** – An alternative to the *hierarchical* approach given by the agglomerative clustering method is the  $K$ -Means approach. Given a number of clusters  $K$  this minimises the squared distance between each dot and its closest cluster centroid. A full description of this method can be found in [6] but we assert that it is impractical to use it as a descriptor. While faster than an agglomerative approach there is no easy way of scoring the clustering it produces as to how well the it fits the data; this means that when iterating through possible values of  $K$  there is no definitive point at which to stop. We have tried several approaches, including balancing the number of clusters against the variance from the centroid for each cluster and minimising the nearest neighbour distance for each cluster, but with unsatisfactory results.

The agglomerative clustering method has to perform a large number of computations as it requires the nearest neighbours for each dot to be found (not estimated nearest neighbours as we will consider later) and involves an iterative process comparing cluster distances. As a result it is infeasible to use as the basis for a change identifier.

<sup>5</sup> Guaranteed to be no less than the length of the diameter

<sup>6</sup> Guaranteed to be no greater than the length of the diameter

<sup>7</sup> In a 2-dimensional pattern these would be the  $x$  and  $y$  coordinates

**Dimensionality:** Measuring the appropriate dimensionality can be performed in several ways and, like connectedness, we can envision both discrete and continuous measures: measuring the apparent dimension the pattern is in and measuring the degree to which a pattern fits a given dimension respectively. Within this work all these measures are assuming a planar space so the dimensionality measures are focused on identifying how 1-dimensional a pattern is.

- **Correlation Co-efficient** – Measuring how closely the pattern conforms to its linear estimator. The correlation co-efficient can be found using the Pearson correlation co-efficient. The Pearson correlation co-efficient makes use of the covariance of the coordinates; if we are using PCA to find the gradient, then we already have the covariance matrix and may be able to save processing time.
- **Principal Component Eigenvalue Difference** – Taking the pattern’s eigenvalues and finding how weighted one is over the other. In 2-dimensions we can measure how 1-dimensional the pattern is by the difference between the principal eigenvalue and the orthogonal eigenvalue divided by their sum. The closer to 1 this value returns, the more 1-dimensional the pattern.

**Dispersion:** This is possibly the most far-reaching of the classes in that it attempts to describe the layout of the pattern: How dense is it? How homogenous is its density? etc. As a result it has a large number of potential descriptors with a range of different complexities. It may be the case that multiple descriptors from this class are required to accurately measure change.

- **Cardinality** – Simply the number of dots in the pattern.
- **Global Density** – The global density of the pattern: Cardinality divided by an extent measure, usually the bounding box area but variance is an equally valid option.
- **Estimated Nearest Neighbour Distance Variance** – This is a method that returns a value for how clustered a pattern is, and is computed as the variance in distances between estimated nearest neighbours. To avoid the high computational complexities suffered when finding nearest neighbours we use the nearest neighbour in the axis aligned dimensions. If the patterns are stored in a data structure that is sorted by all dimensions of the space the pattern is embedded in (e.g., in a 2-dimensional space a structure sorted by  $x$  and  $y$ ) then this can be estimated in  $O(\log n)$  time (assuming a  $O(\log n)$  search time). It is not possible to be sure that the actual nearest neighbour has been found as there maybe a closer dot than those closest along the axis.
- **Skewness** – Skewness is a measure of the how uneven the distribution of a pattern is from the mean, often thought of as how much the histogram of the data is skewed to the left or right.
- **Kurtosis** – Kurtosis is the measure of how even the distribution of the pattern is, often thought of as how flat its histogram would be. Kurtosis makes use of the fourth moment about the mean<sup>8</sup> and is therefore related to skewness which uses the third.

Before moving on to the discussion and description of the change identifiers that arise from the presented descriptors, we note that there is analysis that can be performed on the descriptors themselves. Preliminary experimentation has been undertaken to show the correlation between their measures, however there is no space to detail that

<sup>8</sup> Moments about the mean are values used to describe probability distributions and have the general form  $\mu_k = E[(X - E[X])^k]$  for the  $k^{\text{th}}$  moment about the mean, for example the second moment about the mean is the variance.

work here. It suffices to note that between the classes there is little correlation, but distribution proves to be the exception. There may also be tripartite dependencies and finding these is an interesting direction for future work.

As mentioned earlier, the change identifiers are measures of change in a dynamic dot pattern, with each identifier relating to a specific descriptor. To indicate when change has been too great to continue processing the dynamic dot pattern without updating the footprint we need a way of thresholding the change identifiers. Ideally this threshold should be cognitively salient because the live nature of the proposed system precludes being able to ‘fiddle’ with the threshold value to get the desired results. That the threshold is difficult to set can be best demonstrated with a change identifier that measures the area difference of the bounding box. If we imagine two phases,  $\phi_1$  and  $\phi_2$ , from two dynamic dot patterns,  $DDP_1$  and  $DDP_2$ . The increase in bounding box area from  $\phi_1$  to  $\phi_2$  is the same for both patterns, however the bounding box of  $DDP_1$  was far smaller than  $DDP_2$  at  $\phi_1$  and has doubled in size whereas  $DDP_2$  has only increased by 50%. It would not be unfair to state that the change in  $DDP_1$  has a greater impact than the change in  $DDP_2$ . A threshold is required to signal that the footprint must be updated when sufficient change has occurred. Should the threshold be ‘concrete’ (i.e. it is a fixed value and not relative to the dot pattern) then the identifier is not tracking the impact that the change is having on the dynamic dot pattern. The thresholding concern can be satisfied if the requirement that all identifiers return a proportional value is introduced; a value that represents proportional change in the property the identifier measures since the last timestep at which the footprint was updated. The threshold now becomes a percentage value and is, therefore, more cognitively identifiable than a concrete value. While this still relies on user input we feel that it represents less of a mental leap than intuitively ‘knowing’ by how many units<sup>2</sup> a pattern’s bounding box area will need to change before its footprint is no longer a suitable representation. The definition of the change identifier can now be formalised as:

#### Descriptor Change Identifier

A descriptor change identifier is a measurement that compares two phases of a dynamic dot pattern ( $\phi_u$  and  $\phi_\tau$ ) and returns the difference in a descriptor of the dot patterns expressed as a proportion of the value of that descriptor on the dot pattern  $\phi_\tau$ .

$$\forall \phi \in DDP_i$$

$$change_x(DDP_i, \tau, u) = \left| \frac{desc_x(\phi_\tau) - desc_x(\phi_u)}{desc_x(\phi_u)} \right|$$

where  $change_x$  is the change identifier corresponding to descriptor  $desc_x$ ,  $\phi_\tau$  is the phase of the dynamic dot pattern  $DDP_i$  at time  $\tau$ ,  $\tau$  is the current time and  $u$  is the time of last update.

The identifiers are combined into *change identifier sets* which can then provide an overall measure of change for the dynamic dot pattern since the footprint was last updated. The sets have a group threshold allowing a user to state that every time total change exceeds, for example, 10% the footprint will need to be updated. Alternatively the set can have a threshold indicating the amount of its identifiers that are allowed to break their personal thresholds. From testing it appears that this latter approach appears to be more cognitively salient than using the threshold on the combined values.

## 4 Change Identifiers Assessment

To establish the fitness of change identifiers for their purpose, we need to be able to measure the ‘quality’ of the footprint. It should be stressed that we are not commenting on how well the footprint algorithm can create a footprint that represents the pattern; we assume that the algorithm used was chosen for its suitability to the application. The ‘quality’ we measure is how close the stored footprint is to the footprint which would result if it were recomputed from the current dot pattern using the chosen algorithm at any given step. The overall quality for a sequence of dot patterns is obtained by combining the quality values for each step. Our goal is to maximise the quality while minimising the computation time. These are conflicting objectives: to maximise quality is to minimise the difference between the stored and true footprints and this can only be achieved by updating the footprint at every timestep, resulting in a maximal value for the computation time. Conversely, the computation time would be minimised by never updating the footprint, typically resulting in catastrophic loss of quality. We therefore need to seek a middle course which optimises the trade-off between the objectives.

In order to compute the total time taken, we will need to make use of the following quantities:

- $t_{FP}(i)$  is the time taken to compute the footprint from the dot pattern at step  $i$ .
- $t_{CI}(i)$  is the time taken to evaluate the change identifier(s) at step  $i$ .
- $r(i)$  is a Boolean variable, set to 1 if the change identifier(s) evaluated at step  $i$  exceed(s) the pre-set threshold, and 0 otherwise.

The footprint has to be computed at least once, namely at the first timestep ( $i = 0$ ). At subsequent timesteps it is only recomputed if the change identifiers return a value above threshold. The total computation time over a run of  $n$  dot patterns is thus

$$T_{CI} = t_{FP}(0) + \sum_{i=1}^n (t_{CI}(i) + r(i)t_{FP}(i)).$$

The value of  $T_{CI}$  is minimum when the change identifier threshold is set so high that the footprint is never recomputed after the start of the sequence (so  $r(i) = 0$  for  $1 \leq i \leq n$ ):

$$T_{\min} = t_{FP}(0) + \sum_{i=1}^n t_{CI}(i).$$

It is maximum when the change identifier threshold is set so low that the footprint is recomputed at every time step (so  $r(i) = 1$  for all  $i$ ):

$$T_{\max} = t_{FP}(0) + \sum_{i=1}^n (t_{CI}(i) + t_{FP}(i)).$$

If change identifiers are not used at all, and the footprint is recomputed at every timestep, then the total time taken is:

$$T_{NCI} = \sum_{i=0}^n t_{FP}(i) = t_{FP}(0) + T_{\max} - T_{\min}.$$

If it is assumed that always  $t_{CI}(i) < t_{FP}(i)$  (for if not, there would be little point in using change identifiers) then  $T_{\min} < T_{NCI} < T_{\max}$ , so the relative size of  $T_{CI}$  and  $T_{NCI}$  — which provides a measure of the time advantage, if any, gained by using change identifiers — depends on the threshold settings.

It will be convenient to consider an inverse form of the quality measure, which we shall refer to as *error*. Our goal is therefore to seek to minimise both time and error. To measure error, we need a way of quantifying the extent of the mismatch between the stored footprint and the true footprint. The difference between two footprints can be measured in various ways, (e.g., using Hausdorff distance, or symmetric area difference) but for this paper we will be using symmetric area difference. The symmetric difference between two regions comprises the parts of each region that do not overlap the other; it is given by

$$R_1 \Delta R_2 = (R_1 \setminus R_2) \cup (R_2 \setminus R_1) = (R_1 \cup R_2) \setminus (R_1 \cap R_2).$$

We use the area of this as a measure of the dissimilarity between two footprints; and since we are only interested in comparisons, not absolute values, we normalise this area by expressing it as a fraction of the area of the ‘true’ footprint ( $footprint(\phi_u)$ ). Thus the aggregate mismatch between the stored footprint and the true footprint over a dot-pattern sequence of length  $n$  is given by

$$error = \sum_{i=0}^n \frac{||footprint(\phi_i) \Delta footprint(\phi_u)||}{||\phi_u||},$$

If the footprint is recomputed every time, corresponding to total computation time  $T_{\max}$ , we have a footprint for every phase, so  $error = 0$ . At the other extreme, the maximum value of  $error$  is obtained when the footprint is never recomputed, corresponding to  $T_{\min}$ . There is thus a trade-off between  $error$  and computation time, where different choices of change identifier thresholds correspond to different positions on the curve. The optimal setting for the change identifier threshold depends on the relative importance attached to the conflicting goals of minimizing both computation time and accumulated footprint error; but in any case no time advantage can be obtained for error below the value at which  $T_{CI} = T_{NCI}$ .

## 5 Results

To provide a dynamic dot pattern that would provide enough variance to test the change identifiers fairly we have used an implementation of the ‘Boid’ behaviour described by Reynolds [19]. Boids produce a reasonable mimicry of real-life bird movement by having each entity attempt to align itself with its local neighbours while maintaining a distance that is neither too far away or too close. The results presented here are from a run that made use of three change identifier set types, a set containing all of the change identifiers, a set containing the fastest descriptor from each class and a set that uses identifiers that were selected explicitly for the dynamic dot pattern used (containing a cardinality identifier, the estimated diameter squared identifier and the estimated nearest neighbour distance identifier). Both the ‘all’ identifiers and ‘fastest’ identifiers set types have versions with differing thresholds of the number of identifiers allowed to breach their individual thresholds, and neither type includes the agglomerative clustering descriptor because it is too slow. This range of change identifier sets was used as they represent a set where we wish to measure every type of change we can (the all set), a set to measure each of the classes of descriptor individually (the fastest descriptor set) and a set to represent the identifiers chosen by human intuition about the types of change the phenomenon being measured can undergo. Arguably this last set is the most important as it is how we may envision the change identifier framework actually being used. The footprint algorithm used is the  $\chi$ -hull [8] because it can produce a variety

of different footprint types (it is not limited to the convex hull) and completes in a comparatively fast time to other footprint algorithms.

Fig. 6(a) gives the error as a proportion of the expected footprint for every timestep. Every timestep where a line has dropped to 0 indicates that the footprint was updated at that timestep. Of the sets, Fastest-0.9 (the set using all of the fastest processing descriptors with a proportion of allowed fails of 0.9) and Fastest-0.5 do not ever cause an update apart from at the very first timestep. This indicates that neither of them is sensitive enough to the change occurring in the dynamic dot pattern. Comparatively Fastest-0.1 causes the most updates. All-0.1 and All-0.9 (the sets that use all of the descriptors) are hard to distinguish on the graph because they update at exactly the same times. Because All-0.9 has a higher threshold this means that any time an update occurs for either set, the change must have been sufficient to cause at least 90% of the identifiers to fail.

Fig. 6(b) shows the computation time for each timestep and the lines correlate with Fig. 6(a); showing a jump on Fig. 6(b) for each drop on Fig. 6(a). Note that all of the sets fall well below the computation time for a run without change identifiers. Interestingly All-0.1 consistently takes longer to compute than All-0.9, this is likely an anomaly arising from the computer the tests were running on using the processor for other tasks. The logarithmic scale makes the difference appear larger; for comparison the average difference between All-0.1 and All-0.9 is 0.003 seconds whereas the average difference between All-0.1 and the run without identifiers is 0.527.

The final graph (Fig. 6) displays the sets on a graph of average time against average error. The sets fall much where we'd expect given the above graphs. Two aspects of particular interest on this graph are that Fastest-0.1, UserSelected-0.1 and Fastest-0.5/9 have formed the suggestion of a curve much like that suggested for an individual identifier in § 4. Also of note is that the UserSelected set has provided a balance of just over 20% error per step for around 0.004 seconds, an improvement on Fastest-0.1 in time for a small increase in error and an improvement on Fastest-0.5/9 in error for a small increase in time. Such a result demonstrates that it is certainly possible for a user to make intelligent choices on how to select a set for a dynamic dot pattern assuming they know something about its expected behaviour.

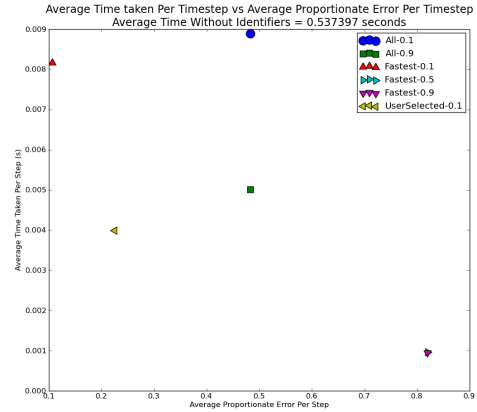
## 6 Conclusions

Constraints on space have meant that we can only display a small selection of the tests that have been performed. However, even with this small sample size, it can be seen that identifiers can be used to reduce the average computation time across a dynamic dot pattern for a controllable level of error. The results show that the thresholds and sets can be altered in a straight-forward manner to traverse the time-error trade-off curve.

Further experimentation with different dynamic dot pattern types has confirmed that the change identifiers are not limited to solely workin with Boid-like behaviour patterns. But to guarantee that the change identifiers are useful future work will involve more real-world examples of large data sets. Future work may also involve extending the range of descriptors to take into account dots with attributes beyond their location, for example identity, intensity and territorial extent.

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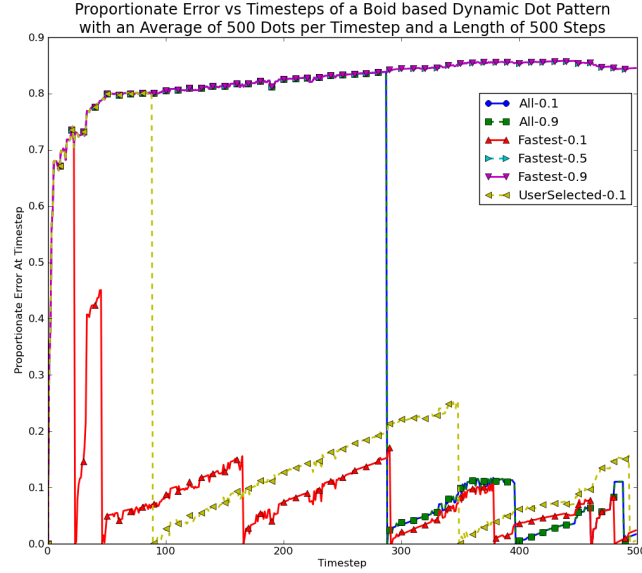
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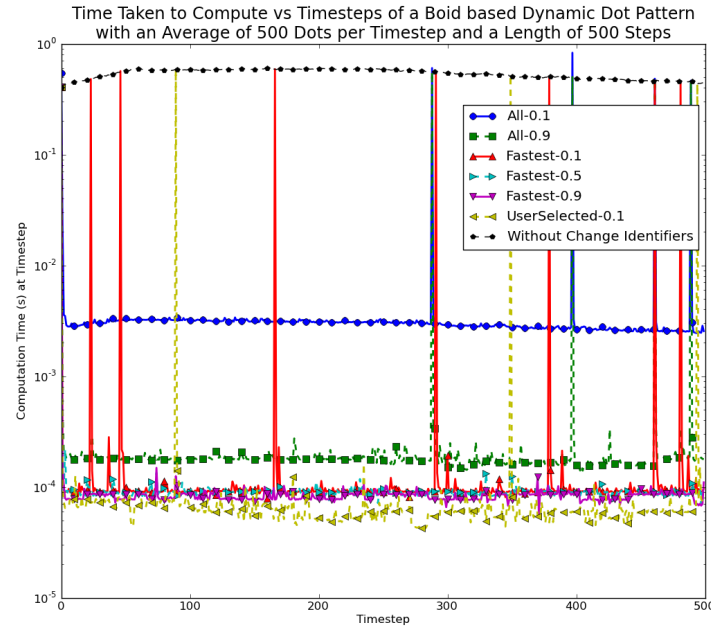
**Figure 6.** Graph of average computation time in seconds per timestep vs average proportionate error found by symmetric area difference per timestep.

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(a) Graph of proportionate error found by symmetric area difference for each timestep.



(b) Graph of computation time taken in seconds for each timestep; note that, to make the run without change identifiers visible, the  $y$ -axis has been plotted on a logarithmic scale.

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# From collective actions to “actions of organizations”: an ontological analysis

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**Abstract.** Here, we propose an ontological analysis of organizations that covers both structural and behavioral aspects. By distinguishing between the *object* and the *process* when studying group phenomena, we analyze both the *object*-organization and the organization’s *processes*-actions. For the *object*-organization, we defend the hypothesis whereby the notion of *collection* (as commonly defined in formal ontologies) is not appropriate for founding the concept of an organization; we prefer the notion (taken from the social sciences) of a *collective*, i.e. *a set of humans unified by a joint intention – that of forming a group capable of acting*. This leads us to consider the philosophy of actions (and social actions in particular), in order to clarify the nature of this collective agent and account of its intentional behaviors. Lastly, we compare our ontological framework with existing formal ontologies of organization, by referring mainly to the work of Bottazzi and Ferrario at the Laboratory for Applied Ontology (LOA) in Trento.

## 1 INTRODUCTION

The work presented in the present article is situated within the domain referred to as “applied ontology”, which is at the interface between formal ontology (philosophy) and knowledge representation (artificial intelligence). The applied goal of this work is to define knowledge bases with inferential abilities and that serve as components of information systems.

It is only recently that this domain has focused on collective phenomena (i.e. those involving a plurality of entities). The literature primarily contains work centered on the notion of *collection* (or “collective”, a synonymous designating a set of entities) and that assesses the value of using this notion to describe anatomical structures [1] and human organizations [2]. More recently, Wood and Galton [3] proposed a general ontological framework for classifying these collections/collectives according to various criteria. However, with the notable exception of Galton’s analysis of “dynamic collectives” [4], this work essentially addresses the static (i.e. structural) aspects of collective phenomena and ignores dynamic (i.e. behavioral) aspects. The objective of the work presented here was to articulate these structural and behavioral aspects and thus account for the actions of organizations.

To this end, we adopted a basic ontological principle that can be summarized as follows: the *object* and the *process* are two

complementary aspects of any reality. This principle corresponds to a widely shared view in formal ontology concerning the reality of the physical world. The complementarity of the objects and processes is explained by strong mutual dependence, as stated by Galton and Mizoguchi [5, p. 72]: “(a) *matter and objects by nature presuppose the participation in processes or events*, and (b) *processes and events by nature presuppose the existence of matter or objects*”. This principle is already firmly anchored in most upper-level (foundational) ontologies, including BFO and DOLCE. In the latter [6] (adopted here as our reference framework), the principle corresponds to the distinction between *endurants* and *perdurants*, applied so far to the analysis of individual phenomena. In our work, we make this principle a precept and therefore seek to apply it to the analysis of collective phenomena and, more precisely, social phenomena generated by collectives of humans. We distinguish between *objects*-collectives on one hand and the *processes*-behaviors generated by these groups on the other.

It is useful to note that by attributing groups (and then organizations) with their own existence, we distance ourselves from Searlian naturalism and, more generally, from methodological individualists in the philosophy of social science [7]. Our main argument for this is linguistic. In everyday language, there are many cases in which properties that cannot be attributed to individuals are assigned to groups (the jam “paralyzed the downtown area”, the crowd “dispersed in silence”, the flotilla of boats “filled the bay”, etc.). By correlating this observation with the stated purpose of DOLCE in “capturing the ontological stands that shape natural language and human cognition” [6, p. 7], we consider our strategy of distinguishing between objects-groups and the latter’s behavior as worthy of further consideration. In any case, this position underlines the fact that an ontology necessarily commits to a theory (in the social sciences, in our case) and explains the choice of research work referred to here, in our ontological analysis.

In the remainder of the article, we first present an ontological reference framework structured around the foundational ontology DOLCE (Section 2). Next, to address organization actions, we proceed in two steps. In a first step, we ground our research on work in the social sciences, in order to clarify the concept of *social group* (or *collective*) as a solid basis for accounting for collective actions (Section 3). In a second step, we focus on the structured, formal collectives that are *organizations* (Section 4). To account for organizations and their actions, we respectively borrow on Bottazzi and Ferrario’s ontological work [8] and on philosophy of collective actions (including Tuomela’s work [9][10]). Lastly, we compare our ontological framework with existing formal ontologies of organization by referring mainly to the work of Bottazzi and Ferrario.

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## 2 THE ONTOLOGICAL REFERENCE FRAMEWORK

Before turning to our analysis of collective phenomena itself, we shall first review background information on the foundational ontology DOLCE [6] and present a set of basic concepts which we have added (notably to account for the notion of *action*).

### 2.1 Particulars (DOLCE)

DOLCE’s domain is that of Particulars<sup>3</sup>, that is to say entities that cannot be instantiated (e.g. “my car”) rather than universals (e.g. “being a car”). One can distinguish between four sub-domains of Particulars (see Fig. 1):

- Endurants are entities “enduring in time”<sup>4</sup>. Within Endurants, Physical Objects (e.g. a paper copy of this article) are distinguished from Non-Physical Objects (e.g. the content of this article resulting from your interpretation); this distinction corresponds to a difference between two realities or *modes* of existence for the entities. Basically, Non-Physical Objects exist insofar as agents [11, p. 267]: “... by means of some sort of convention, constitute, make use of, communicate and accept [them]”. The domain of Non-Physical Objects covers entities whose existence depends on either a single agent (for Mental Objects) or a community of agents (for Social Objects).
- Perdurants are entities “occurring in time” (e.g. your reading of this article) in which Endurants temporarily participate (*participatesInDuring*). Perdurants encompass entities such as States (e.g. “sitting”), Processes (e.g. “running”), and Events (e.g. “a soccer match”), all kinds of entities that we designate in the article as “behavior” by Endurants.
- Endurants and Perdurants have Qualities that we perceive and/or measure (e.g. the weight of a print copy of an article or the time it takes you to read this article).
- Qualities take on “values” or “magnitudes” referred to as Qualia (e.g. 25 grams, 20 minutes) within values spaces called Regions.

To complete this short introduction, we have to make one remark on the notion of *social object* and concerning DOLCE’s position vis-à-vis Searle’s [12] social ontology.

As we shall see in Section 3, consideration of a class of Social Objects turns out to be critical for our conceptualization of organizations and their actions. It is important in this respect to note that this standpoint is in strong contrast to Searle’s [12] social ontology. Indeed, according to Searle, social reality is above all constituted of social *facts* that

are dependent on collective intentions of humans (or animals capable of collective intention). This is the case (for a group of agents) for the fact of considering that a piece of paper with a special green inscription *counts for* a one dollar bill, or the fact that a specific individual human *counts for* the President of the French Republic. According to Searle, neither the dollar bill, nor the President of the French Republic exists as object; only the piece of paper and the human individual exist. In contrast, the authors of DOLCE recognize that there are social objects (such as *money*, *governments* and *universities*) that have an existence analogous to that of material objects. Indeed, one of their research projects involves defining the essence of these social objects [11][13]. Our proposed ontology of collectives and organizations is fully encompassed by this perspective.

### 2.2 Actions, participation roles and participatory capacities

Our goal here is also to account for the actions of collectives. According to a common belief (introduced by Davidson [14]) in the philosophy of action, a behavior may be qualified as an *action* as soon as one can describe it as having been performed intentionally. Indeed, the notions of *action* and *intention* are inextricably linked. To account for these notions, we have expanded DOLCE with a minimum set of concepts. These concepts (summarized in [15]) come from work in the philosophy of (individual) action. Their extension to the framework of collective action will be discussed in Section 3.

- Actions are Perdurants controlledBy at least one Intention<sup>5</sup>. They contrast with Happenings which lack an intentional cause<sup>6</sup>.
- Deliberate Actions are premeditated Actions. They are controlledBy a Prior Intention which consists in planning the action (before its initiation) and then in controlling it in a rational way<sup>7</sup>. In contrast, Non-Deliberate Actions (which include routine actions) are only controlledBy one Intention In Action.

<sup>5</sup> In the current state of our ontology, the different concepts of *intention* introduced here are defined without reference to their content (i.e. whether conceptual or not). The definition of these contents would require an ontology of mental objects, such as that laid out by Ferrario and Ultramari [16] as an extension of DOLCE. We shall leave this for further work.

<sup>6</sup> In DOLCE-Lite-Plus, a notion of action was informally introduced as “an Accomplishment exemplifying the intention of an agent” [6]. By more generally defining Actions as arbitrary Perdurants controlled by an Intention (as recently proposed by Trypuz [17] in an extension of DOLCE to actions), we allow other categories of Perdurants (namely States and Processes) to be intentionally realized.

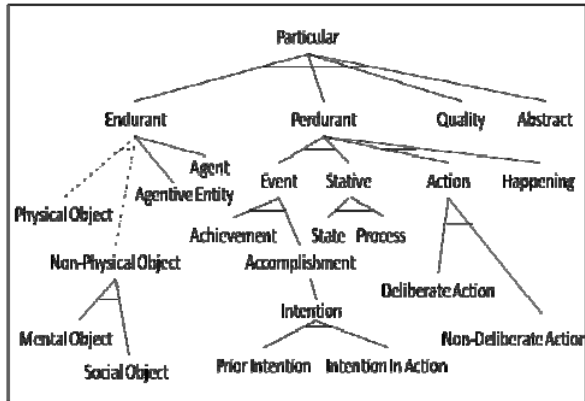
<sup>7</sup> Although we use a Searlian terminology to designate this intention, the proposed concept is somewhat different. Thus, based on Pacherie’s [15] dynamic theory of intentions, we consider that Prior Intention does not stop at the point where the Action begins. In contrast, the Prior Intention continues and has a controlling role in guiding the Action and determining its success.

<sup>3</sup> With respect to our notation, the informal labels on DOLCE’s categories appear in the text in the Courier New font with First Capital Letters for concepts and a javaLikeNotation for relations. In order to identify the extensions made to DOLCE, the labels of the categories introduced in the article are underlined.

<sup>4</sup> Due to space limitations, we are only able to provide a very brief introduction to DOLCE’s categories and we have limited our description to those required for our analysis. For a comprehensive presentation of DOLCE, the reader is invited to refer to [6].

Various entities participate to these Actions in various ways, i.e. by playing different roles. To account for specific ways in which Endurants temporarily participate in Actions, we introduce an equivalent number of specializations of DOLCE's participation relation participatesInDuring (e.g., isAgentOfAt, isInstrumentOfAt and isResultOfAt). In turn, these relations are used to define *participation roles* that specialize the concept Endurant (e.g., Agent, Instrument and Result).

These different roles are played by entities with specific *capacities* or *dispositions*. Indeed, only entities capable of Intentions can have the role of Agent. The Agentive Entity concept classifies precisely these entities with the ability to perform Actions (i.e. to implement Intentions). An Agentive Entity only has the role of an Agent during the performance of particular Actions.



**Figure 1.** Taxonomy of the main concepts defining our ontological reference framework. A descending line between two concepts represents a subsumption link. A dashed line reflects the existence of intermediate concepts. A horizontal line between edges from a father concept indicates that the sibling concepts are incompatible.

### 3 COLLECTIVE PHENOMENA

The term “collective phenomenon” refers to a phenomenon demonstrated by a plurality of entities. This term encompasses a wide variety of situations such as a *charge by a herd of buffalo*, the *deforestation of a geographical area* or the *formation of a traffic jam*. As one can see, these phenomena relate to a broad variety of fields. However, they all correspond to a global effect resulting from several individual effects. In this article, we focus on collective behaviors (and, more particularly, intentional behaviors) that result from the contribution of individual humans – a *performance of a piece of music by an orchestra*, for example. In accordance with our precept of distinguishing between an *object* and a *process*, we postulate the existence of a plural entity (referred to as a “collective”) to which we attribute the responsibility for such behavior.

In the literature on formal ontologies, researchers have recently suggested defining this type of a collective notion by deriving it from a broader notion of collection and thus equating a collective (and an organization) to a “complex” collection

[2][3]. We believe that this conception is not justified and instead propose two distinct notions of *collection* and *collective*; the former corresponds to an embodied set (dependent on agents) and the latter (coming from the social sciences) corresponds to a plurality of individuals capable of acting (3.1). Below, we start to characterize the actions of these *collectives* (3.2).

#### 3.1 Collections and collectives

The starting point for our concept of *collection* is the concept of a naturalized (embodied) set similar to that proposed by Bottazzi et al. [2]. A Collection is thus a whole to which entities *belong*. The membership relation between an entity and a Collection (isMemberOfAt) is identified by connecting a content to a container: the member is “in” the Collection. The criterion for membership of an entity in the Collection is a property that temporarily classifies the said entity<sup>8</sup> (e.g. the property of “being a stamp that I keep for its value” for the Collection “my collection of stamps”). It follows that: (i) over time, the members of a given Collection can change and (ii) two distinct Collections can be extensionally equivalent (if they have the same members)<sup>9</sup>. Moreover, Bottazzi et al. also consider that a Collection is a Non-Physical Object that depends on agents, in as much as one (or more) agent(s) conceive it; the Collection ceases to exist as soon as it ceases to be conceived by the agent(s). We have adopted this minimal characterization for our ontological framework<sup>10</sup>. However, to emphasize the representational nature of a Collection, we distance ourselves from the original proposal by constraining a Collection to be a Non-Agentive Object (see Fig. 2).

The question is now whether this notion of collection is a good starting point for defining an organization. We think that it is not. By means of an explanation, let us consider the example of a physical object such as a brick wall. If the wall is made of bricks of different shades, an observer will be able to clearly identify a collection of light-shaded bricks, a collection of dark-shaded bricks and many other collections that he/she may come up with. However, according to the above-mentioned definition of Collection, the bricks that are members of the collections are considered as objects satisfying a property, rather than as physical objects. The forces that bricks exert on each other and that ensure the solidity of the wall are abstracted. This is also

<sup>8</sup> For the purposes of this article, we (like Bottazzi et al. [2]) shall only consider sets that are intensionally defined by a property. In future work, we plan to expand the scope of our concept of Collection to cover extensional sets – the equivalent of arbitrary sums of entities (an Arbitrary Sum, within the meaning of DOLCE), but gathered together into a whole by thought by an agent.

<sup>9</sup> The Collections’ membership criteria are, in this case, two different but extensionally equivalent properties.

<sup>10</sup> In particular, we consider the isMemberOfAt relation to be primitive. In fact, and in contrast to a common held belief (cf. for instance [3]), we do not define our isMemberOfAt relation as an isPartOfAt subrelation. This allows us to consider that Physical Objects are members of a Collection (a Non-Physical Object) without violating the constraint imposed by DOLCE whereby a Non-Physical Object has for parts Non-Physical Objects only.

true of their position in the wall, giving the latter its overall form and strength. In other words, by basing our argument on a very general notion of organization implying relations between entities (others than those conceived by an observer), we can say that a Collection sets aside any form of organization.

An apparently different approach has been adopted by Rector et al. [1]; they suggest the notion of a *collective* made up of a generally indeterminate number of *grains*. The latter all have the same role (e.g., a *collective* of cells forming a skin tissue, a *collective* of grains of sand forming a beach and a *collective* of stars forming a galaxy). In terms of conceptualization, Rector et al. suggested identifying *collectives* as Amounts of Matter (in the sense of DOLCE). Thus, a collective of cells is treated as an Amount of cells. Skin (or piece of skin) is therefore notably *constituted by* a collective/Amount of cells. By analogy, our brick wall would be constituted by (amongst others) a collective of bricks. The problem that we see with this conceptualization is that it fails to provide these collectives with a criterion of identity. We have a concept of a “specific sum of grains” but lack information on the *specific* features. This notion is just as conceptually weak than the Collection concept when seeking to account for a particular *organization* of bricks, in the general sense (as we understand it here)<sup>11</sup>. Moreover, with regard to our objective of accounting for human organizations, this concept defines physical objects while organizations are commonly deemed to be non-physical objects (intuitively, it is impossible to beat with a stick a baseball team!). Again, we must seek another approach.

To this end, we turn to the social sciences (and the philosophy of the social sciences) by focusing on a research topic (introduced the sociologist French [18] and culminating today with the work of List and Pettit [19], notably) that aims at defining organizations as groups of humans able to act and that are morally accountable for their actions (like human beings). To move in this direction, French [18] proposed drawing a distinction between two categories of human groups (or “collectivities”), which he calls “aggregate” and “conglomerate”<sup>12</sup>. According to French, the identity of “aggregate collectivities” changes as their membership changes. Furthermore, these aggregate collectivities are unable to act. In contrast, “conglomerate collectivities” have their own identity (over and above that of their members) and are capable of actions. However, as other researchers (e.g. Pfeiffer [20]) subsequently demonstrated, this distinction is at best one of degree and not of category and the suggested classifications are largely erroneous: some “aggregate collectivities” (such as people gathering in an emergency to rescue a person in danger) are certainly capable of actions. As sociologists and psychologists have shown in their studies of group dynamics, decision-making structures may develop spontaneously over a very short time. Moreover, some “conglomerate collectivities” (such as a duo of singers, a sports team or a corporate) can change their identity as their members change (insofar as the

assessment of this identity depends on external agents – the baseball team’s fan, for example [21]). So, we still lack a set of concepts that define a satisfactory starting point (intuitively, a generic concept of group of individuals) for characterizing (by specialization) human organizations.

Finally, we turn to a more recent line of research (illustrated by the work of Pettit and Schweikard [22] and List and Pettit [19]) that highlights the notion of *group agent*, which is distinct from that of a *joint action*. The analytical strategy involves defining (i) conditions prompting humans to form a group able to act and (ii) the conditions under which such groups act collectively. In both respects, the notion of *joint intention* is at the heart of the analysis. In as much as this notion is still subject to much debate (see section 3.2), we shall simply follow the above strategy for the purpose of our current research, without committing to a precise, definitive notion of *joint intention*.

Thus, we introduce a Collective concept (see Fig. 2) that we assimilate to a *group of humans unified by a joint intention - that of forming a group able to act*. In doing so, we leave the door open to the existence of broader pluralities of individuals that are not able to act. Nevertheless, by taking account of the above-mentioned social psychology research highlighting the spontaneous development (over very short time spans) of control and decision structures, we decided to include most of French’s “aggregate collectivities” in the extension of our concept Collective (including aggregates that form during circumstantial actions)<sup>13</sup>. In addition, by ascribing Collectives with the capacity of intentions, we espouse the idea (as expressed by Sosa [24]) that these Collectives have, in some sense, a mind or a locus of consciousness where these intentions form (p. 215): “The persons that are members of the group have minds, and the group’s mind (in whatever sense it has one, its beliefs and desires) is some sort of construct from those minds.” The group’s mind is based on a set of representations (consisting of objectives, plans and beliefs about the world) that are collectively recognized by the Collective and enable it to control actions in the manner of individuals. In this sense, one can speak of *collective intentions*. In contrast to an individual, a Collective does not have (at least directly) a physical body at its disposal – it is a Non-Physical Object. However, this does not prevent it from acting (on the physical world, in particular), since its actions are carried out through individuals and their physical bodies. Before considering collective actions (and for completeness’ sake), we introduce an isPartyToAt relation into our ontological framework; this expresses the fact that an individual is involved (by way of a joint intention) in a Collective; the isPartyToAt relation differs from the isMemberOfAt relation in that it does not depend on external agents.

### 3.2 Collective actions

An action is intuitively considered to be a *collective* (or “joint”) action because it results from the combination of several individual actions. This condition is, however, commonly

<sup>11</sup> It should be noted that these authors consider examples of collectives whose grains are different compounds of blood (white blood cells, red blood cells, plasma, etc.) which we consider to be very close to our Collections.

<sup>12</sup> Examples of “aggregate collectivities” cited by French are: one’s neighbors, teenage groups and mobs; Examples of “conglomerate collectivities” are: clubs, political parties, universities and companies.

<sup>13</sup> It is worth noticing, in this respect, that we distinguish our Collective concept from List and Pettit’s notion of *group agent* [19] relying of more constrained notions of *agency* and *joint intention*. For reasons of space, we cannot justify this choice. The interested readers may refer to Thalos [23] for the presentation of a close viewpoint.

regarded as insufficient by philosophers, who wish to avoid considering that any collection of individual actions aimed at the same goal and independently combining to achieve the said goal is a collective action. Intuitively, use of the adjective “collective” assumes the presence of a shared commitment or even some form of cooperation. In the literature, several treatments reflecting this idea have been suggested, the most influential of which include proposals by Tuomela and Miller [9], Searle [25], Brachman [26] and Gilbert [27]. All these various conceptions highlight a plural entity (designating individuals engaged in the action) by use of the pronouns “we” (or “us”).

In a first step towards the conceptualization of collective actions, we hypothesize that it is reasonable to give a full ontological existence to the entities designated by the pronoun “we” or “us”. The natural candidate for embodying this role is, of course, our Collective. This conception amounts to endowing collective actions with a Davidsonian intuition, according to which each action is necessarily controlled by an agent. It should be noted that there is no requirement to form a new Collective for each performance of a collective action. By adopting the viewpoint of Pettit and Schweikard [22], we consider that a Collective (by analogy with their “group agent”) may perform several actions. However (unlike Pettit and Schweikard), we consider that a Collective may occasionally form when a spontaneous action takes place. In any case, the Collective must exist before the collective action is performed.

In a second step (and in order to justify our conceptualization), we argue that (to the best of our knowledge) there is nothing on a theoretical level to contradict our choice. We note here (as we did above) that different treatments of the notion of *joint intention* have been suggested. Most of these treatments placed a number of constraints on the existence of joint intent (e.g., awareness on the part of the agents participating in a joint action of its joint character and of the attitudes of the other participants). However, other conceptions (described by Pacherie [28] of “minimalist”) exist; for example, that of Butterfill [29] requires only the existence of a *shared goal*. It should be noted that the broad notion of Collective that we have adopted here (and, by implication, the weak constraints for the formation of these Collectives) is entirely consistent with this minimalist conception of intention.

Formally, we expand our relation hasForAgentAt to encompass these situations of Action controlledBy a Collective. At the same time, we refine our concept of Intention to introduce Collective Intentions. We therefore define a Collective Action as an Action controlledBy a Collective Intention and comprising at least one contributory Individual Action.

In the next section, we detail our model of collective action by placing it in an organizational context.

## 4 ORGANIZATIONAL PHENOMENA

As we have seen above, our concept of a Collective (defined as an *agentive whole consisting of individuals*) covers a broad reality of groups. It notably covers some of French’s “aggregative collectivities” [18], including short-lived groups that constitute themselves on the occasion of an action (which may not necessarily be deliberate). In this section, we focus on

the *organizations* described as groups with a perennial and often formalized structure and which are able to carry out complex premeditated actions – the equivalent of French’s “conglomerate collectivities”. In line with our precept of distinguishing between the *object* and the *process*, we first propose a model for organizations (by refining our model of Collectives) and then present a model of their actions.

### 4.1 Organizations

A first, essential feature of the organizations defined here is that they are highly structured. This structure begins with formalization of the conditions of membership of the organization. One can consider these conditions as an affiliation agreement specifying the affiliate’s rights and duties. Once an individual has become a member of the organization, he/she has (according to List and Pettit [19]) two main roles: the first (corresponding to an attitude) is to allow the organization to act instead of its members; the second (concerning actions) is to act mindfully in pursuit of the organization’s objectives. The second role amounts to performing parts of the group’s actions. These parts are commonly specified by ascribing specific and differentiated active roles. Lastly, the performance of complex actions by the organization may prompt the formation of subgroups of individuals. These subgroups may then carry out some (or, parts) of the complex actions. The organization will then present a hierarchical structure.

As one can see, the organization’s structure is based on rules specifying contracts at the level of both affiliated individuals and the organization itself. The individual’s commitment to these rules is a condition of the organization’s formation and structuring.

Organizations are further characterized in that they are social constructs; in other words, they are intentionally built entities to which a function (a mission) is socially attributed. This characterization is important when defining the identity of an organization because it equates to the addition of an extrinsic dimension (an enjoyment of external recognition) to an intrinsic dimension (the disposition to act). One can consider (like Slater and Varzi [21]) that these two dimensions are combined within an organization’s identity criteria. The origin of existence of the social group (an intentional construction, rather than a mere emergence), the social group’s dependence on external agents (including other organizations) and the formalized character of the group’s structure are usually put forward to distinguish between Organizations and informal groups within the broader set of Collectives.

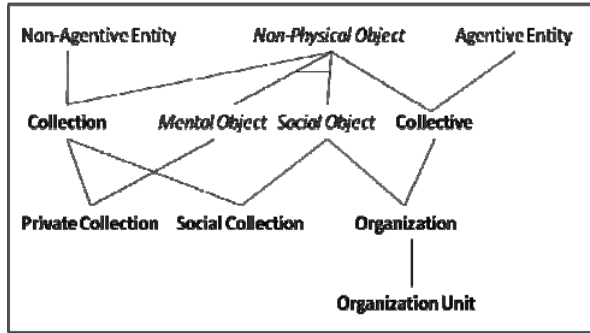
For our conceptualization of organizations, we strongly rely on Bottazzi and Ferrario’s formal ontology of organizations [7]<sup>14</sup>. For the purposes of this article, we shall merely list a few of the main relations and concepts that structure our ontological framework:

- The relation isValidFor models the Organization’s social commitment to Propositions. This fundamental relation (on which most of the other concepts and relations depend) enables one to include descriptions (or representations) within the

<sup>14</sup> In the Related Work section, we present a detailed comparison of these ontological frameworks.

structure of an Organization (i.e. objectives, plans, various norms, roles and so on).

- The relation isAffiliatedToAt (a subrelation of isPartyToAt) models the fact that an Agentive Entity (a Human or an Organization, in the case of systems of organizations) *formally* and temporarily belongs to an Organization. This relation implies that the affiliate satisfies rules set by the Organization.
- An Organization Unit is an Organization that isManagedByAt (a subrelation of isProperPartOfAt) the Organization upon which it depends. The only parts of an Organization that we consider are Organization Units.



**Figure 2.** Collections and Collectives are Non-Physical Objects. A Collective is an Agentive Object. An Organization is a Collective and a Social Object. An Organization Unit is an Organization (in its own sake) managed by (and dependent on) an encompassing Organization.

## 4.2 Actions of organizations

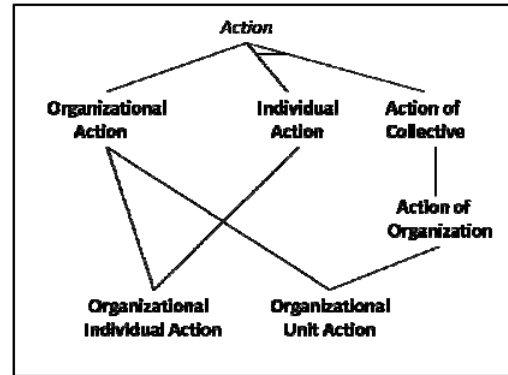
Our conceptualization of the organizational actions relies chiefly on the work of Tuomela [9][10]. Over the past 20 years, this philosopher has developed a detailed theory of social action that (under certain conditions) gives an organization the status of an actor. The ontological choices we have made so far are full consistent with this theory. In this section, we present a synopsis of this theory and introduce a set of concepts that complement our ontological framework.

In essence, Tuomela considers that an Action of Organization (in as much as an action that can be attributed to an organization) is an action consisting of joint actions of persons. In general, for an action  $X$  performed by the organization, a few members of the organization (and possibly just one) perform actions  $X_1, X_2, \dots, X_n$ , corresponding to their part of action  $X$ . These members are called “operant agents”. The term “joint action” means that operant agents unite their efforts in order to achieve something that (by convention and according to social and normative right conditions) is considered to be an organizational action. Ontologically speaking, two categories of actions can therefore be distinguished: action  $X$ , which we call Action of Organization, and actions  $X_i$ , which we call Organizational Actions (cf. Fig. 3). To

account for the contribution of the latter to the former, we propose considering the isProperPartOf relation.

Organizational Actions entail a specific action mode for their agent (called “we-mode”) and the implementation of specific intentions (called “we-intentions”). In short, a “we-intention” can be paraphrased as “we will collectively do  $X$ ”. The “we” refers to the Organization and the intention to perform the Action of Organization  $X$  is to understand as the “we-intention” shared by members of the organization. When an operant agent acts according to the “we-mode”, she/he commits to collectively achieve his/her part of action  $X$  (i.e.  $X_i$ ). It is important to note that there are no constraints placed on the way in which the  $X_i$  actions are carried out [30, p. 67]: “Even if on the group level, so to speak, the members are jointly seeing to it that  $G$ , they may act separately or jointly to achieve this goal and use whatever “tools” (e.g. hiring agents to do something) that are believed to be useful”. One should also note in this respect that an Action of Organization  $X$  may be composed of a single Organizational Action  $X_i$ , as in the case where a government decision ( $X$ ) is announced by the government’s spokesperson ( $X_i$ ).

For the purposes of the present paper, we shall not discuss how “we-intentions” are formed. Likewise, we shall not discuss the “we-intentions” possible contents (for a review, please refer to [10]). To establish a link with our model of the organization, we simply note that these Organizational Actions may have either an Organization Unit or an individual affiliated to the Organization as an agent. To distinguish between these two cases, we distinguish explicitly between two types of Organizational Actions, referred to as an Organizational Unit Action and an Organizational Individual Action (see Fig.3).



**Figure 3.** An Action of Organization is a special case of an Action of Collective. Every Organizational Action is ProperPartOf an Action of Organization.

## 5 RELATED WORK

In addition to the actions of collectives of individuals (for which we rely on existing theoretical frameworks) our present contribution bears mainly on the characterization of these collectives. We introduce the concepts Collective and Organization, which differ from the Collection concept. In this final section, we position our proposal with

respect to reference works in the field of formal ontologies of organizations.

As we have seen, our proposals are principally inspired by (and similar to) Bottazzi and Ferrario's work [8] on the formal ontology of organizations. In line with the latter authors, we adopted the foundational ontology DOLCE [6] and the LOA project to define social objects that are "missing" from Searle's social ontology. These *Social Objects* are defined *a minima* as *Non-Physical Objects* (namely, objects not directly located in physical space) that depend on a community of agents. *Organizations* are further defined by Bottazzi and Ferrario [8] as *Social Objects*. To fill the conceptual space between *Social Objects* and organizations, the LOA project adopted two approaches.

One corresponds to the definition of the intermediate notions of *collection* and *collective*, with a *collective* being considered as a special case of *collection* [2]. As stated above, we adopted a different position by accepting the notion of a *Collection*-embodied set (as defined by Bottazzi et al.) but by using a different foundational basis for the notions of *collectives* and further of organizations: The difference lies in the fact that our *Collective* is founded by relations between individuals (from which the *Collective* derives its existence), whereas this type of relation is absent from our *Collection* concept). Slater and Varzi [21] appear to have adopted a similar position by distinguishing between the sports team and the group of team members. The latter authors state that a same group of individuals (a *Collection* of individuals, in our ontology) can constitute different teams (*Organizations*, in our ontology) depending on the roles played by the said individuals in these teams. Furthermore, we consider that, when observers want to analyze how the membership of a team changes over time, they may very well consider various *Collections* of its members at different times. It should be noted in this respect that in their subsequent treatment of the notion of organization, Bottazzi and Ferrario [8] did not reuse the notion of *Collection*. The approach of defining an organization as a complex collection seems, therefore, to have been abandoned.

The second approach is an ambitious project that seeks to define a general theory of social objects and their links with the physical world. To this end, the concepts of *qua-individual* ([11], [13]) and, more recently, *perspectile* [32] have been defined. The general idea is to admit the existence of new objects - social objects - inhering in physical objects and *counting* for the latter in contexts that involve particular social conventions (e.g., the social object "John *qua* (as) President of OntoBusiness Inc." *counts* for the physical object "John" in his role of President, recognized by the company). According to Bottazzi and Ferrario, the consideration of these new objects enables one to account for problems of organizational identity by considering that these social objects (rather than their physical hosts) correspond to the parts of the organization<sup>15</sup>. It should be noted that in our case, we do not consider that members affiliated to an organization are parts of the organization: the relation *isAffiliatedToAt* is

not a subrelation of the relationship *isPartOfAt*<sup>16</sup>. At the same time, the only parts of organizations that we consider (*Organization Units*) are themselves organizations. We are therefore open to the fact that *qua-individuals* (whose theorizing is still in draft form) may correspond to individual parts (or, rather, constituents) of an organization.

In Section 4.1, we summarized the common features of our conceptualizations of the notion of *organization* itself. Here, we emphasize two important differences. Firstly, Bottazzi and Ferrario [8] consider that organizations are distinct from social groups. The researchers argue that members of an organization may not necessarily be aware of the existence of the other members, which can never be the case for a social group (according to Gilbert [27] cited by these authors). In contrary, our concept of *Collective*-social group, that encompasses organizations, is based on "minimalist" conception of the notion of *joint intent* [28][29]. In this respect (in a second contrast to Bottazzi and Ferrario), we attribute the capacity to act to *Collectives* and, *a fortiori*, to *Organizations*. Curiously, Bottazzi et al. have suggested that an organization is an agent in [31] but this idea was not accounted for in the axiomatic presented in [8]. This same question was recently posed by Robinson in his comparative analysis of the concepts of *legal person* and *organization* [33, p. 122]: "If the surface structure of natural language is intended to have ontological relevance in DOLCE, then philosophical discussion of whether or not organizations, legal persons, and other social objects are "really" agentive is not necessary relevant [...] there is natural language surface structure evidence to consider moving the governments of states (and even organizations more generally) to the agentive category as well." Boella and van der Torre adopt a similar degree of caution concerning the agentive status of an organization [34]: "Inspired by Searle's analysis of social reality we define organizations, functional areas [a sub-class of ours *Organization Units*] and roles as *socially constructed agents*. These agents do not exist in the usual sense of the term, but they are abstractions which other agents describe as if they were agents, with their own beliefs, desires and goals, and with their own autonomous behavior." The pseudo-agent status granted by Boella and van der Torre to *functional areas* and *roles* is accompanied by a homogeneous pseudo-part status [35, p. 83]: "The decomposition hierarchy of the organizational structure, however, is not based on the part-of relation of objects." Our conception for these entities differs markedly: we consider *Organization Units* to be both *genuine* parts and (as *Organizations*), *genuine* agents. In contrast, roles are *concepts* and therefore non-agents; even though one can consider *concepts* to be parts of the *structure* of the organization, they are not parts of the organization itself. Overall, the only agents that we consider to participate in the actions of the organization are the *Organizations* (and their *Organization Units*) and the *affiliated* persons.

<sup>15</sup> Technically, two entities with exactly the same parts are considered identical. If individual members of an organization are identified with parts of the organization, having the same members should imply that the organizations are identical – which is obviously not the case.

<sup>16</sup> In order to maintain the homogeneous nature of the relations *isPartOf*, we consider that an *Organization* may only have sub-organizations (namely *Organization Units*) as parts. Thus, if the *Organization Units* are the same, the *Organizations* are the same.

## 6 CONCLUSIONS & FUTURE WORK

In the present paper, we have proposed an ontological framework that brings together a set of basic concepts accounting for actions of collectives of humans and, more particularly, of organizations. The novelty of this framework relates to the clear distinction between the notion of *collection* (as an embodied set) and that of *collective* (as individuals intentionally forming an agent). In order to characterize this concept of *collective*, our framework is based on theories from the sociology of organizations and the philosophy of collective action. Lastly, we have shown that our framework extends the work of Bottazzi and Ferrario at the LOA by linking the structure of organizations to their intentional behavior.

Several bricks in the framework require further characterization. However, we are hopeful that this solidly-grounded framework will guide future developments. Our group is particularly committed to an analysis of the *processes* of the organizations – processes that are a part of organizational actions [36]. One of the challenges in this respect is to understand how individual behavior and collective behavior are interfaced within organizations.

## ACKNOWLEDGMENTS

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# Understanding the Social Cascading of Geekspeak and the Upshots for Social Cognitive Systems

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**Abstract.** Barring swarm robotics, a substantial share of current machine-human and machine-machine learning and interaction mechanisms are being developed and fed by results of agent-based computer simulations, game-theoretic models, or robotic experiments based on a dyadic communication pattern. Yet, in real life, humans not less frequently communicate in groups, and gain knowledge and take decisions basing on information cumulatively gleaned from more than one single source. These properties should be taken into consideration in the design of autonomous artificial cognitive systems construed to interact with/learn from more than one contact or ‘neighbour’. To this end, significant practical import can be gleaned from research applying strict science methodology to human and social phenomena, e.g. to discovery of realistic creativity potential spans, or the ‘exposure thresholds’ after which new information could be accepted by a cognitive agent.

The results will be presented of a project analysing the social propagation of neologisms in a microblogging service. From local, low-level interactions and information flows between agents inventing and imitating discrete lexemes we aim to describe the processes of the emergence of more global systemic order and dynamics, using the latest methods of complexity science. Of particular interest is the ability to track those novel linguistic expressions which are *idiosyncratic* to the system (i.e., not used in offline discourse). This allows us to plot the dynamics of the spread of the items *in a closed, hermetic circuit* relative to its structure and size.

We will consider the following issues: 1) how linguistic innovation becomes a norm, 2) that the distribution of the general lexical innovativeness of Internet users scales not like a power law, but a unimodal, 3) that the exposure thresholds characterising users’ readiness to adopt new lexemes from their neighbours concentrate at low values, suggesting that—at least in low-stakes scenarios—people are more susceptible to social influence than may erstwhile have been expected, and 4) that, contrary to common expectations, the most popular tags are characterised by high adoption thresholds. Hypotheses will be investigated which may account for the observed phenomena.

Whether in order to mimic them, or to ‘enhance’ them, parameters gleaned from complexity science approaches to humans’ social and humanistic behaviour should subsequently be incorporated as points of reference in the field of robotics and human-machine interaction.

*Why is it that when robots are stored in an empty space, they will group together, rather than stand alone?*

—Dr. Alfred Lanning in *I, Robot* (2004)

## 1. THE ORIGINAL TURING TEST

The year 2012 marks the centenary of the birth of Alan Turing. Yet it is an unjust legacy that to this day few, even in the AI field, seem aware of what Turing originally had in mind when, in his 1950 paper *Computing machinery and intelligence* [29], he introduced his concept of a test examining a machine’s ability to exhibit intelligent (or, to be more precise, humanlike) behaviour. For it was not merely a matter of whether a computer could interact with a human in such a way that the interrogator would be deceived into thinking s/he were ‘conversing’ with another human being. The design of the imitation game was much more subtle: to see whether a computer pretending to be a woman could be more convincing than a man also pretending to be a woman.<sup>3</sup>

## 2. LANGUAGE SIMULATIONS

Regrettably, this necessary proviso of ‘other things being equal’, so forcefully emphasised in Turing’s original scenario, all too often seems to be overlooked in much of current research literature which either has the ambition to serve as input for developing AI, or which could potentially be applied by the field.

For instance, over the past decade much space has been devoted to language simulations, from workshops devoted exclusively to that topic<sup>4</sup> to articles posted on arXiv and published across scientific journals. Many of the papers, devoted to phenomena such as language evolution, language competition, language spread, and semiotic dynamics, were based on regular-lattice *in silico* experiments and as such are glaringly inadequate, especially to the scenery of the 21<sup>st</sup> century:

- the models take into account only Euclidean relationships (whereas the current telecommunication technology and the global accessibility of mass media mean that more and more of our linguistic input reaches us from afar, and—especially with services such as VoIP calls and social networking sites—spatial

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<sup>3</sup> For an interesting distant but convincing analogy in popular culture, think for instance of the title protagonist of Mankiewicz’s 1950 film *All About Eve*, whose faked femininity is more compelling than that of the remaining, genuinely heterosexual heroines.

<sup>4</sup> E.g. the GIACS Workshop on Language Simulations, which took place at the University of Warsaw in the year 2006.

proximity can no longer be equated with social proximity);

- are ‘static’ (while mobility has been a distinctive feature of humankind—but also the animal world—as evidenced by warriors, refugees, missionaries, civil servants, and tradespeople long before the time of the Hanseatic League);
- assume a limited, identical number of ‘neighbours’ for every agent ( $4 \vee 8$ ;<sup>5</sup> first of all, an underestimate, secondly, again unrealistic given that persons vary in terms of the number of their close friends, acquaintances, or relatives – suffice it to think of the growing number of nuclear and patchwork families, the multi-generation families of the not-so-distant past, or the divide in China between urban couples who have had to abide by the one-child policy and the rural countryside where the restriction was not stringently enforced, but where in turn male offspring have often been valued more than female);
- presuppose identical perception of the prestige of a given individual by each of its neighbours (while, again, take a single person known to a group, be it a celebrity or an insider, and their perceived prestige and respect is again going to fluctuate from individual to individual), as well as
- invariant intensity of interactions between the different agents,
- absence of multilingual agents (with a few notable exceptions, e.g. [4]);
- and sometimes more technical issues such as lack of memory effect or zero noise (while noise may be the indicator and initiator of pattern change).

### 3. ALTERNATIVES

This is why there still remains much work in front of the AI circles to move from coarser-grained game-theoretic (e.g. [19]) and agent-based models (e.g. [18]) which not infrequently only manage to capture the initial and final states and the general trend of the phenomena they are purported to describe, towards increasingly accurate and sophisticated work based on the results of rigorous data-driven research and empirical studies that recreate the necessary conditions and parameters as faithfully as possible. One solution is experimental designs involving actual cognitive agents. A new quandary that arises with many designs involving interactions between and learning by (embodied) artificial intelligent agents (for a good overview cf. e.g. [26], [27]) is the fact that they are often restricted to dyadic scenarios. This can naturally be justified when the process in which the robots engage is akin to the initial stages of language acquisition in humans, where a baby can conceivably find him-/herself in situations where s/he only interacts with a single caretaker. However, sooner or later the child’s interaction becomes more social, with an increased number of input sources and persons against whom linguistic hypotheses can be tested. This calls for research paradigms involving more agents engaging in

interactions with the subject under investigation, and luckily more and more robotics teams are moving in this direction.

Another, often more time-, cost- and resource-effective alternative is rigorous re-search fuelled by data from genuine human interactions. In the case of linguistic phenomena such as language learning and the uptake of new linguistic expressions, such data can be gleaned by either interviewing each member of a community and additionally verifying their responses against a more objective benchmark such as e.g. standardized test scores (in the case of foreign language acquisition; cf. e.g. [21])—admittedly still a time-consuming process, and one laden with the limitations posed by self-assessment—or, an easier way, utilize readily available repositories of user-generated content such as Web 2.0 sites.

The recent information explosion with exponentially increasing vast quantities of rich sources of data, and their widespread availability, has enabled access to huge amounts of data allowing us to investigate human behaviour from new angles. The increased use of the World Wide Web, and the recent availability of user-generated text in particular, provides evident and unprecedented new research opportunities. The data stored on the Internet is virtually unregulated, essentially uncensored, spontaneous, immediately registered, interconnected, and amenable to relatively easy search and exploration with the use of statistical and concordancing tools. Web 2.0 services, with content (co)generated by the users, especially the ones which allow enriching their analyses with information concerning the structure of the connections and interactions between the participating users, are particularly useful for multi-angle explorations of language and social phenomena, such as humans’ communicative behaviour. By tapping into the repositories of language data nearly perfectly suited to fine-grained large-scale dynamic linguistic analyses and applying novel, transdisciplinary research methodology, most of the formerly-mentioned limitations can be addressed and bypassed.

### 4. LANGUAGE ON THE INTERNET

Erstwhile research on language evolution and change focused on large time-scales, typically spanning at least several decades. Nowadays, observable changes are taking place much faster. According to [12], a new English word is born roughly every 98 minutes (admittedly a rather overrated estimate owing to methodological problems).

The uptake of novel linguistic creations in the Internet has been commonly believed to reflect the focus of attention in contemporary public discourse (suffice it to recollect the dynamics and main themes of status updates on Twitter following the presidential elections in Iran, Michael Jackson’s death, Vancouver Olympic Games, and the recent Oscar gala, last July’s L.A. earthquake, the Jasmine Revolution—by some also called the “Internet Revolution”—in Tunisia, the developments in Libya, the 2011 Tōhoku earthquake and tsunami, or ibn Laden’s death, see e.g. [11]). However, even where the topics coincide, the proportions in the respective channels of information are divergently different (correlation at a level of a mere .3; e.g. [23], just as television ratings cannot be used to predict online mentions; [20]), just as not infrequently the top stories in the mainstream press are

<sup>5</sup> We use the  $\vee$  operator to symbolise exclusive disjunction.

markedly different than those leading on social media platforms (e.g. [24]). The emotive content of comments on different social platforms is also distinctly different ([2], [7]).

## 5. A CASE IN POINT: TAGS AND SOCIAL COORDINATION

In a recent empirical research project [22], we investigated the creation and adoption of tags (metalabels) on the Polish microblogging site Blip.pl (roughly analogous to Twitter), with special emphasis on neological expressions. At the time of the data dump the site had 20k users (with over half logging on daily), with 5.5k users in the giant component<sup>6</sup> (density: 0.003), 110k relations, 38k tags and 720k tagged statuses. The data were analysed in Python.

The intended purpose of tagging systems introduced to various Web 2.0 services was to provide ways of building *ad hoc*, bottom-up, user-generated thematic classifications (or “folksonomies”; [31]) of the content produced or published within those systems. However, the tagging system of Blip became much more than that, as users redefined the meaning and modes of using tags. In the site, tagging is not merely a mechanism for retrospective content classification, but also provides institutional scaffold for on-going communication within the system. From the point of view of *individuals*, using a tag within a status update still provides information about what the update is about, but also implies joining the conversation defined by the tag, and, consequently, subscribing to the rules and conventions governing conversation. In this sense, the system of tags can be thought of as an institution (as sociologically understood), regulating and coordinating social conduct — here, mostly communication. From the *systemic* point of view, tags-institutions define what Blip.pl is about, the meaning of its dynamics, and its culture.

## 6. THE LONG TAIL OF THE BLIP CULTURE

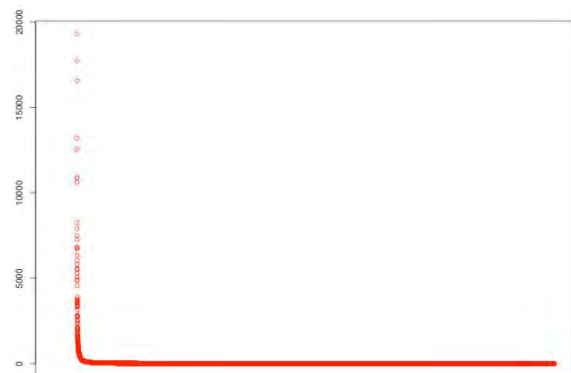


Figure 1. Tag popularity distribution in Blip

<sup>6</sup> By the term ‘giant component’ we mean the unique largest connected cluster (subgraph), containing a majority of the entire graph’s vertices.

One of the preliminary results obtained from the data analysis carried out concerns tag popularity, whose distribution scales like a power law (Fig. 1), a feature Blip shares with a wide range of natural, technological and socio-cultural phenomena (cf. e.g. [5], [17]). Our assumption is that at least a considerable proportion of popular Blip tags constitute the “meaning” and structure of the system, its cultural and institutional establishment, while the long tail consists of more or less contingent representations.

## 7. SOCIAL INFLUENCE AND DIFFUSION

The most important mechanism we are looking for has to do with diffusion of innovation. Diffusion and creation of novelty has been traditionally assumed to be among the most important social processes [8]. In our case, each of Blip’s tags, a potential communication coordinator, had been first created by a user, then spread throughout the system with greater or smaller success (see Fig. 2). Some of the most successful, most frequently imitated tags have become Blip’s culture and structure.

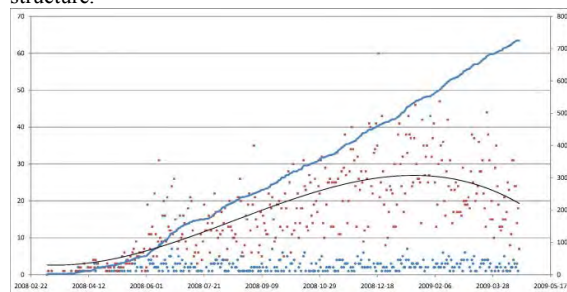


Figure 2. Evolution of the popularity of an idiosyncratic tag, relative to system size; abscissae: time, ordinates left: percentage of saturation; ordinates right: absolute count; blue rhomb dots: first usages; red square dots: subsequent usages; thin black line: subsequent usage trend (multinomial); thick blue line: first usages cumulative

There are a number of theories explaining the mechanisms of diffusion of novelty, and one of our goals is to find out which best accounts for our data. Memetic theory assumes that ideas (here coded as words-tags) are like viruses which “use” the mechanisms of the human mind to reproduce. The most successful reproducers would be those optimally adapted to the environment of the mind — its natural dispositions and the ecosystem of already established ideas ([6], [9]).

The theory of social influence proposes that individual behaviour (including adoption of innovation) is contingent on peer pressure. The threshold model of collective behaviour postulates that a person will adopt a given behaviour only after a certain proportion of the people s/he observes have already done the same. This proportion—the “adoption threshold”—constitutes the individual characteristic of each member of the group [13]. The network version of this theory proposes that an individual (“ego”) observes only a fraction of the social system, namely, the alters in his/her ego-network. The exposure of the ego to an innovative idea is hence defined as the proportion of his/her alters/neighbours that had already adopted the relevant innovation by the time concerned, and an individual’s adoption threshold is computed as his/her

network exposure at the time of adoption [30].

A third point of view is offered by the social learning theory [1], which assumes that innovation or behaviour adoption is a result of a psycho-cognitive process which involves evaluation of other people's behaviour and its consequences. In this case the adoption process is perceived as more reflexive and less automatic than the previous two ([14], [25]).

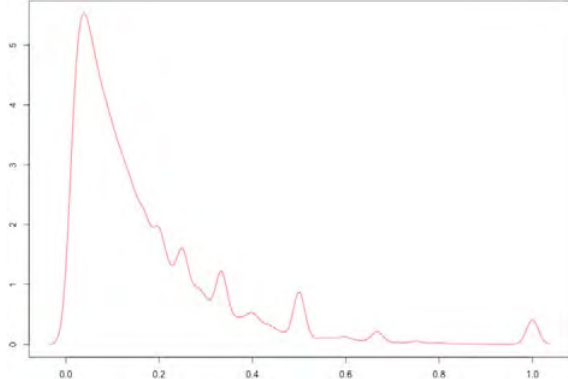
The preliminary analysis conducted involved calculating thresholds for all tag adoptions (i.e., their *first* usages). We describe the user-tag network with a bipartite graph  $G = G(U, X, E)$ , where  $U$  is the set of users,  $X$  is the set of tags, and  $E$  represents the edges between users and tags. The user-user network we define using a directed graph  $D = D(U, H)$ , where  $H$  is the set of edges, and  $e_{u \rightarrow x} \in E$  is an edge connecting user  $u$  to tag  $x$  added in time  $\tau_{u \rightarrow x}$ . Using this notation, we calculate the (mean) measure of the number of alters (neighbours) who had adopted a given tag before user  $u$ . We only consider first usages:

$$\beta_u = \frac{\sum_{e_{u \rightarrow x} \in E(u)} \frac{A(e_{u \rightarrow x})}{H_{(t)}(u)}}{|E(u)|}$$

where:

- $A(e_{u \rightarrow x})$  is the number of neighbours of  $u$  who are already connected to  $x$  at time  $\tau_{u \rightarrow x}$ ;
- $H_{(t)}(u)$  is the number of neighbours of  $u$  at time  $t$ ;
- $E(u)$  is the total number of (unique) tags used by  $u$ .

The smoothed distribution of  $\beta_u$  is plotted below



**Figure 3.** Distribution of tag adoption thresholds in Blip

Fig. 3 shows the general characteristics of the innovativeness of Blip's users: the distribution of adoption thresholds based on all instances of tag adoption events. Contrary to Granovetter's assumption of normality of thresholds' distribution in populations, the resultant distribution of adoption thresholds is considerably skewed, with a median of 0.11 and a long tail of higher values<sup>7</sup>. This suggests that the population of Blip's users is generally innovative and/or corroborates the viral model of diffusion over the two alternative mechanisms (social influence and social learning) mentioned earlier. The prevalence of low thresholds indicates that adoption is less contingent on social

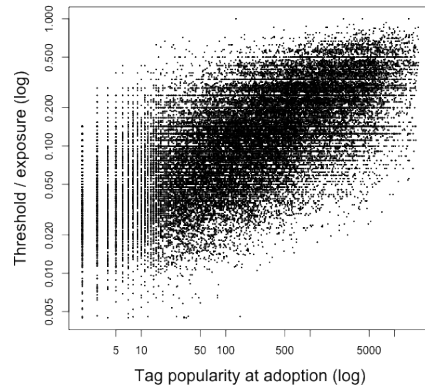
<sup>7</sup> The "humped" feature of the distribution tail stems from the skewed distribution of the variables used to calculate the threshold values.

pressure to adopt, or elaboration of the way the tags are being used by alters, than on individual, cognitive mechanisms of attention and knowledge integration. However, we expect other factors (such as tag and user characteristics) to play an important role as well.

Another finding is the general correlation between tag popularity and adoption threshold. Figure 4 is a scatterplot showing the relationship between the adoption threshold and the general, systemic popularity of a tag at the time of a singular adoption. It shows that the more popular tags tend to be adopted at higher values of exposure (which constitutes the adoption threshold of a given user for this tag) than those less popular. This may run contrary to common-sense expectations that the more popular an item is, the more readily it should be adopted. There are two alternative and yet to be verified hypotheses that may account for our observation.

One account supports the social influence approach, and explains the observed relationship by the fact that a lower popularity of a tag *implies* that only people with low adoption thresholds had adopted it by the moment of measurement. The greater popularity of the other tags may simply mean that their diffusion took long enough for people with higher threshold to pick them up. This suggests the classical diffusion process with population division into early adopters and laggards: thresholds rise with tags' popularity because users with lower thresholds had adopted them earlier (when the expressions were not yet popular).

The other hypothesis, corroborating the premises of the social learning theory, postulates that a higher threshold is consistent with later adoption, the adoption lag being needed for observation and evaluation how an innovation is being used by others and works in the social context. The positive correlation between threshold and popularity may stem from the fact that the most popular tags constitute the institutional and cultural structure of the system and so more time is needed for their evaluation, learning and adoption.



**Figure 4.** Relationship between tag popularity and exposure threshold

There are obviously only a subset of preliminary findings. The next step is to develop a formal model and simulation that will include these factors in explaining diffusion mechanisms in order to gain not only a controlled understanding of their dynamics, but also predictive potential.

## 8. INSIGHTS FOR AI?

Such rigorous data-driven research offers the chance of not only approximating to descriptive adequacy, but also moving beyond explanatory adequacy to approaching principled explanation. Results like the above are conceivably useful to answer questions how a) creative, and b) susceptible to the influence of alters an artificial cognitive agent should optimally be. The established parameters can also be helpful in the development of interactive dialogue systems, HCI, and intelligent machines that acquire knowledge via interaction with other (human and non-human) agents (rather than all their knowledge being put in by their creators). Naturally, the question needs to be posed to what degree observed online behaviour—which may naturally be affected by the medium—can be treated as a realistic proxy for offline behaviour. If we grant the assumption that any difference that may exist is insubstantial, such and similar data-driven research can have practical import for the discipline of artificial (social) intelligence, providing a reference point for at least three aspects of cognitive systems' behaviour:

- (i) interaction<sup>8</sup>,
- (ii) learning, and
- (iii) collective intelligence.<sup>9</sup>

Where the agents are expected to pass off as humans, exhibiting performance indistinguishable from that of mankind, e.g. in affective contexts (where, for instance, their task is that of companions), the established data could then be used to emulate human behaviour as closely as possible (bearing in mind the desirability of optimal distinctiveness (cf. [3], [15]) and the uncanny valley problem; [16]). In other scenarios, it may be more desirable for the agents to outperform humans<sup>10</sup> (think, for instance, of Deep Blue defeating Kasparov in 1997, or IBM's another wonderkind, Watson, the computer capable of answering natural-language queries, which in February 2011 won the Jeopardy quiz show against two of its all-time human champions). In that case, it is still useful to have a reference point or benchmark. Only subsequently, given the growing sophistication of tools for ABMs, can fine-grained simulations be employed to try to emulate and explain the behaviour observed. This is what Alan Turing would appreciate.<sup>11</sup>

## ACKNOWLEDGMENTS

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<sup>8</sup> And each utilizable cognitive system must be interactive.

<sup>9</sup> Consider e.g. the "wisdom of the crowd" effect ([10], [28]).

<sup>10</sup> To use the words of Gigolo Joe from *A.I.* (2001), "Man made us better at what we do than was ever humanly possible."

<sup>11</sup> Even if computational cognitive systems may be *non-Turing*, with non-terminating computations, interactivity, and non-uniform evolution [32].

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# A Comparative Investigation of Herding Algorithms

Brandon Bennett and Matthew Trafankowski<sup>12</sup>

**Abstract.** This paper gives an overview of a system for simulating flocking and herding of sheep. The system implements a number of different algorithms and includes functionality for batch testing their performance over large numbers of randomised situations. This allows one to perform tests to compare different algorithms and different parameter settings.

We suggest an algorithm inspired by the herding commands and techniques used by actual shepherds and use our simulator to obtain results of that indicate that in many situations our method is more effective than other published sheep herding algorithms.

## 1 Introduction

There is a large body of literature on explaining and simulating the flocking behaviour of animals [11, 8, 10, 2, 9, 3, 14, 6]. However, the literature on herding is far less extensive [1, 12, 15, 4, 5, 7]. This paper presents an algorithm for herding and compares it to several other proposed algorithms. We also describe an implementation of a herding simulation system that we have used to test these algorithms. We give some experimental results that give indicate the effectiveness of the algorithms. Most of the material in this paper has been taken from the project report of Matthew Trafankowski [13].

In constructing our simulation, we have taken the herding of sheep by a sheepdog to be our paradigm case, and our descriptions will normally refer to this particular herding example. However, our algorithms are formulated in terms of quite general behaviour patterns and could potentially be applied to other herding situations. Our behaviour model involves a superposition of several different movement control mechanisms, each of which can vary in its specific details and the strength of its effect according to a number of parameters. By changing these parameters we can potentially model a range of different herding situations, and we can also examine whether a herding algorithm works robustly over a range of different parameter settings.

Although our primary aim is to model and simulate herding (in particular sheep herding) a model of flocking will also be needed. Herding without flocking is clearly much more difficult to achieve and, in reality, herding is (as far as we know) only used to control animals that have some flocking instinct. Hence, we implement a flocking algorithm that is simple but somewhat generic in that it combines a number of recognised flocking mechanisms controlled by separate parameters that determine the degree to which they affect the overall flocking behaviour.

The effectiveness of herding is strongly affected by the flocking behaviour of the sheep. In particular, if sheep have a strong tendency

to flock into tight groups, herding will obviously be easier. Published works describing herding algorithms often also present a particular flocking algorithm which has been used to test it. But we wanted to test the herding algorithms in their own right rather, so in our experiments we used the same generalised flocking algorithm for testing all the different herding algorithms. Because herding is so sensitive to flocking behaviour we used two different parameter configurations for our flocking algorithm, one setting produced strong, tight flocking behaviour and the other gave rise to much weaker flocking, allowing wide scattering of the sheep. Each herding algorithm was tested in relation to each of the flocking settings.

## 2 Sheep Movement and Flocking

Our system simulates movement in terms of a series of discrete time steps. At each time point a sheep will be associated with position ( $x$ ,  $y$  coordinates) and a trajectory. The trajectory is a two-dimensional vector whose magnitude is constrained to be less than the value of a threshold parameter. This vector will then be modified according to several different movement control mechanisms. After these adjustments to the trajectory vector, the sheep's position will be modified by applying the vector as a displacement to its position coordinates.

### 2.1 Movement Control Mechanisms

Our model of sheep movement behaviour contains three components:

- Random movement.
- Repulsion from obstacles (at close proximity).
- Repulsion from other sheep (at close proximity).
- Fleeing from the dog.
- Flocking movement.

Our sheep continually undergo a small random perturbations to their trajectory. They are kept separate from each other and from obstacles by applying a repulsive vector when they are in close proximity. The dog exerts a repulsive force directly away from itself on any sheep within a certain radius. Flocking movement is more complex and is described separately below. The magnitudes of these forces and the ranges at which they are active are all controlled by parameters that can be easily altered by means of sliders on our simulator interface.

### 2.2 Flocking

Our model of flocking behaviour incorporates several mechanisms to modify the trajectory of a sheep. All the mechanisms involve the sheep being attracted towards a certain point, but differ as to how the attractor point is determined. (In the case of attraction to all sheep, the net attraction is the vector sum of attractions to many different

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<sup>2</sup> This paper is based on work carried out by Matthew Trafankowski for his final year project in the School of Computing, University of Leeds. It builds on earlier project work by Geoffrey Knight and Rolari Segrun.



points.) In particular we have implemented the following attraction modes:

- Attraction to the nearest sheep.
- Attraction to the centroid of the set of sheep.
- Attraction to a random sheep.
- Attraction to all sheep.

The strength of each of these is controlled by a separate parameter allowing the factors to be combined with arbitrary weighting of each.

Attraction to the nearest sheep is a simple flocking mechanism and it is plausible that this does correspond to an actual behaviour tendency in real sheep. However, it does not by itself give rise to flock cohesion because it allows the flock to fragment into pairs or threesomes, which are attracted towards each other but not towards any other more distant sheep.

Attraction to centroid of all sheep locations is a convenient way to achieve some degree of global cohesion of the flock. However, it may be criticised for being unrealistic, since it is not plausible that sheep can accurately compute the centroid of a flock, nor that they would head towards the centroid even when no sheep are actually near the centroid.

Attraction to a random sheep or to all sheep are similar in average affect; although, as one would expect, attraction to random sheep results in more unpredictable flocking behaviour. Both these methods achieve global cohesion of the flock and are intuitively more plausible than attraction to the centroid.

As well as having parameters setting the strength of each flocking mechanism, we also have parameters that determine when each flocking mode is active. This is given by a *minimum flocking separation* parameter. If the distance to an attractor point is less than the value of this parameter then no modification is made to the sheep's trajectory.

Our flocking model is clearly very simplified and not realistic in its details. However, we believe it is sufficient for our purposes. We are primarily interested in herding and want to test whether a herding algorithm can work effectively under a range of flocking conditions. Our flocking model simulates general characteristics of flocking behaviour and its parameterisation allows the strength of flocking tendencies to be varied, ranging from no flocking at all to very tight bunching.

### 3 Herding Models and Algorithms

We shall be comparing a number of published algorithms for modelling and simulating herding behaviour: [12, 15, 4, 7]. Of these, the most detailed description is given in [15]. [12] covers the same algorithm as [15] but gives less detail. [4] and [7] are short papers that give only an outline of the algorithms used. We have had to make some assumptions in recreating these, but we believe that our implementation captures the essential features of the proposed algorithms.

#### 3.1 Vaughan and Sumpter's Algorithm

Perhaps the first herding algorithm in the literature is that proposed by [12] and further developed in [15]. This is also arguably the most elaborate algorithm in terms of its mathematical specification. It based on a *force* model of both flocking and herding behaviour. Vaughan and Sumpter's algorithm was actually implemented on a small robotic vehicle and tested on a flock of ducklings. But they suggest that the algorithm is also appropriate to sheep herding.

As well as the use of ducklings, a further unusual aspect of the setting in which this algorithm was developed and tested is that the flock and herding robot are both constrained to move within a circular enclosure, and the goal of the herding is always to get the flock to a region that is at the edge of the enclosing circle. This is very different to the setting assumed in all the other algorithms, where the sheep are in a largely open area (possibly with some obstacles) and are to be herded into an un-contained region within this.

Duckling behaviour is modelled by an equation giving the movement vector of each duckling at any given time in terms of its distance from other ducklings, obstacles and from the robotic duck-herder:

$$\vec{d} = \sum_{n=1}^N \left( \left( \frac{K_1}{(|\vec{DD}| + L)^2} \right) \widehat{DD_n} - \left( \frac{K_2}{|\vec{DD}|^2} \right) \widehat{DD_n} \right) - \left( \frac{K_3}{|\vec{DW}|^2} \right) \widehat{DW} - \left( \frac{K_4}{|\vec{DR}|^2} \right) \widehat{DR}$$

Here,  $D$  is the position of the duckling whose movement we are computing; each  $D_n$ , with  $n \in [1 \dots N]$  is the position of one of the other  $N$  ducklings;  $W$  is the position of the nearest point on the surrounding wall and  $R$  is the position of the herding robot. The notation  $\vec{XY}$  refers to the vector from  $X$  to  $Y$  and  $\widehat{XY}$  refers to the unit vector with the same direction as  $\vec{XY}$ .

The other ducklings exert both an attractive flocking force and a repulsive force, to prevent them moving too close to each other. The strength of the flocking force is determined by the constants  $K_1$  and  $L$ , with  $L$  preventing the force from becoming excessively strong at short range. The strength of the repulsive force is given by constant  $K_2$ . The surrounding wall and the herding robot also exert repulsive forces, whose magnitudes are determined by  $K_3$  and  $K_4$  respectively. All the forces work according to an inverse square law, similar to gravitational attraction.

The movement of the herding robot is governed by two factors, one attractive and the other repulsive: The robot, at position  $R$  is attracted to the centroid of the duckling flock at position  $F$ . The magnitude of this attraction is proportional to the distance from the centroid of the flock to the designated goal position at  $G$  and is scaled by the constant  $K_{r1}$ . The robot is also repelled away from the goal with a strength determined by the constant  $K_{r2}$ . So, the net movement vector applied to the robot is given by:

$$\vec{r} = K_{r1}(|\vec{GF}| \widehat{RF}) - K_{r2}(\widehat{RG})$$

The rationale behind the herding robot control equation seems to be that the further the flock is away from the goal, the more robot should push it by advancing towards the flock. Also in order to direct the flock in the right direction, the robot should be on the opposite side of the flock to the goal and hence should be repelled by the goal.

#### 3.2 The Algorithm of Lien *et al*

The herding algorithm suggested by Lien *et al* is very different to that of Vaughan and Sumpter [4, 5]. The herding behaviour is divided into two stages.

First, the dog moves to the opposite side of the flock relative to the goal. The paper describes some different methods in which this could be done. One is to move straight to this point (which risks scattering the flock). A better way is to avoid disturbing the flock by moving round it. Two further alternatives are considered: one is to avoid going within a certain distance of the flock; the other, is a



more elaborate method of moving along a roadmap that is imposed on the environment in such a way as to minimise the number of sheep that are near each node that is visited. In our reconstruction of this algorithm, we have used the simpler mechanism, where the dog simply moves round the flock so that it avoids coming within a certain distance of any sheep.

Once it has positioned itself at a point behind the flock relative to the goal, it pushes the flock towards the goal by using a movement pattern of the form shown in Figure 1. Here, small movements towards the flock are interspersed with side-to-side motion, which is intended to keep the flock together.

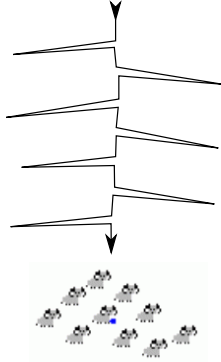


Figure 1. Lien *et al* Herding Trajectory

The papers [4, 5] do not give an exact specification, so we have had to make some assumptions in our reconstruction. The published description indicates that the Lien *et al* system includes a mechanism for gathering up an initially scattered flock, but it seems that this was treated as a separate functionality and not as part of the actual herding operation. It is also possible that the system was tested using relatively strong flocking tendency of the sheep, which would mean that the ability to gather sheep is less of a problem during herding. Because some of our experiments are carried out using relatively weak flocking tendency of the sheep we have added a phase of the algorithm that gathers up stray sheep before beginning the actual herding process.

We believe we have captured the essential behaviour of the algorithm although it seems that the original implementation is more sophisticated than ours and would most likely perform somewhat better than our results indicate. However, it may also be that our added sheep gathering functionality provides achieves some enhancement of the original algorithm.

### 3.3 Miki and Nakamura's Algorithm

Miki and Nakamura [7] published a short paper describing a herding algorithm somewhat similar to that of Lein *et al* [4, 5].

There are two main differences between the algorithms. One difference is in the way that the dog moves into position behind the flock relative to the goal. The second is in the way that the dog herds the sheep. Miki and Nakamura do not mention the side-to-side movement behaviour described by Lien, so we assume that the dog moves directly towards the flock in the direction of the goal. (From our experiments, we have found that this is only effective, when sheep have a high flocking tendency, otherwise the flock is likely to become scattered).

Figure 2 shows the shepherding trajectory proposed by Miki and Nakamura. The motion is controlled by the angle  $\theta$  between the guidance direction (the direction to the goal) and the animal to be herded (which they refer to as the 'object'). This angle is calculated at the current position of the sheepdog.<sup>3</sup>

Their paper does not give an actual equation for determining the trajectory of the sheepdog, but it is clear from the diagram they give that the dog will move round the object in an approximately circular trajectory until it reaches a position almost directly behind the object, with respect to the guidance direction. When it reaches this position it will turn towards the object. If it is directly behind the object it moves directly towards it. If it is slightly to one side or other of the object, relative to the goal, it will move at an angle so as to get more directly behind the object.

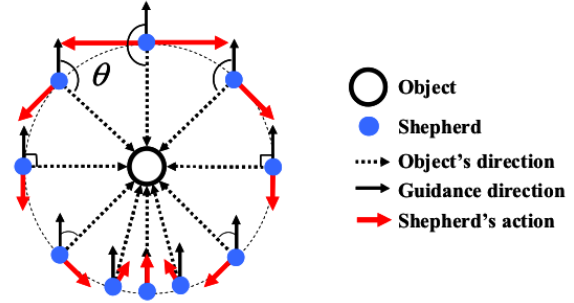


Figure 2. Miki and Nakamura's Herding Trajectory

Judging by the brief description and diagrams they give regarding flocking, it seems that Miki and Nakamura use a flocking algorithm that causes quite tight flocking. They state that this is based on a cohesion rule, which guides sheep to move close to their nearest neighbour. (Their sheep movement model also includes collision avoidance, movement away from sheepdogs and a random factor.) It is not clear from their description why they get the tight flocking shown in their diagrams, as in our experiments we found that implementing flocking in terms of movement towards nearest neighbour often results in a flock fragmenting into pairs and threesomes.

### 3.4 Our Algorithm

A simple program for simulating flocking and herding was first implemented by Bennett in 2003. This has been subsequently developed in a number of student projects. The algorithm has been refined and a variety of tests carried out to determine the best parameter settings for the algorithm and also to compare it with other algorithms.

Bennett's algorithm was directly inspired by the set of command signals that shepherds typically use to communicate with sheepdogs, when rounding up sheep. The exact set of commands can vary and different shepherds use different command words or signals (often whistles). The following list includes most of the commonly used commands with typical names:

- **Stay!** — the dog should halt and remain still.
- **Lie Down!** — the dog should lie down.

<sup>3</sup> They refer to the herding agent as the shepherd and indicate that they have in mind some kind of autonomous herding robot.

- **Easy!** (or **Steady!** or **Take Time!**) — the dog should move more slowly.
- **Walk Up!** — the dog should approach the nearest animal slowly and stop at a certain distance, which is normally just far enough that the sheep will not flee (though it may move away).
- **Look Back!** — the dog should leave the sheep it is currently working and look around for other sheep.
- **Get Back!** or **Get Out!** — the dog should move back away from the sheep.
- **That'll Do!** — the dog should return to the shepherd.
- **Come By!** — the dog should circle the sheep in a clockwise direction.
- **Away to Me!** — the dog should circle the sheep in a counter clockwise direction.

Although all these commands are useful, the last two, **Come By** and **Away to Me!**, seem to be key to successful herding. These cause the dog to move around the flock of sheep, either one way or the other. Such circling maneuvers tend to keep the sheep together, but also push them steadily away from the dog. Driving a flock of sheep is normally achieved by alternating between circling in each direction.

Figure 3 gives some indication of the way the circling algorithm works and the variable parameters that are involved. To herd effectively, the dog must circle at an appropriate distance. Rather than setting the circling distance directly, we compute a motion vector based on the position of either the leftmost or rightmost sheep as seen from the point of view of the dog. The dog will move at a certain angle wide of this vector.

The dog's movement alternates between clockwise and anti-clockwise movement patterns. The initial movement pattern is determined as follows:

From the position of the dog, determine whether the centroid of the flock is to the left or right of the goal. If the flock centroid is to the left of the goal start a 'circle clockwise' movement behaviour. If the flock centroid is to the right of the goal start a 'circle anti-clockwise' movement behaviour.

To circle clockwise, first determine the sheep that is furthest left, when looking from the position of the dog to the centroid of the flock. Take a trajectory a number of degrees (determined by a configuration parameter) to the left of this leftmost outlying sheep. To circle anti-clockwise, do the same as above but with respect to the sheep that is furthest right when looking from dog to flock centroid.

Once in a circling pattern (clockwise or anti-clockwise), the dog will stay in that pattern until a termination condition is met. The leftmost or rightmost sheep, that determines the dog's trajectory, is computed dynamically, so may change during the circling. This means that the dog always circles the flock at a small angle wide of the outermost sheep.

The timing of the dog's alternating between two directions of circling is crucial. The circling direction depends primarily on the position of the sheep in relation to the goal. If the sheep are to the left of the goal (from the point of view of the dog) the dog will mainly circle clockwise. However, if the dog were to change direction of circling too often, it will not sufficiently flank the sheep to keep them grouped together (it may split the flock). Hence the need to herd the sheep by continuing to encircle the flock, must be balanced against the need to drive the flock in a certain direction. Typically the dog should describe a circle of around 1/4 to 1/3 of the way round the flock. But the dog should go further in one direction than the other depending on the position of the sheep relative to the goal.

The angle  $\theta$  that the dog has travelled round the flock relative to the direction of the goal is given by the following equation, where  $D$  is the position of the dog,  $C$  is the position of the centroid of the flock and  $G$  is the position of the goal:

$$\theta = 180^\circ - |\angle(\vec{CD}, \vec{CG})|$$

The dog switches the direction of its circling when  $\theta$  is greater than a given threshold parameter.

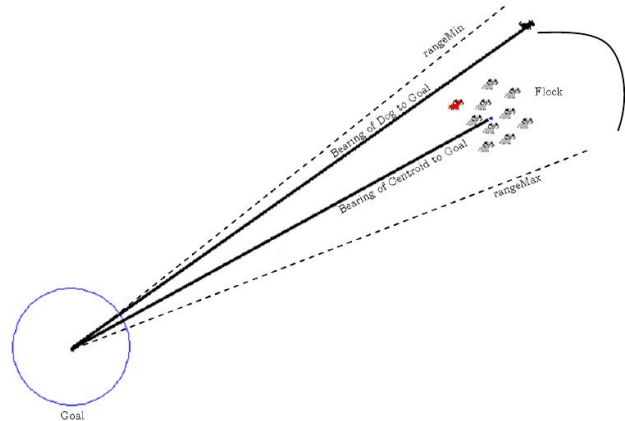


Figure 3. Dog Movement

## 4 A Simulator Software System

The main part of the simulator is a simple animated graphic display, which represents the herding scenario using simple bitmap images. A typical graphic display is shown in Figure 4 (which is just a section of the much larger display window). The circle is the goal region. The dog has to get all the sheep into this circle to complete the herding task. (The sheep shown is red is the current outlier and the dog is moving towards, but slightly to the right of this sheep.)

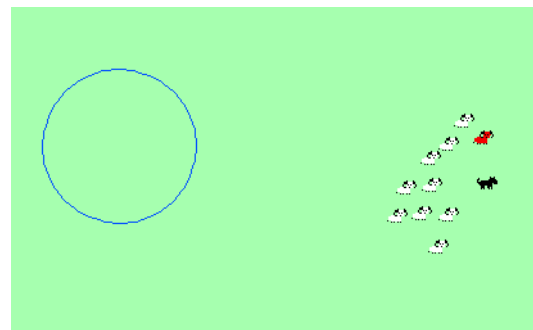


Figure 4. Simulator Screen-Shot

The system also has an extensive GUI for setting the many parameters relating to flocking and herding behaviour, choosing the algorithm to be run and setting up the initial configuration of sheep, goal region. The simulator also provides functionality to enable a large number of tests to be run in batch mode, recording the results

and computing averages over large numbers of randomised test situations. One of the main windows of the configuration GUI is shown in Figure 5.

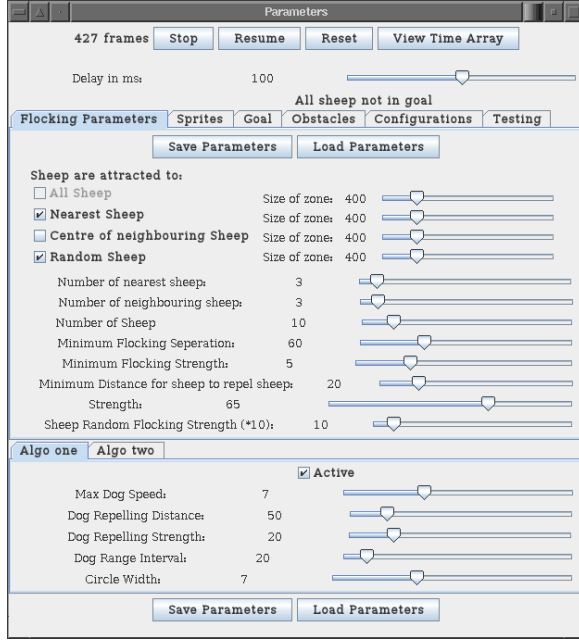


Figure 5. The Parameter Selection GUI

## 5 Comparison Tests

We began our appraisal of the algorithms by visual inspection of the simulator display and by adjusting parameters using intuition and trial and error in order to achieve reasonable herding behaviour.

We found serious problems with the Vaughan and Sumpter algorithm. Apparently the robot duck herder was always tested within a fairly small walled enclosure (10m radius). Our simulation suggests that the algorithm cannot work in an open environment. We noted that the force vector approach cannot give rise to circling behaviour. Instead, herding relies on the fact that ducklings are repelled from the enclosing wall. The movement factor that repels the herder from the goal in order that it get behind the flock could only work if the flock centroid was at a narrow range of distances from the goal. The herder would typically move into the flock scattering it, or, if the goal repulsion force was set high, it would stay far away from the goal. We decided that this algorithm would not be viable in our setting and so did not carry out further test on it.

The algorithms of Lein [4] and Miki [7] both performed reasonably well, although they were quite sensitive to parameter settings and tended to perform poorly when dealing with sheep with weak flocking tendencies. Our algorithm gave good results, although it proved to be very sensitive to the parameters used to determine when the dog changes direction of its circling behaviour.

### 5.1 Algorithm Parameter Tweaking

We then used the system to evaluate different parameter settings for each algorithm to determine values that gave good herding capabilities in a range of different herding situations. It is probably im-

possible to find optimal parameter values, because herding performance will vary according to the flocking model used. Moreover, since each herding algorithm also involves between 4 and 8 configuration parameters the space of possible configurations is enormous. Although there is no theoretical reason why the separate parameters for a herding algorithm can be optimised independently, in practice we found that by varying one parameter at a time, keeping the others, we were able to tweak the parameters independently and find parameter combinations that are locally optimal and give good herding performance. We believe that these are also global optima, although this would be difficult to prove, given the very large space of parameter combinations.

Details of the parameter testing experiments together with graphs of herding performance plotted against each parameter variable can be found in [13].

### 5.2 Herding Algorithm Results

In order to test the algorithms under different herding conditions, a large number of different tests were carried out. We varied the number of sheep to be herded, the type of flocking attraction that was implemented and the range over which the flocking attraction extended.

Four types of flock attraction were used:

- $n$ -nearest — each sheep is attracted to each of the  $n$  nearest sheep in the rest of the flock.
- $n$ -centroid — each sheep is attracted to the centroid of the  $n$  nearest sheep in the rest of the flock.
- random — each sheep is attracted to one random sheep (which will be picked fresh each movement cycle).
- all — each sheep is attracted (to a small degree) to all of the other sheep in the flock.

The ‘Attract Range’ is in somewhat arbitrary screen pixel units. This is a maximum distance over which the attraction components to random sheep and to all sheep operate. Thus, the experiments with this range set to 200 involve sheep with a considerably weaker flocking tendency than those using an attraction range of 400.

We give results for each of the 3 viable algorithms for each of the 15 different test settings, specified in Table 1. The tests are numbered corresponding to the numbers of the tables in which the results were presented in [13]. The details of each test are as follows:

Test	Num Sheep	Flocking Type	Attract Range
T63	10	5 nearest + random	400
T64	10	5 centroid + random	400
T65	10	random	400
T66	10	all	400
T67	10	5 nearest + random	200
T68	10	random	200
T69	10	all	200
T70	15	8 nearest + random	400
T71	15	random	400
T72	15	all	400
T73	20	10 nearest + random	400
T74	20	random	400
T75	20	all	400
T76	25	13 nearest + random	400
T77	25	random	400

Table 1. Flocking parameter settings used in each of 15 different tests.

For each setting and each algorithm, 50,000 runs were executed and average values for number of frames taken to herd the flock were computed. A frame limit of 20,000 was used for each individual run. Although the averages were always much less than this, there were a small number of cases where the sheep could not be herded. Thus percentage success rate was also recorded. The results are given in Table 2. The final column of the table gives the initial of the algorithm that had the quickest average herding time for that test.

Test	Lien		Miki		Bennett		Best time
	Time	Success	Time	Success	Time	Success	
T63	4094	99.98%	5305	99.99%	3968	99.61%	B
T64	4242	99.99%	5361	99.99%	3902	98.57%	B
T65	4939	99.99%	5575	99.99%	4098	99.47%	B
T66	2903	99.99%	4133	97.96%	3036	95.44%	L
T67	5462	99.99%	7001	99.99%	5355	99.68%	B
T68	6720	99.99%	7380	99.99%	5647	98.68%	B
T69	8135	99.91%	11031	89.49%	6284	87.27%	B
T70	4652	99.98%	5989	99.98%	5076	99.21%	L
T71	5391	99.99%	6218	99.99%	5153	99.76%	B
T72	3828	99.99%	4903	99.16%	3036	99.46%	B
T73	5482	99.98%	5664	99.95%	6730	98.81%	L
T74	6415	99.99%	6220	99.97%	6132	99.78%	B
T75	6367	99.99%	6822	99.15%	3640	99.28%	B
T76	5482	99.97%	5663	99.98%	5995	99.13%	L
T77	12686	96.02%	10179	99.90%	8259	99.87%	B

**Table 2.** Results comparing algorithms for 15 different test settings.

## 6 Conclusion

Our algorithm based on explicit modelling of the circling behaviour used by real sheepdogs, under the guidance of shepherds, achieves effective herding over a wide range of flocking characteristics. In most cases its performance was found to be better than the algorithms proposed by Lien *et al* and by Miki and Nakamura. However, the comparison may not be entirely fair, because we only used a reconstruction of those algorithms from limited information, so their original implementations could well have been better. We also found that, despite our algorithm's average herding times being generally better than the others, we had a somewhat lower rate of success at accomplishing herding within our allotted time limit.

We believe that our simulation system provides a very useful testbed for developing and comparing flocking and herding algorithms. And it could also be adapted to simulate other kinds of collective movement behaviour.

Although we conducted a large number of tests with many different parameter settings and algorithm variants, we became very aware that the space of possible flocking and herding behaviours is vast and our analysis so far is extremely limited in scope. Nevertheless, we believe that we have made some contribution to the understanding of how herding can be simulated by algorithmic specification of movement behaviour.

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