Experimental comparison of collective behavior in physical systems versus populations of living organisms

This report was written by Bertrand Roehner but it relies on the contributions of several researchers (listed below) who made experiments and/or provided help, advice and encouragements.

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Abstract The report provides some theoretical yardsticks for interpreting various experiments in collective behavior done with insects or fishes. The long-term objective is to develop a form of statistical mechanics which applies to systems of living organisms and would constitute a generalization of standard statistical mechanics in a sense which will be explained.

To this aim, we discuss transport phenomena between two containers initially out of equilibrium. We recall that for a gas there are two different regimes depending on the section of the pipe connecting the containers. One consists in molecular effusion, the other in flows as described by the standard equation of fluid dynamics. It will be seen that in experiments with living organisms the phenomena are more similar to effusion.

Our final objective is to find experiments suited for measuring inter-attraction forces with good accuracy and reproductibility.

28 August 2012. Preliminary version, comments are welcome

Key-words: Effusion, diffusion, statistical mechanics, temperature, insects, ants, fishes, attraction.

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Contents

A bee collecting nectar from a flower or an ant carrying a pine needle toward its nest does not look very different from a butterfly flying from one flower to another. At first sight there is nothing to tell us that bees and ants have strong interactions with their nestmates whereas butterflies live alone. Yet, as soon as foraging bees come back to their colony, they interact with worker bees waiting to take over the pollen and move it toward storage places. This comparison suggests that in order to measure the interactions between living organisms, one must choose situations and circumstances in which the inter-attraction can and will manifest itself.

Over the past three years we have conducted a series of experiments with groups of insects and small fishes. Our initial objective was to set up techniques which would allow to define and measure interaction strengths in systems of living organisms. This lead us to investigate several basic phenomena of statistical physics, e.g. evaporation diffusion, effusion, phase transition (gas to liquid), and so on. In the course of these investigations we came to realize that in order to make sense of our results, we should develop an alternative form of statistical mechanics.
In this report (i) we suggest some parallels between physical systems and systems of living organisms that we hope to be useful. (ii) we present some preliminary experimental results and (iii) we propose ideas for experiments to be done in the future.

Most of the experiments that we will describe have been done in 2010 and 2011 by students and researchers at Beijing Normal University, the Chinese National Academy of Science in Beijing, the South China Agricultural University in Guangzhou and the Eastern Bee Institute of Yunnan Agricultural University in Kunming, Yunan. We would like to thank all participants including those who are not explicitely named in this report.

Agent based modeling versus physics based modeling

Our objective is to present a set of models which will serve as yardsticks for evaluating various escape experiments performed on insect or animal populations. In such experiments a fraction (or in some cases all) units move from a container A to a container B in a given amount of time T.

Such models can be set up in two different framewoks.

- One of them is what is currently called agent based modeling. It mean to build a model based on our intuitive understanding of such experiments. For instance, individual units would have a more or less random motion and would also be able to detect the presence of their neighbors and rule their own behavior according to what they perceive around them.
- A second way is to present different *physical* models in which a gas or a liquid flows from one container to another and to try to determine which one is best suited to describe what is observed in our experiments on living units.

Which one of these approaches will be the most fruitful?
At first sight it seems that the first approach is the best because it leaves us complete freedom in designing the model. On the contrary, in the second approach modeling is conditioned and constrained by physical arguments which one may find irrelevant for *living* units. This sounds quite convincing. Nevertheless it is the second approach that we will try here. Why?

Our choice is motivated by several reasons.

(1) Our objective is not to model our experimental results at all cost. Our objective is to understand what they tell us about the interaction between individual units. If in the first approach we introduce an inter-individual interaction in a plausible but in fact fairly arbitrary way it will be of little usefulness for determining the values of the parameter(s) which define this interaction because this will not provide any useful *yardstick*. Determining these parameters will just replace our observational estimates of the interaction strength by more theoretical parameters which will not necessarily be more transparent[1].

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[1] Without going into technicalities, it is fairly obvious that the two main facets of the model, namely the randomness and the interaction will not be independent. If one selects a random motion with a large standard deviation one will need a stronger interaction in order to describe a given behavior. In fact, this kind of agent based modeling would become satisfactory only if one would be able to pre-determine *all* parameters of the model from observations that are independent from those that one wants to describe. This would transform the model into one without free parameter would make the comparison with observation really significant.

(2) Physics offer a set of cases corresponding to interactions covering a whole range of strengths. From a gas with very little interaction such as helium to a liquid or a solid, physical phenomena display a broad set of yardsticks.

(3) Physics also offers a number of concepts which characterize the *collective behavior* of a set of molecules. The notions of temperature, pressure, viscosity are not trivial. It took centuries to physicists to identify them and define them properly. As a matter of fact, we do not yet know how these notions should be transposed to systems composed of living units. This goal sets a stimulating challenge.

(4) In the same line of thought, one should mention what is probably the most important reason for using physical analogies. Phase transitions (from gas to liquid or from liquid to solid) are non-trivial phenomena which are very difficult to describe through agent based models[2]. Phase transitions are likely to play an important role for insect populations as shown by the very existence of the clustering effect for social insects.

(5) If molecules and living units were to obey completely different rules it would make little sense to take the properties of gases or liquids as a guide. Yet, several observations suggest that there are in fact deep similarities. This question was discussed in an earlier paper (Roehner 2005). As an illustration one can mention an observation which will be discussed later on in this paper, namely the fact that non-social insects seem to behave like a gas whereas the behavior of social insects is more that of a liquid. If social insects are put in a container they cluster together without filing the whole volume whereas non-social insects will spread over all available space.

In the next section we discuss the possibility of a common framework for physical systems on the one hand and biological or socio-economic systems on the other hand.

Physical systems versus systems of living organisms

Role of environment

At first sight it may seem that systems of living organisms are so different from physical systems that attempting to build a statistical mechanics of living organisms is an hopeless objective.

One of the main obstacles is the fact that living organisms may have different types of behavior. As an illustration consider bee workers in a beehive versus foraging bees collecting nectar from the flowers around the beehive. In the beehive the workers are closely packed together and do not fly; on the contrary, foraging bees fly to flowers hundreds of meters (or even one or two kilometers) away from the beehive

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[2] Remember in this respect how tricky it is to describe phase transitions either analytically (e.g. through Onsager's model for a set of spins) or by computer simulations.

and they do so mostly alone. It would be difficult to imagine situations with a sharper contrast.

Yet, there is a similar difference between molecules inside a liquid and molecules of vapor which escaped from the liquid. In the liquid the molecules are closely packed together [3] whereas the vapor molecules can travel large distances. What accounts for the difference between liquid and vapor? The molecules are the same, their velocities are almost the same, what is different is the average inter-molecular distance d. Basically, $d_{\text{vapor}} \sim 1000 d_{\text{liquid}}$.

This analogy does not completely solve the question however. It may be that workers and foragers are different in some fundamental aspects. In order to determine what are these differences (if any) one must compare their behavior in identical and controlled conditions. This is one of the objectives of the experiments which will be described later.

Energy in physical systems

The notion of energy plays a fundamental role in all fields of physics and especially in statistical mechanics. Do we have something similar in systems of living organisms? What would be the energy of a system of living organisms. The answer is fairly simple.

In a system of particles there are basically two forms of energy:

- kinetic energy E_c and
- potential energy E_p.

Kinetic energy manifests itself through the movements of the molecules. This is an easy notion. The notion of potential energy is less clear. The potential energy is due to the interaction between the molecules. In order to make this notion more intuitive imagine the interaction between two molecules as being materialized by a thin thread of rubber. When the molecules are far apart their potential energy is (by convention) equal to zero $E_p(\infty) = 0$. Then, when one leaves the molecules to move toward one another the force between them produces positive work (the work is positive because the force is in the same direction as the velocity, it is the same process as when a ball falls from a height h_1 to a height h_2) thus the energy of the system becomes lower which means that it becomes more and more negative. A simple illustration is provided by the system composed of the Earth (whose center we denote by E) and a mass m. When m and E are far apart, the system has a high potential energy. When the mass falls toward E the potential of the system will decrease. If, nonetheless, we assume that by convention the "far apart" situation corresponds to an energy equal to

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[3] Similarly, for a gas contained in a closed vessel the molecules collide with their neighbors every 10^{-10} second whereas molecules which escape into vacuum through a small hole in an effusion process can travel large distances.

zero[4], then, of course, all cases where m is closer to E will correspond to a negative energy.

The total energy of the system is the sum: $E = E_c + E_p$. Let us consider some special cases.

For an ideal gas, such as argon, $E_p \simeq 0$ which means that $E \simeq E_c > 0$. On the contrary, for a solid at a temperature near 0 degree Kelvin the velocities of the molecules are very small which means that $E_c \simeq 0$ and therefore $E \simeq E_p < 0$.

Between these extreme cases, there is a whole range of intermediary situations. For instance, for a solid at room temperature $|E_p| > E_c$ which means that $E < 0$. For a gas (not necessarily an ideal gas) at a temperature of 1,000 degree Kelvin the potential energy is negligible compared to the kinetic energy which means that $E \simeq E_c > 0$.

An obvious consequence is that in order to transform a piece of metal at 0 K ($E = -E_1 < 0$) into a gas ($E = E_2 > 0$) one must inject into the sytem a huge quantity of energy (namely $E_2 - (-E_1) = E_1 + E_2$); usually this is done by heating the system; however, as demonstrated by microwave owens, this can also be done by giving more kinetic energy to the molecules (which has of course the same end result although the device is different).

Energy of a system of living organisms

What parallel notions can be defined for a system of living organisms?

More specifically, let us consider a population of a few hundred bees contained in a glass container.
They move around walking on the walls or occasionally flying. It is possible to define (and to measure) the distribution of their velocities exactly in the same way as for the velocities of the molecules of a gas. In other words, the kinetic energy of the bees can be defined in the same way as for a physical system.

What about the potential energy? This notion seems less clear because (so far) we have little knowledge regarding the force of attraction between bees. However, the existence of such a force is clearly demonstrated by the fact that, left to themselves, bees will attract one another eventually (after about half an hour at 20 degree Celsius) forming a cluster. Although fairly compact with bees closely packed together, this cluster is not completely steady like a solid. In other words, this cluster of bees is something between a solid and a liquid, very much like foam or cream.
So, there is certainly a potential energy. As the bees are almost motionless in the

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[4] Although simple, this assumption is not really "natural" because we are not used to the fact that something which is large is equal to zero. In other words, we are not used to considering 0 as a "big" number, which it is, nevertheless, if all other numbers in the series are negative.

cluster, one can even say that, the energy of the system is almost entirely in the form of potential energy, i.e.: $E \simeq E_p < 0$.

On the contrary, if the bees are in a larger box and all flying around $E \simeq E_c > 0$

What about energy conservation?

The principle of energy conservation is a fondamental law of physics. Do we have something similar for systems of living organisms?

A simple observation will convince us that for systems of living organisms energy is *not* conserved, at least not in the same instantaneous sense as in physics.
Consider a group of about one hundred fruit flies, e.g. drosophila, contained in a test tube: many may rest on the layer of food at the bottom of the tube while others may slowly climb on the walls of the tube. If one hits the glass of the tube with a plastic ruler, suddenly all flies begin to move: some quickly walk up to the top of the tube, others fly to the top just to fall back as they hit the cap. Obviously, the kinetic energy of the drosophila jumped instantaneously when the tube was hit with the ruler. Somehow the drosophila switched to a kind of “panic mode” in which they momentarily expense a great amount of energy. Then, in the following minutes the system relaxes to its previous state.

In short, the difference between living organisms and molecules is that living organisms can store energy which can then be released in bursts.

Another (and related) difference is that populations of living organisms need a permanent input of energy for remaining alive that is to say for keeping a substantial amount of kinetic energy.

Although these two differences seem quite significant, it is important to realize that they are not fundamental differences. Indeed the same phenomena also exist for molecules albeit not on the same scale.

- A big molecule (e.g. a protein counting several thousands atoms) has many modes of internal vibration. These modes can be excited by targeting the molecule with a laser beam. The energy stored in these excited vibration modes is similar to the energy stored in living organisms in the form of stored carbohydrates or lipids. What is different, is the time scale of the relaxation process. The energy stored in vibration modes is released through “vibrational energy relaxation” (or VER[5]) in a matter of a few picoseconds (10^{-12} s). In contrast, the relaxation time of energy stored in living organisms can range from a few hours to several weeks.
- We may think that, in contrast with living organisms, molecules contained in a container can keep their kinetic energy for ever. However, this is only true as long as the container remains at room temperature.

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[5] See for instance Fujisaki and Straub (2005).

For a physicist living near the South Pole during the months when the Sun is under the horizon, any container left unattended outside of the living quarters would cool down to average outdoor temperature (around -40 degree Celsius). As a matter of fact, even the polar station itself would return to the same temperature in a matter of a few days once its fuel reserve is exhausted.
This example helps us to understand that the kinetic energy of molecules ultimately relies on a source of energy which is basically the solar energy received by the earth. In the absence of this energy flow the temperature at the surface of the earth would cool down to a few degree Kelvin. It is the natural radioactivity of the earth which would keep the temperature a few degrees above zero.

Yet, from a practical perspective our observation that molecules and living organisms are not *fundamentally* different does not solve the problem. The fact remains that systems of living organisms will have a much broader range of regimes than systems of molecules. As a result, experiments will be more difficult to repeat. In order to reduce variability, one will have to control the state of living organisms at the beginning of the experiment. A possible control-method is to record the distribution of velocities of the organisms. Such a test will reveal whether the organisms are in a excited, subdued or “normal” state. In this way, one does not need to be concerned with the actual reason of this situation, a question which would be difficult (if not impossible) to settle anyway.

Toward a statistical mechanics of living organisms

Physical systems with weak interactions

Over the past three centuries physicists have studied many systems involving either weak or strong interactions. The most well known systems with weak interactions are gases such as helium of argon as well as (albeit with greater variability) most other real gases. This case is particularly important from a theoretical point of view because the theory which was developed for gases, namely the kinetic theory of gases, has brought about several key-concepts of statistical mechanics e.g. temperature, energy, entropy, phase space.

Physical systems with strong interactions

Systems with strong interactions comprise the study of liquids or solids. Although the theory of such systems is fairly difficult they are of more importance for our purpose because they provide many examples of phase transitions. Why are phase transitions important?

Defined in a fairly general way, a phase transition is a change in the internal structure of a system. The transitions from gases to liquids and solids are well known but in a sense they do not provide the best examples of phase transitions because they result in sweeping changes which completely unravel the original structure. Gases have no internal structure and therefore have no phase transitions. On the contrary, solids have intricate internal structures and therefore undergo many phases transitions. Most metals exist in different crystallographic structures For instance, tin exists in two allotropic[6] forms, namely α-tin and β-tin, more commonly known as gray tin and white tin, respectively[7]. Two more allotropes, γ-tin and σ-tin exist at temperatures above 161 degree celsius and pressures above 10,000 atmopheres.

The existence of many allotropic forms is not unique to metals but is also observed for most non-metallic solids. It is well known that diamond and graphite are two allotropic forms of carbon. Graphene and fullerenes are two others. As another example one can mention sulfur which forms 30 solid allotropes (and also some gas allotropes), more than any other element. Just to mention two of them, α-sulfur is the (solid) form which exists at room-temperature. Above 95.6 degree celsius it is replaced by the β-sulfur form.

Notion of temperature for non-physical systems

First of all it is useful to introduce a distinction between systems for which there is a clear spatial dimension and those for which it is not the case.

Spatial systems versus non-spatial systems

We observed earlier that for systems of living organisms such as populations of bees or drosophila, the velocity and hence the kinetic energy can be easily defined. For such systems the standard estimate of temperature as being proportional to the average kinetic energy can be used.

In contrast many economic and social systems do not have a clearly defined notion of spatial distance. As examples one can mention systems composed of companies, commodity markets or stocks. For such systems one cannot just transpose the standard physical notions of energy and temperature; thus, in order to define meaningful parallels one needs to understand the core concepts on which the notions of energy and temperature rely. This is what we intend to do on this section.

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[6] The meaning of the word “allotropic” is “to exist in different stable forms”. The Greek word “allotropia” means “variability”.

[7] β-tin has a tetragonal structure ans is a malleable metal whereas α-tin has a diamond cubic crystal structure and has the aspect of a grey powder. The transition from the β to the α form occurs under 13.2 degree celsius. This, however, requires ideal laboratory conditions in terms of purity and even on such conditions the transition is very slow. The transition temperature is much lowered in the presence of impurities. In the presence of traces of bismuth the transition may not occur at all.

Before coming to this, let us come back to systems of living organisms. Once, energy and temperature have been defined it is of crucial importance to perform consistency checks in order to confirm the significance of such notions for such organisms.
One possible test is the following.

The equipartition theorem of statistical mechanics tells us that $(1/2)m < v^2 >= kT$, where m is the mass of the particle, v its velocity, k the Boltzman constant and T the Kelvin temperature. Although this formula is only an approximation in the sense that it assumes a continuous and unbounded distribution of energy levels, let us accept it as a first step. An obvious consequence is that, for a given temperature, v should be proportional to $1/m$. For the sake of brievity, this effect will be called the "bigger means slower" effect.

Does such a prediction make sense for systems of living organisms?
At first sight the answer seems to be "no". For instance, in a system of fishes of the same species but of different sizes (e.g. young fishes mixed with adult fishes), big fishes can swim faster than small fishes. This seems even more obvious for a population which comprises fishes of two species, one which is of small size and the other of a bigger size.
What answers can be given to these objections?

- First, it must be emphasized that although some scaling corrections may be allowed, there *must* be a "bigger means slower" effect. Otherwise, there will be no thermalization through mutual interaction, hence no global equilibrium. If there is no global equilibrium statistical mechanics does not apply.
- Secondly, it must be emphasized that so far there are very few data about the distribution of velocities in systems of living organisms. We need more experimental results before trying to answer the previous question.
- In interpreting experimental results one should make a clear distinction between "free velocity" and "diffusion velocity". Free velocity is the velocity observed in effusion experiments that is to say in the absence of mutual interaction. Diffusion velocity is the velocity observed *within* a system of elements in mutual interaction.

These velocities are ruled by different formulas. For free velocities, the rule is $v = \sqrt{2kT/m}$ whereas for diffusion (in a liquid), the rule will be:

$$\bar{x}^2 = 2Dt \Rightarrow v_d \simeq \sqrt{2D/t} \sim \sqrt{1/t}1/m^{1/6}$$

(the Stokes-Eintein relation which is only valid in liquids was used in the last step).

It can be seen that the expected dependence with respect to m is not the same.

- So far, we have considered systems in equilibrium. In order to check whether thermalization occurs or not, an alternative method is to inject elements whose velocity is widely in excess of prevailing thermal velocity. In physics this occurs for instance when fast neutrons which are emitted as a result of a nuclear reaction are slowed down through interaction with surrounding atoms. In water, in the course of about 16 collisions with surrounding atoms, the velocity of fast neutrons is reduced by a factor of almost 10^5 and this occurs within 10^{-10} second (for more details see the discussion in Roehner (2007, p. 63-65)).

Similarly, it would be interesting to observe what happens when a living organism A_0 moving with a high velocity V_0 (for instance because of an external excitation) is introduced into a system of slowly moving organisms A_i. If there is an interaction between A_0 and the A_i one would expect thermalization to occur. As a result one should observe that V_0 decreases until it becomes equal to the average velocity of the A_i. Needless to say, the decrease rate must be faster than the one observed in a group of only A_0s once the external excitation has been switched off[8].

The relaxation time of such a process would provide an estimate of the coupling strength between A_0 and the A_i. The longer the relaxation time the weaker the coupling strength.

For such an observation the following experimental procedure can be suggested. For the sake of illustration, we describe it for ants but it can of course also be tried with other living organisms.

First one must measure the distribution of velocities in a group of ants at different temperatures, say 10, 15, 20 and 25 degrees Celsius. This is easily done by shooting a film and analyzing it image by image on a computer. Knowing that the time interval between two images is 1/20 s, the velocities can be obtained from the displacements between successive images.

For the second step a group of ants is put at a temperature of 10 degrees for about 20 minutes. Then, it is removed from the cooling box and left at room temperature (25 degree). Progressively, the velocity distribution will converge toward the distribution at 25 degree. Let us denote by τ_0 the corresponding time constant.

The third step is similar to the second step except that, after being taken out of the cooling box, the ants are mixed with a group of ants which have been kept permanently at room temperature. Before being put into the cooling box the ants had been marked with a white dot so that they can be identified on the film. In the same way as above, we measure the time constant τ_1 which characterize the convergence of the white dotted ants toward their velocity distribution at 25 degrees. If the difference $\Delta\tau = \tau_0 - \tau_1$ is positive, $\Delta\tau$ can be seen as a measure of the interaction between ants[9].

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[8] Even in the absence of any water, the fast neutrons will also eventually be slowed down as a result of their collisions with the wall of the container, but this process will take a longer time.

[9] This experiment relies on the belief that there is indeed a collective effect and that the warming up process is not just the result of a physiological mechanism at individual level.

An alternative form of the experiment would be to replace the ants from the cooling box by ants of a different species which has a slower velocity distribution. If the velocity is purely determined by species identity their distribution will be the same when the species are mixed as when they are kept separate. On the contrary, if the velocity distributions

- Finally, let us consider a case which is well known by beekeepers. In European honey bees (Apis Mellifera) males are about twice as big as females and they are known to fly or walk more slowly. In fact, males can be readily recognized not only because their slower flight but also because their wings make more noise.

Can this case be considered as illustrating the "bigger means slower" requirement? We do not think so.

The flight velocity of the males is lower not as a result of their interaction with the females but rather as a consequence of the fact that their wings are undersized with respect to their higher weight which implies that although their wing frequency is higher (hence the louder humming) they cannot match the velocity of the lighter female bees. In short, this case has nothing to do with thermalization.

Temperature as seen as a manifestation of dispersion

When the order "March, forward" is given to an US Army squad all soldiers start marching at the same moment, in the same direction and at the same pace. This can be considered as the analog of what happens in physical systems at a temperature of zero degree Kelvin.

For instance, if an external magnetic field is applied to a paramagnetic material, *all* magnetic moments will immdediately align themselves in the same direction. This will happen no matter how small the external field. In our military illustration, one would say, that the soldiers will all start to walk even under a slightly whispered order.

On the contrary, at a non-zero temperature, only a specific proportion of the moments will become parallel to the external field and this proportion increases when the external field becomes stronger as illustrated in the graph. In the military analog this would mean that even when the order is shouted fairly loudly not all soldiers will start to march.

A social parallel: effects of the Fukushima accident

What parallel with social phenomena can one suggest? Consider the accident that occurred in mid-March 2011 at the nuclear power plant of Fukushima in Japan. It resulted in a permanently increased level of radioactivity in Fukushima prefecture. In a limited area around the plant *all* people were evacuated. This was the analog of

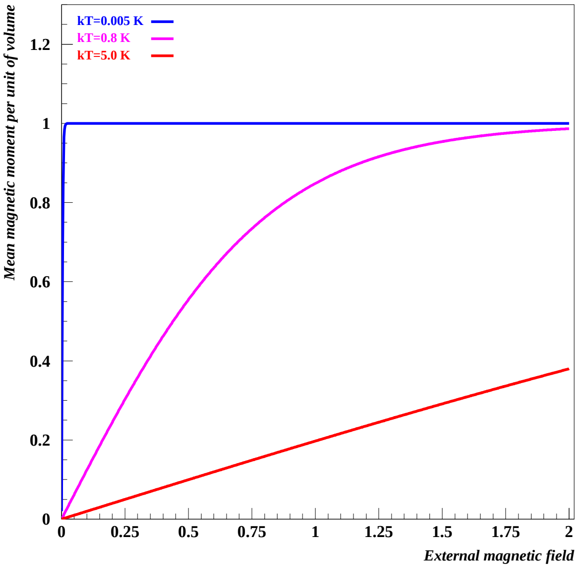

Fig.xx:Effect of non-zero temperature on the mean magnetic moment of a paramagnetic substance. When an external magnetic field is applied to a paramagnetic substance at a temperature of zero degree Kelvin, 100% of the magnetic moments become parallel to the external field which results in a maximum mean magnetic moment per unit of volume. At a non-zero temperature only a fraction of the moments will become parallel. As a result, for a given external field, the mean magnetic moment $\bar{m}(H)$ per unit volume will be smaller. The formula is: $\bar{m}(H) = \mu \tanh(\mu H/kT)$ (Reif 1965. p. 207)

the “Forward march” order[10]. On the contrary, outside of the evacuation zone in the rest of Fukushima prefecture, some people moved to other prefectures while other people remained in their homes. For instance, most pregnant women or families with small chidren moved to other places. Needless to say, many other reasons may have played a role in the decisions made by people. Outside of the evacuation zone, the response to the accident can be described as a non-zero temperature effect. That is why non-zero temperature can be seen as a manifestation of diversity.

Notion of diversity at atomic level

At atomic level, the fact that not all magnetic moments respond to the external field in the same way is also, in a sense, due to diversity. How should the notion of diversity be understood in this case?

Of course, all magnetic moments are identical but at a given moment, due to their vibrations, they will be in *different states*. Therefore, their responses to an external field will not be the same which will lead to the gradual effect observed in systems at non-zero temperature. For instance, from a classical mechanics perspective if at a given moment the particles do not have the same velocity they will not experience the same force. A particule with a high velocity will experience a stronger force than

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[10] However, some people came back to work into the evacuation zone. For instance, large quantities of stones continued to be extracted from quarries located in the area.

a particle with a slow velocity. When the temperature increases the particles vibrate more strongly which means that their velocity range will become broader.

In order to convince ourselves that this argument is indeed correct, one should study a system of two magnetic moments in the framework of quantum mechanics. In that framework the moments would be described by their wave functions $\psi_1(t), \psi_2(t)$ and these wave functions would be governed by two time-dependent Schrödinger equations. These equations would include a term representing the interaction between the moments as well as terms describing the effect of the external field on each of them. Once the equations have been solved their solutions will certainly show that the responses of the two moments to the external field are *not* identical. Needless to say, the role of temperature cannot be seen on such a two-moment system because the notion of temperature only exists for a system that has many particles.

In short, provided the word is understood in a fairly broad sense, diversity is the key-factor that causes dispersion. Let us illustrate this through a second example.

An economic parallel: wheat markets

In 19th century Europe there were weekly (or bi-weekly) wheat markets in in all cities and twns of some importance. In France for instance, price records are available for hundreds of them from 1825 to 1913. On all these markets prices fluctuate more or less randomly.

What would for such a set of markets be the analog of the zero Kelvin degree limit. At this limit everything is “frozen” which means that the price fluctuations are reduced to zero. What are the economic conditions that will lead to such a situation? First, suppose that wheat is harvested not once a year but everyday in the same way as for the production of industrial goods. Next, suppose that the supply is flexible enough to follow the fluctuations of the demand (including unexpected fluctuations due for instance to an army spending some time in the area) on a daily basis. As a result, wheat prices would become very stable. As stable indeed, as the prices of cars are nowadays in most industrialized countries. In such a situation, the volume of sales would be just sufficient to satisfy the needs of every buyer.

What would be in such a market the effect of a sudden increase in demand? For instance, one can assume that troops are staying temporarily in the area which results in demnd jump ΔD. We said that supply side would respond with great flexibility, but this flexibility would have a cost nevertheless. Indeed, in order to increase the supply (whether for cars or for wheat) new production facilities must be called upon and these facilities most likely will have a lower productivity than the facilities already in operation. If the production cost of the most productive facilities is p_1 and if $p_2 > p_1$ is the production cost of the new ones, the market price p' which will satisfy the higher demand will lie somewhere between p_1 and p_2. In such a flexible market (from which all friction factors which exist in real markets have been removed) the arrival of the troops will make the price jump from p to p'. As in in the graph with the magnetic field at zero degree, the jump will occur overnight and only once. On the contrary, in real markets there are all sorts of delays and frictions which will make the change more gradual. Among such friction factors one can mention the time required to grow wheat in new fields, the harvesting and transportation time and so on.

In the conception delineated above, each producer will be characterized by a typical production cost P_i reflecting its level of productivity. Thus, the n producers can be ranked from lowest to highest production cost. If the production capacities of the producers are Q_i, then the production cost for a demand D will be given by:

$$P = (1/D) \sum P_i Q_i, \text{ where } \sum Q_i = D \tag{1}$$

PD is the analog of the total energy of a physical system and PD/n, the average production value per producer, is the analog of the average energy per state.

What will be the temperature in this example? The graph tells us that the higher the temperature, the stronger must be the external shock in order to achieve a sizeable response of the system. In other words, a market with high temperature would be a market beset with much noise and many frictions and which does not well adapt to a new situation.

Remark Equation (1) is a perfectly deterministic rule. The statistical analog of (1) would be:

$$P = (1/D) \sum (P_i Q_i) q_i, \text{ where } q_i = \exp[-\beta(P_i Q_i)]/[\sum \exp[-\beta(P_i Q_i)]]$$

Interpreting temperature as a manifestation of diversity is probably not the most common way to look at it. Most often it is with movement that temperature is identified. That is what we explain in the next section

What is the significance of temperature in physical systems?

When thinking about temperature the first idea which comes to mind is the following relation from the kinetic theory of gases:

$$(1/2)m\overline{v^2} = (3/2)kT \tag{I.1}$$

where v is the velocity of a molecule, T the Kelvin temperature and k the Boltzmann constant. This relation establishes a connection between T and the average of the kinetic energy of a molecule.

Several important qualifications are in order.

- It is important to realize that for the absolute temperature of a system to be defined, the system must be in thermodynamic equilibrium. For systems which are not in equilbrium it may be possible to define local and more or less ad hoc temperatures but one cannot define absolute temperatures in an unequivocal way. We will come back to that point shortly.

Moreover, the system must also be ergodic in the sense that ensemble averages are identical to time averages. While this condition is ensured for physical systems, it may be more problematic for non-physical systems.

- The velocity defined by equation (I.1) cannot be measured inside a gas or a liquid because of the many collisions between the molecules. In a sample of nitrogen in standard conditions of pressure and temperature the mean time between two successive collisions is $\tau = 6 \times 10^{-10}$ s and during this time, in spite of the fact that its velocity (as measured outside of the system) is $v = 500$ m/s, the molecule covers only a distance of $l = 0.3$ μm. The velocity v is measured through effusion experiments in which the molecules escape from the system through a small hole of a diameter that is smaller than l. Once outside, thanks to a quasi-vacuum, they can travel in a straight line over a distance of several centimeters. Yet, this measure gives only a rough estimate of the velocities inside the system (see Fig. xx)

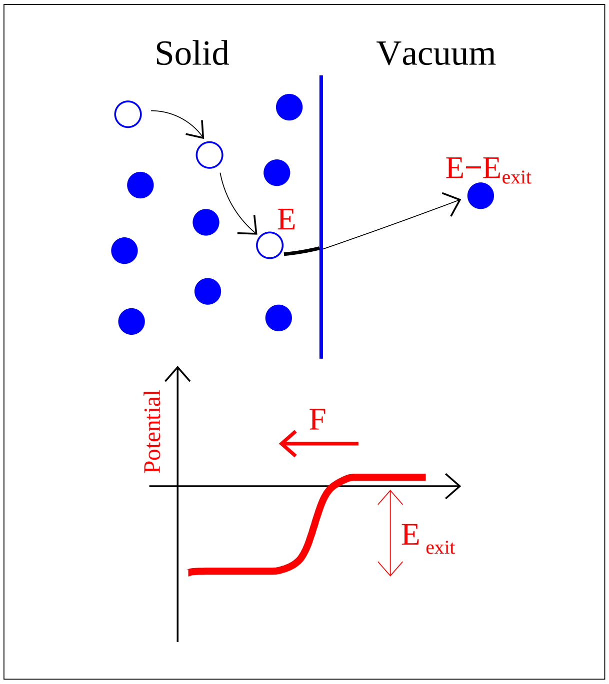

Fig.xx: Velocities inside and outside of a solid. Inside the solid atoms can move by jumping from one vacancy to another. Atoms whose energy is high enough can escape from the solid. These atoms produce the cloud of vapor that exists over solids. By direct measurement or indirectly by measuring the pressure of the vapor one can determine the velocity of the atoms in the vapor. However, in order to be able to estimate the velocity of the atoms *inside* the solid one should also know the energy Eexit.

For the purpose of extending the notion of temperature to non-physical, relation (I.1) can be considered as the *definition* of temperature[11]. However, if (I.1) is taken as the very definition of temperature, then we need some criterion for ensuring that this T is not just a formal and meaningless parameter but has indeed the the basic properties of a physical temperature. One possible criterion is to check that (I.1) holds for *different masses*. Broadly speaking, this means that big things should move slover than small things. We will come back to that point later on.

In short, (I.1) says that *temperature is motion and vice versa.*
At this point it is important to realize that the movements of molecules are not limited to their translational velocity but include also rotational or vibrational movement. For instance in a solid the molecules oscillate around their average central positions.

Does equation (I.1) mean that everytime that there is a system with agitated individual units it is possible and useful to define a temperature that would characterize that agitation? Such a definition is undoubtely possible. The main question is whether it may be useful.

In order to see this point more clearly, we first discuss the significance of movement in physical systems.

Significance of movement in physical systems

To make this point clearer let us for a moment try to imagine what systems without movements (that is to say at 0 degree kelvin) would look like. First, we list several features and then we explain them in more detail.

- In such systems any disequilibrium would remain for ever.
- The physical properties (e.g. the density) of any system would be different from one point to another.
- All materials would have zero compressibility and therefore infinite hardness. As a result no sound transmission would be possible.

In order to explain the first two points we consider a fluid at room temperature. Let us assume that at time t_1 one injects an additional quantity of the same fluid at a specific location M_1. In the course of time, this excess fluid will diffuse to the neighboring area and eventually to the whole volume of fluid. However, this diffusion process occurs only because through their random movements the molecules which are around M_1 will be be able to explore the surrounding area where the density is smaller[12]. Without these movements the excess fluid will remain for ever at point M_1.

The third point results from the fact that the elasticity of a solid comes from the vi-

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[11] It is true that in statistical mechanics the definition of temperature is different, namely: $T = 1/(\partial S/\partial E)$ where S and E are the energy and entropy of the system respectively. As, a priori, we do not know how to transpose these notions to non-physical systems the present definition is fairly useless.

[12] The process of equalization is very similar to the process invloving two compartments that are considered below.

bration of the molecules around their central position. A vertical impact through the stroke of a hammer at a location M_1 will create a deformation. The vibration center of the molecules around M_1 will move downward and this will also temporarily push downward their neighbors. As a result the deformation will be transmitted through the whole solid. If frozen in their central position the molecules will not be able to transmit any deformation[13].

In short, it is the agitation of the molecules which smoothes out temporary fluctuations and ensures spatial uniformization. Without this agitation all materials would be fragmented into small cells each of which would have different properties. It would be impossible to produce an homogeneous beam of steel[14].

In our previous argument we considered the extreme case of a system at 0 degree. That may sound unrealistic because, as is well known, it is not possible to reach such a temperature. In fact the same argument would also apply to a system whose temperature is close to zero, say around 0.01 degree. The only change that needs to be made is that sentences such as "equilibrium will never be reached" should be replaced by "equilibrium will be obtained only after a very long time". In other words, systems at 0.01 degree will have very long relaxation times which means that if submitted to frequent shocks they will be out of equilibrium most of the time.

Our previous discussion has an important implication. Apart from temperature there are many other intensive variables (e.g. pressure or concentration of a given species of molecules), but temperature is the key-factor because it is associated to movement and without movement no equlibrium would be possible for any of the other variables. In the term movement one must include not only translational velocity, but all forms of movement including vibrations, spin switching, or electrons jumping from one level to another.

Distinctive property of a heat-bath

Formula (I.1) has an important implication which can be considered as a distinctive characteristic of a "real" temperature.

Consider a fluid which is a mixture of two particles of different masses m and M. Let us assume that $M = 100m$; for instance if m represents the mass of a water molecule, i.e. $m = 18g$, then $M = 1,800g$, M can possibly be the mass of a

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[13] The fact that some metals become superconducting under a critical temperature does not contradict this argument for in this case one applies an electical field which is experienced throughout the material and brings about the movement of the electrons. In this case there is no need for a local deformation to be transmitted from one end of the system to the other.

[14] In our previous discussion we considered a fluid not a solid. However, it also applies to steel because in most of the production process steel is in fact liquid. It is mainly in this phase that the uniformisation takes place. However, it should be observed that uniformisation by diffusion occurs even in solids. Indeed, when the temperature of a solid becomes close to its melting point there are more and more vacancies that is to say sites which are not occupied by atoms. By jumping from one vacancy to the next atoms can move and bring about uniformisation.

macromolecule[15].

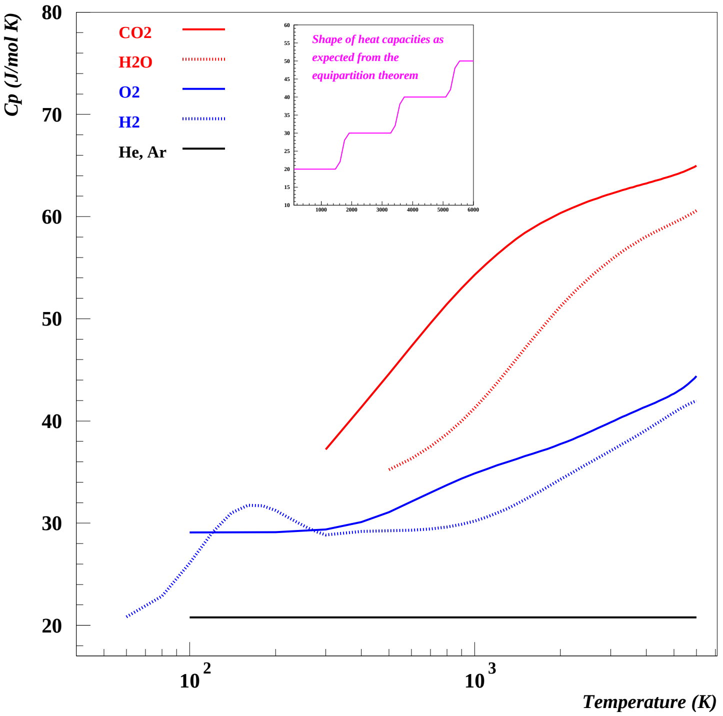

Fig.xx: Heat capacities of gases. The figure shows that, except for helium and argon (two monoatomic noble gases), the heat capacity curves are very different from what is expected from the equipartition theorem. This theorem relies on classical mechanics, an approximation that in principle is better for high temperatures than for low temperatures. But we can see that the approximation does not work well even for high temperatures.As the temperature increases a larger number of vibration modes contribute a well as the excitation modes of the electrons. *Sources: CRC handbook of chemistry and physics (2009-2010) section 6-26; website of the National Institute of Standards and Technology*

Formula (I.1) tells us that the velocity of this molecule of mass M will be 10 times smaller than the velocity of the water molecules. If the later is around 500 m/s the bigger molecule will have an average velocity of 50 m/s.
The equipartition theorem states that the mean value of each independent quadratic term in the expression of the energy is equal to $(1/2)kT$ (Reif 1965, p. 249).
The fact that this statement does not seem very plausible can be seen readily. Let us consider the rotational degrees of freedom. The equipartition theorem tells us that the averages of kinetic energy of two rotations around different axes $E_1 = (1/2)I_1\dot{\theta}_1^2$ and $E_2 = (1/2)I_2\dot{\theta}_2^2$ are both equal to $(1/2)kT$ even if I_1 is arbitrarily larger than I_2, say for instance $I_1 \sim 10^6 I_2$. Intuitively this does not seem reasonable because, unless $\dot{\theta}_2$ becomes a million times larger than $\dot{\theta}_1$, the term E_2 would be much smaller than E_1.

A quantum mechanical argument indeed shows that the equipartition statement is not true. The argument goes as follows. Apart from the form that we have already

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[15] For instance the mass of a molecule of insulin $hboxC_{257}\mathrm{H}_{383}\mathrm{N}_{65}\mathrm{O}_{77}\mathrm{S}_6$ is $M = 5,807$.

used the kinetic energy for a rotation can be also be written as a function of the angular momentum $L = I\omega$; this form, namely $E = L^2/(2I)$ is best suited from a quantum mechanics perpective because it is L which is the variable that is quantized: $L = l(l+1), \quad l = 0, 1, \ldots$. So, the lowest possible level is $E_0 = 1/(2I)$. As long as $E_2 < E_0$ the rotation $\dot{\theta}_2$ will not contribute at all. This rotation will only start to contribute when $E_2 \sim E_0$; when I_2 is very small it implies E_0 is large and therefore $\dot{\theta}_2$ must be very large. But $\dot{\theta}_2$ will become large enough only when the temperature is very high, say $T \leq T_2$. In other words, under T_2 this mode will not contribute at all, and above T_2 it will contribute not all at once (as stated by the equipartition theorem) but *progressively* by starting from zero, increasing and reaching a maximum[16].

Real velocity versus diffusion velocity

Definitions

It is important to make a clear distinction between the *real velocity* of a particle in a fluid and its *diffusion velocity*.

- The real velocity v is the velocity of the particle between two successive collisions (Fig. xx). For molecules the time τ between two successive collisions is of the order of $\tau \sim 10^{-10}$s. A bigger particle experiences more collisions per second which means that τ is even smaller. It is impossible practically to measure such velocities inside the fluid. The only possible measurement consists in allowing the particle to leave the fluid and to let it move into a quasi-vacuum envrionment. This reduces drastically the number of collisions and allows the velocity to be measured through the distance covered in straight line.
- The diffusion velocity v_d is defined as the average distance travelled by a (large enough) sample of particles. As noted above the trajectories of these particles will contain a lot of direction changes. Despite this great diversity in shape, it is possible to define a meaningfull average. For instance, in the case considered in Fig xx, it was sufficient to consider some 500 particles to get a fairly significant estimate for their average velocity. One way to define a diffusion velocity is to consider that in $t = 5$ s the average distance travelled by the particles is the distance corresponding to one half of the height of the histogram. It is known that for a gaussian frequency curve $y = \exp\left[-x^2/(2\sigma^2)\right]$ the $x-$value at half maximum is 1.18σ. So, if the histogram of the displacements x is well described by a gaussian curve, the diffusion velocity will be $v_d = 1.18\sigma/t$. For most practical applications the simpler approximation

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[16] A theoretical calculation shows that the heat capacity of an assembly of rigid rotators has the shape that can be seen on the graph for the case of hydrogen. For more details see see the following website of the Gary Morris School of physics in New South Wales:
ruelle.phys.unsw.edu.au/ğary/...files/SM3_5.pdf

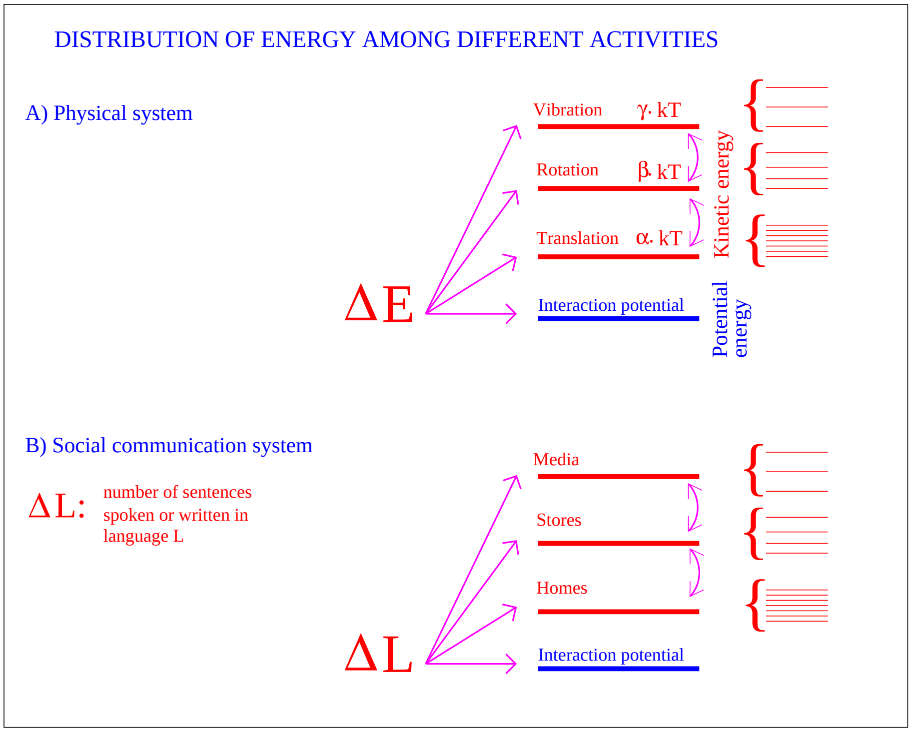

Fig.xx: Distribution of "energy" between different "activities". In a physical system energy exists in several forms: different kinds of kinetic energies and also potential energy due to the inter-attraction of the molecules. As we have seen elsewhere this last aspect becomes important in fluids or solids. These forms can be seen as being diverse "activities" of the molecules. The figure draws a parallel with a facet of a social system, namely the distribution of a given amount N of sentences spoken or written in a minority language L. For instance, L can be German in the eastern part of France or Spanish in Los Angeles. An increase ΔN will result in its distribution among the different types of activities for which a language is used. The analogs are as follows: molecule - person, energy - quantity of sentences in language L, energy level - sentence multiplication factor corresponding to the activity under consideration. All these activities are more or less inter-dependent. Low levels activities will be "filled" first while high level acivities will have to wait until the temperature of the system becomes higher.
Incidentally, it is by purpose that we did not replace α by kT/m (for a one-dimensional system). Although this would be correct at room temperature it will not be true at a sufficiently low temperature as shown by the curve of the heat capacity of hydrogen.

$v_d = \sigma/t$ will be sufficient.

Connection between (real) velocity and diffusion velocity

At first sight it may seem that there is no way to establish a link between v and v_d. The shapes of the trajectories defining v_d are so diverse and chaotic that it seems very difficult to find a link between their straight-line parts and the global curves.

Because within the system the trajectories are so erratic the position of a particle in the course of time is a random fonction (which we write with capitals as is customary in probability calculus) $X(t)$. For $X(t)$ one can define an ensemble average by considering a sample of similar particles. We will denote by $E(.)$ this kind of expectation. More precisely we will consider a sample of particles all starting from a

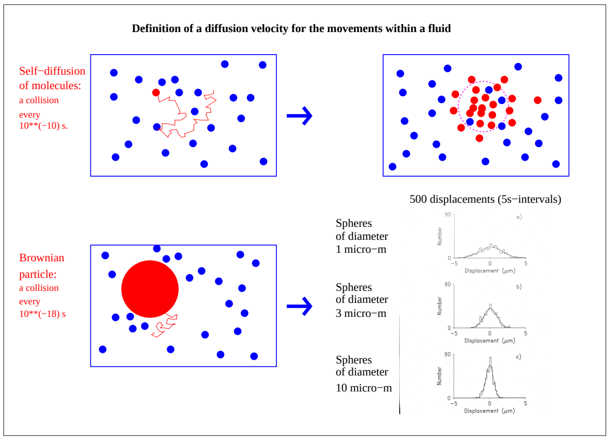

Fig.xx: Self-diffusion and brownian motion. Because of the many collisions that any molecule experiences there is a phenomenon of self-diffusion (Reif 1965 p. 483-488). This effect is basically the same as the diffusion of a big particle which is referred to as brownian motion.

given point O at time $t = 0$ and we want to know the distance covered on average by these particles. As a measure of this distance $E[X(t)]$ will not work because this expectation will be zero on account of the fact that the particles will go equally in all directions (or equally to the left and to the right if one considers a one-dimensional system as will be done later). A possible measure of this distance would be $E(|X|)$. In order to avoid the absolute value one prefers usually to use the standard deviation: $\sigma[X(t)] = \sqrt{E\left[X^2(t)\right]}$. It is $\sigma[X(t)]$ which corresponds to the dotted circle in Fig. xx. Once this quantity has been computed, the diffusion velocity can be obtained just by dividing by the time t: $v_d = \sigma[X(t)]/t$.

What information do we have in our hands in order to compute $\sigma[X(t)]$?

- The fact that the predictions of the kinetic theory of gases agree with observation show that the particles in a gas follow the law of newtonian mechanics in spite of their small size. This allows us fairly easily to write an equation of motion for the particles.
- From the kinetic theory of gases we already know the moments of first and second order of the velocity $V(t)$ of the particles between successive collisions[17] . They are given by the following formulas:

$$m_1 = E(V) = \sqrt{\frac{8}{\pi}\frac{kT}{m}} \quad m_2 = E(V^2) = \frac{kT}{m}$$

Incidentally, from these formulas one can compute the variance $\sigma^2 = E(V^2) - [E(V)]^2$ and the coefficient of variation $CV = \sigma/E(V)$ of the module of the velocity; one finds: CV=67%. Such a coefficient of variation corresponds to a variable which is “moderately random”. In contrast $X(t)$ is much “more erratic”. As $E[X(t)] = 0$, one can say either that its coefficient of variation cannot be computed

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[17] $V(t)$ denotes the module of the velocity. In one dimension it would be its absolute value.

or that it should be very large because for a real sample $E[X(t)]$ is never strictly equal to zero

From the above results is it possible to find v_d as will be seen later on. Before giving this derivation we wish to present the results. One gets:

$$\sigma^2\left[X(t)\right] = \frac{2m_2}{\alpha}$$

where m_2 is the second-order moment of the velocity (defined above) and α denotes the friction coefficient defined by the fact that αV is the force experienced by the particle in its movement. In this form the result is valid for a gas, liquid or solid. A more detailed expression can be given under additional assumptions.

- If the equipartition theorm holds m_2 can be replaced by kT/m. This assumption will be valid at room temperature.
- When there is no turbulence (that is to say when the Reynolds number is smaller than 1) the friction force can be written in the form given by Stokes' formula, namely: $\alpha = 6\pi\eta a$, where a is the radius of the particle and η the dynamic viscosity (expressed in Pa.s). As the Reynolds number is proportional to the size of the particle, this assumption is certainly fulfilled for particles of a size of the order of 1 micrometer or less.

Derivation of a formula for the variance of x

In what follows, for the sake of simplicity, we consider a one-dimensional system. For a particle of mass m_p and velocity V it is reasonable to assume the following equation of motion:

$$\frac{m_p dV}{dt} = -\alpha V + F(t)$$

where

- $F(t)$ is a random function which describes the interactions (whether in the form of shocks or distant interactions) due to surrounding molecules.
- The velocity $V(t)$ is also a random function. Although small, the time interval between two successive shocks is a positive number which means that the derivative of V is meaningful (actually it would be more appropriate to write a discrete time equation rather than an equation in continuous time).
- The term $-\alpha V$ is a friction force which is due to the fact that when the particle is moving to the right it will experience stronger shocks on its right-hand side than on its left-hand side. If the average velocity of the molecules is v_{mol}, the shocks on the right-hand and left-hand side side will have an average velocity $v_{\text{mol}} + V$ and $v_{\text{mol}} - V$ respectively. By difference this gives rise to a drag force which must be a function of V, of the vertical section of the particle, and of 3 variables giving the

characteristics of the molecules: their velocity v_{mol}, their density per unit area n, and their mass m [18].

As we wish to compute $E(X^2)$ we express the previous equation in term of X and in order to generate a term X^2 we multiply both sides by X

$$m_p X \frac{d^2X}{dt^2} + \alpha X \frac{dX}{dt} = X(t)F(t)$$

We take into account the following relations:

$$X\frac{dX}{dt} = \left(\frac{1}{2}\right)\frac{dX^2}{dt}$$

$$\frac{d^2X^2}{dt^2} = 2\left(\frac{dX}{dt}\right)^2 + 2X\frac{d^2X}{dt^2} \Rightarrow X\frac{d^2X}{dt^2} = \frac{1}{2}\frac{d^2X^2}{dt^2} - \left(\frac{dX}{dt}\right)^2 = \frac{1}{2}\frac{d^2X^2}{dt^2} - V^2$$

which gives:

$$\frac{m_p}{2}\frac{d^2X^2}{dt^2} - m_p V^2 + \frac{\alpha}{2}\frac{dX^2}{dt} = X(t)F(T)$$

Now we integrate with respect to time over a time interval $(0, t_e)$, where t_e is the smallest possible experimental observation time.

$$\frac{m_p}{2}\int_0^{t_e} dt \frac{d^2X^2}{dt^2} - m_p \int_0^{t_e} dt V^2(t) + \frac{\alpha}{2}\int_0^{t_e} dt \frac{dX^2}{dt} = \int_0^{t_e} dt X(t)F(t)$$

which leads to:

$$\frac{m_p}{2}[V(t_e) - V(0)] - m_p \int_0^{t_e} dt V^2(t) + \frac{\alpha}{2}[X^2(t_e) - X^2(0)] = \int_0^{t_e} dt X(t)F(t)$$

Apart from the equation of motion (which is rather a plausible assumption) the only solid information that we have in this problem is the average velocity of the particle as derived from the equipartition theorem: $m_p E(V^2) = kT$. In order to use this information we take the ensemble average $E(.)$ over a set of similar particles.

We will assume that one can exchange time averaging and ensemble averaging, i.e.

$$E\left[\int (.)\right] = \int E(.)$$

In principle at least, the validity of this assumption can be checked experimentally in the following way (the discussion refers to the variable x^2 but the same argument can be made as well for any other variable)

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[18] The standard expression of the drag force in a gas, namely $f_d = 6\pi\eta a V = 2\pi m v_{\mathrm{mol}} n a l V$ (Reif 1965 p. 475) contains indeed the expected variables. l is the mean free path (i.e. the distance travelled by a molecule between two successive collisions); the factor nal represents something related to the number of molecules which can hit the particle during the unit of time (without shocks this number would be written nav_{mol}, but if the density is not too low l is much smaller than the distance travelled without shocks in the unit of time.

(1) One selects $N = 100$ particles and for each of them one measures $q_i(t) = x^2$ at time t.

(2) One computes the average $a(t) = (1/N)\sum q_i(t)$.

(3) After following the 100 particles over a time t_e one computes the time average $a = (1/t_e)\int_0^{t_e} a(t)dt$

(4) For each of the 100 trajectories one computes the time average: $b_i = (1/t_e)\int_0^{t_e} q_i(t)$

(5) One computes the ensemble average $b = (1/N)\sum b_i$

(6) If $a = b$ it is proof that time averaging can be exchanged with ensemble averaging.

Ergodicity (of the mean) for the random function $Q(t)$ as defined in probability theory (see Papoulis 1965 p. 328) implies that $a = b$. Indeed, $a(t)$ is the expectation of $Q(t)$ for a given time t, whereas b_i is the time average of $Q(t)$ for a given realization i.

Thus, we get:

$$\frac{m_p}{2}\left[E[V(t_e)] - E[V(0)]\right] - m_p\int_0^{t_e} dtE\left[V(t)^2\right] + \frac{\alpha}{2}\left[E[X^2(t_e)] - E[X^2(0)]\right]$$
$$= \int_0^{t_e} dtE[X(t)F(t)]$$

This equation can be simplified on account of the following observations:

- As $F(t)$ is not correlated with the position of the particle, one gets: $E[X(t)F(t)] = E[X(t)].E[(F(t)] = 0$.
- $E[V(t_e)] = E[V(0)]$. Indeed, as far as the velocity is concerned the diffusion process is stationary (albeit not stationary in x) which means that the ensemble average of $V(t)$ is independent of time. As a matter of fact, the ensemble average of $V(t)$ is zero because there is no reason it to be either positive or negative.
- According to the equipartition rule $E\left[m_pV(t)^2\right] = kT$

Defining $\sigma = E(X^2)$, one gets:

$$-\int_0^{t_e} kTdt + \frac{\alpha}{2}[q(t_e) - q(0)] = 0 \Rightarrow \sigma(t_e) = \sigma(0) + \frac{2kT}{\alpha}t_e$$

If we translate all trajectories so that they start at the same origin point, one will have $X(0) = 0$ which of course implies that $q(0) = 0$. Thus:

$$\sigma(t_e) = \frac{2kT}{\alpha}t_e$$

Extension to non-physical systems

In economics there are many intensive variables, e.g. price, productivity, unemployment rate, interest rate. What is the factor which brings about equilibrium for such variable? The answer is clear. It is exchange and interactiona of all kinds. This includes:

- economic interactions such as trade or financial transactions,
- cultural interactions and in a general way all kinds of social interactions. For instance, linguistic factors, or cultural attitude with respect to learning or working may be important for productivity uniformization.

One should not think that the situation is necessarily much more complicated than in physics. In a molecule of water, although there are also many possible modes of excitations for specific applications one can focus on just one or two of them. In economics, because we are part of the system, we know many modes of excitation. To be able to draw some clear conclusions, one must focus on cases involving only a small number of modes. In the following sub-sections we propose three examples.

Linguistic modes of excitation

It is quite by purpose that we start we a non-economic example.
Consider France and Germany. The languages spoken in these countries are French and German and at first sight it may seem that in the course of several centuries there has be no uniformisation whatsoever. This is not completely true however. There is a diffusion process at work but it concerns only a small area of a width of about 50 km along the border. Indeed, in the French border city of Strasbourg many people are able to speak German. Why? There are many reasons which all refer to some form of interaction.

- As there many German tourists visit Strasbourg, store employees must be able to speak German in order to serve them.
- This region was invaded and occupied by Germany two times during the past 150 years: from 1870 to 1918 and from 1940 to 1944. During these periods, the language that was taught in schools was German
- In Strasbourg as well as in the surrounding area TV sets are equipped for receiving the programs of German TV channels. As a result a substantial number of people watch German programs.
- In the countryside around Strasbourg the mother tongue of a majority of people is Alsatian which is a German dialect almost identical to the language spoken in the German Rhineland.

Thus, one can conclude that there is indeed an ongoing diffusion process but it is very slow. In a study of language diffusion in many areas where two languages are in contact, it was concluded that the velocity of the diffusion front is of the order of 10 kilometer per century (Roehner and Rahilly 2002 p. 106-111).

The parallel in physics would be diffusion between two solids. When two plates made of different metals, for instance gold and lead, are tightly held together and heated there is a diffusion of atoms of each kind into the other metal. Lavoisier (1743-1994) had already observed that when gold is strongly heated, fumes arise which gild a piece of silver held in them.
The first experiment with metals in close contact was performed in 1896 by William Roberts-Austen. A thin plate of gold was fused on to the end of a rod of lead. At a temperature of 250 degree Celsius (the melting point of lead is 327 degree celsius) after a waiting time of 31 days the concentration of gold atoms at a depth of 3.5 cm was 1/10 of the concentration at the separation point. Through adjustement to the diffusion equation the diffusion constant was found to be (Mehrer et al. 2009 section 2.3) $D_{\mathrm{Au}}(523) = 40 \times 10^{-3}$ cm^{2}day^{-1}. At a temperature of only 200 degree celsius, the diffusion constant was five times smaller. $D_{\mathrm{Au}}(473) = 8 \times 10^{-3}$ cm^{2}day^{-1}. Other experiments performed subsequently showed that with fairly good accuracy $\log[D(T)] \sim -1/T$, or in other words: $D(T) = K\exp(-A/T)$. Incidentally, the fact that diffusion in solids obeys a law similar to the law of Arrhenius for the constants of chemical reactions has been realized only in the 1920s[19].

This experiment suggests a method for defining a temperature for the diffusion of languages. We already suspect that in this case the temperature will be an index which summarizes the interactions between the people either of the two languages. So, if one can measure the diffusion constant under different circumstances, for instance as a function of the number of people who cross the border annually, then one will be able to establish a formula similar to the one written above for atoms of gold.

Such an adjustement will *not* prove that the number of people (or any similar variable) has the universality property of the kinetic energy in physics. We are still far away from such a goal because we still do not know how to define a kinetic *energy* for the language problem.

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[19] This law looks very different at first sight from the form of the diffusion constant given by Einstein's law for a fluid, namely: $D = (RT/N_A)(1/6\pi\eta r)$. However, both function are increasing with T.

Effusion experiments and effusion modeling

In order to describe the movement of a gas from a container A to a container B, one must rely on the formulas of hydrodynamics. Unfortunately, because of the inability of physics to describe turbulence in a simple and yet reliable way, hydrodynamics remains a fairly tricky theory. That is why we start with the process of effusion. In this case, as explained below, molecules escape from A to B independently and one after another. As a result there is no turbulence and we are on firm ground. As a matter of fact, this process is fairly similar to a purely random process. This point will become clearer in the following description of the physical process of effusion. Our description is mostly based on Reif (1965).

What is effusion?

Observation shows that when the communication hole between two containers is smaller than the mean free path l of the molecules, they will pass through the hole independently from one another (Fig. 1). In standard room conditions, $l \simeq 0.3\mu$m. Observation shows that molecules escape through a hole smaller than l with the velocity that they have in the container. Incidentally, this property gives an experimental method for measuring the distribution of the velocities in a gas.

Effect of a gap in temperature

From an experimental point of view one distinctive feature of effusion is the one described in Fig. 2. When the containers are maintained at different temperature there will be an equilibrium situation in which the pressures on the two sides are *not* the same. In contrast, a much larger communication hole will tend to equalize the pressure (and also the temperatures). In the effusion case, the equilibrium is realized when

$$p_1/\sqrt{T_1} = p_2/\sqrt{T_2} \tag{1}$$

(for more details see below). p_1, p_2 are the pressures on each side, and T_1, T_2 are the Kelvin temperatures.

Without any communication between the two containers the equilibrium condition would be $p_1/T_1 = p_2/T_2$ as results from the equation of state of an ideal gas: $pV = NkT$ where V denotes the volume and N the number of molecules contained in that volume.

For instance, if $T_1 = 373,\ T_2 = 293$, the pressure ratio p_1/p_2 will be $\sqrt{T_1/T_2} = \sqrt{373/293} = 1.13$ whereas with sealed containers it would be $T_1/T_2 = 1.27$. Such a difference of 12% should be easy to observe.

As one knows from statistical physics, the average velocity of molecules of a gas at temperature T is given by:

$$\bar{v} = \sqrt{\frac{8kT}{\pi m}} \tag{2}$$

where T is the Kelvin temperature, m the mass of a molecule and k the Boltzman constant. One can also recall that $\tilde{v} = \sqrt{2kT/m}$, where $\tilde{v}$ is the most probable speed that is to say the speed for which the distribution function is maximum. As $\bar{v}/\tilde{v} = 1.12$ these expressions are fairly equivalent, so that instead of $\bar{v}$ we may also use the simpler expression $\tilde{v}$. Moreover, for the sake of simplicity, in what follows, we will note v instead of $\bar{v}$ or $\tilde{v}$.

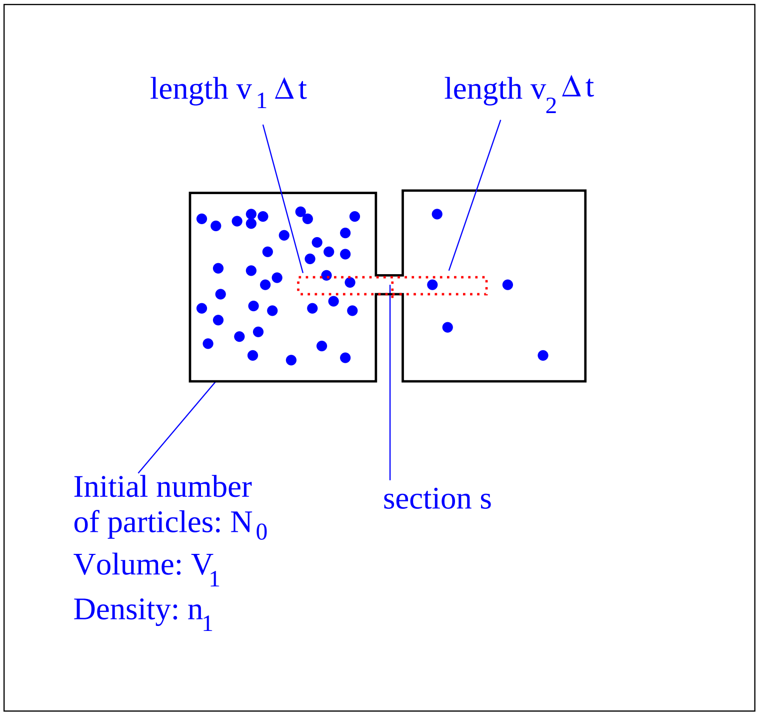

Fig. 1: Effusion experiment. The figure shows the main variables that are needed for describing an effusion experiment. The two red rectangles shematize the volumes occupied by the molecules which will be able to cross from one side to another. We suppose that the temperature is the same on both sides. As a result, the velocity of the molecules will also be the same: $v_1 = v_2$.

When will equilibrium will be achieved?

We start from a situation where the density of the molecules per unit of volume is the same on each side. In each time interval Δt the molecules which will cross from left to right must have a velocity which is in the right direction (that is to say parallel to the axis of the hole[20]) and must be contained in a cylinder of length $v_1 \Delta t$ and section s as represented in Fig. 1.

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[20] Of course, this is an approximation. Molecules with a velocity not exactly parallel to the axis may also be able to cross, but this effect becomes small when the length of the hole is long with respect to l, a condition that is satisfied in all practical cases.

This argument implies that initially the number of molecules which cross from left to right will be $n(v_1\Delta t)$ whereas the number of those crossing from right to left will be $n(v_1\Delta t)$. The fact that $T_1 > T_2$ implies that $v_1 > v_2$ which means that there will be a flow from left to right. Equilibrium will be re-established once the density of molecules on the left-hand side will be increased by an amount Δn such that: $(n - \Delta n)v_1 = (n + \Delta n)v_2$. Replacing v_1 and v_2 by their expressions we see that the variation Δn will be related to the gap in temperature by the following relationship:

$$\Delta n = \frac{n\left(\sqrt{T_1} - \sqrt{T_2}\right)}{\sqrt{T_1} + \sqrt{T_2}} \tag{3}$$

From the equation of state $p = nkT$ results that the changes in numbers of molecules lead to the following pressure changes:

$$p_1' = p_1 - (kT_1)\Delta n, \quad p_2' = p_2 + (kT_2)\Delta n$$

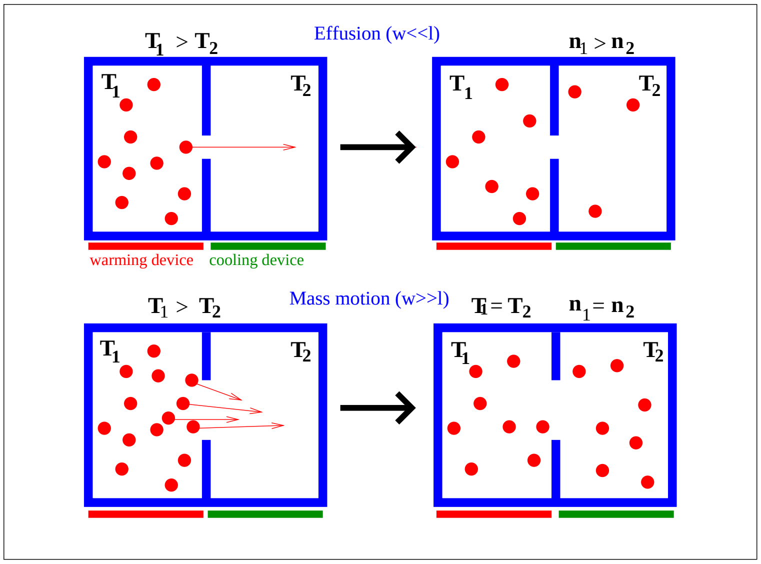

Fig. 2: Effusion versus mass motion. For both experiments the systems are initially out of equilibrium because of a temperature gap $T_1 - T_2$. In the effusion experiment the hole in the partition wall between the two containers has a diameter w that is smaller than the mean free path l of the molecules. For nitrogen at room temperature, l is about $0.3\mu m$. As a result the pressure on the hot side remains higher even when equilibrium is reached:

$$p_1/\sqrt{T_1} = p_2/\sqrt{T_2} \Leftrightarrow n_1\sqrt{T_1} = n_2\sqrt{T_2}$$

In the second experiment the hole is much larger than l. As a result, there will be a hydrodynamic flow from left to right that will result in a quasi-equilibrium characterized by an equalization of temperature and pressure.

Molecules with different masses

N molecules of mass m_a are put in the container 1 on the left-hand side and similarly N molecules of mass m_b on the other side. We assume that $m_a < m_b$. Initially, the system will not be in equilibrium because $v_a > v_b$ implies that the flow of m_a

molecules from left to right will be higher than the flow of m_b molecules from right to left.

In the present problem, there will be two separate equilibrium conditions, one for each kind of molecules. We denote by n_i^a the density of molecules a in container $i = 1, 2$ and similarly by n_i^b the densities of molecules b. The equilibrium conditions read:

$$n_1^a(v_a\Delta t) = n_2^a(v_a\Delta t) \Rightarrow n_1^a = n_2^a, \quad n_1^b(v_b\Delta t) = n_2^b(v_b\Delta t) \Rightarrow n_1^b = n_2^b$$

Equilibrium will be reached when there will be the same numbers of molecules of each kind on each side.

Equilibrium will be reached faster for light molecules than for heavy molecules. We denote by τ_a and τ_b the time constants of the two processes. If $m_a \ll m_b$ the a equilibrium will be reached after a short time τ_a during which the repartition of the b molecules will change only slightly. Thus, between time τ_a and time τ_b there will be $N/2$ molecules a on side 1 and almost no b molecule, whereas on side 2 there will be $N/2$ molecules of type a plus N molecules of type b making a total of $3N/2$ molecules. Thus the pressure on side 2 will be 3 times higher than the pressure on side 1. Subsequently, as $t \rightarrow \tau_2$ the difference $p_2 - p_1$ will tend to zero.

As an example, take $a =$ helium ($m_a = 4$ g/mol) and $b =$ sulfur hexafluoride ($m_b = 146$ g/mol). As will be seen below, the time constants $\tau_a,\ \tau_b$ are proportional to the square-root of the masses. Thus, in this case, $\tau_b/\tau_a = \sqrt{146/4} = 6$.

Effect of intermolecular attraction on molecular velocity

What is the molecular velocity distribution in water (or more generally in liquids)? Does the equipartition theorem hold?

To answer this question the simplest way would be to find some clear experimental results. Surprisingly, however, an Internet search was fairly unsuccesful. Many pressure measurements of the vapor over liquids do of course exist from which the velocity of the molecules of vapor can be derived by using a based on the kinetic theory of gases. The following points provide some further insight.

- In liquids (as well as in gases) some molecules have a speed that is higher than the average speed. As a result they will be able to escape through the surface of the liquid and form a layer of vapor on the top of the liquid. This has two implications (i) As this process allows only the fastest molecules to escape, those which remain will have on average a lower average speed; this is reflected in the the fact that the non-equilibrium process of evaporation results in a cooling of the liquid. However, once equilibrium is reached the cooling stops because the outflow is matched by an

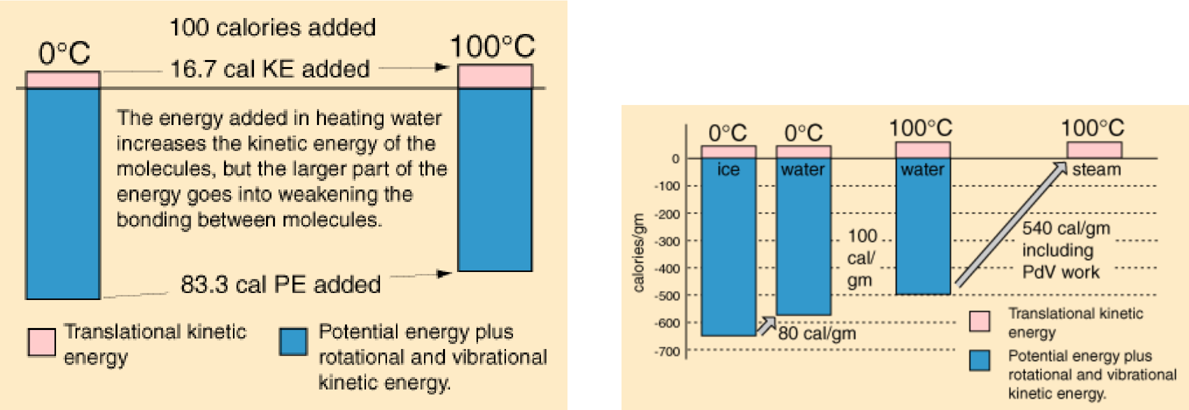

Fig. 3: Comparison of various forms of energy in different states of water. For the understanding of this graph one must recall why the potential energy of inter-attractive forces is seen as a negative energy. Consider two masses m_1, m_2 connected by a string of rubber of length L. Assume that the force due to the rubber decreases to zero when $L \rightarrow \infty$. Then, it makes sense to consider the situation where the two masses are far apart as a free state and to give it (by convention) an energy equal to zero. Now, if m_1, m_2 become closer due to the attraction force of the rubber it is a process which can produce some work (for instance it can be used to rotate a wheel) in the same way as when water falling from a height h_1 to a height $h_2 < h_1$ is used to produce electricity. In other words, when the masses are close to each other the system will have a lower potential energy E_2 than its energy E_1 when they are far apart. As the later is zero, it means that $E_2 < 0$.
An obvious implication is that if one starts from the state where L is small one must provide some energy to stretch the rubber. It is this energy which is represented somewhat schematically by the blue bars. In fact, there should be a different energy $E(T)$ for each temperature and this energy is related to the attraction force $F(r,T)$ by the formula $E(T) = \int_{r0}^{\infty} F(r,T)dr$.
It can be seen that the translational kinetic energy is almost the same in each state but represents a much smaller proportion of the total energy in the solid state than in the state of a gas.
Incidentally, it would be more appropriate not to include the rotation energy into the blue bars because it is truly a form of kinetic energy.
Source: http://hyperphysics.phy-astr.gsu.edu/hbase/thermo/phase.html

inflow of same magnitude. (ii) The fact that molecules cross almost instantaneously from liquid to vapor suggests that they must have almost the same velocity in the two states.

- In a liquid molecules form temporary associations. This means that they so to say coalesce into "collective molecules". Applying to them the Maxwell-Boltzman law will result in reduced velocity.

- One way to identify changes in the interaction strength is to study the heat capacity $C = \Delta E / \Delta T$. In this equation ΔE represents the energy that one provides to the system and ΔT the resulting change in temperature that is to say in kinetic energy[21]. If a process takes place (e.g. the unfolding of a protein) which requires substantial energy but does not affect the kinetic energy, then ΔT will be small and therefore C will be large. In other words, the process will produce a narrow peak in

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[21] In physics, a distinction is made between C_p and C_v, respectively the heat capacity under condition of constant pressure or constant volume. As this distinction is irrelevant for the present argument we omit it here.

the graph of the heat capacity as a function of temperature as in Fig. 4.

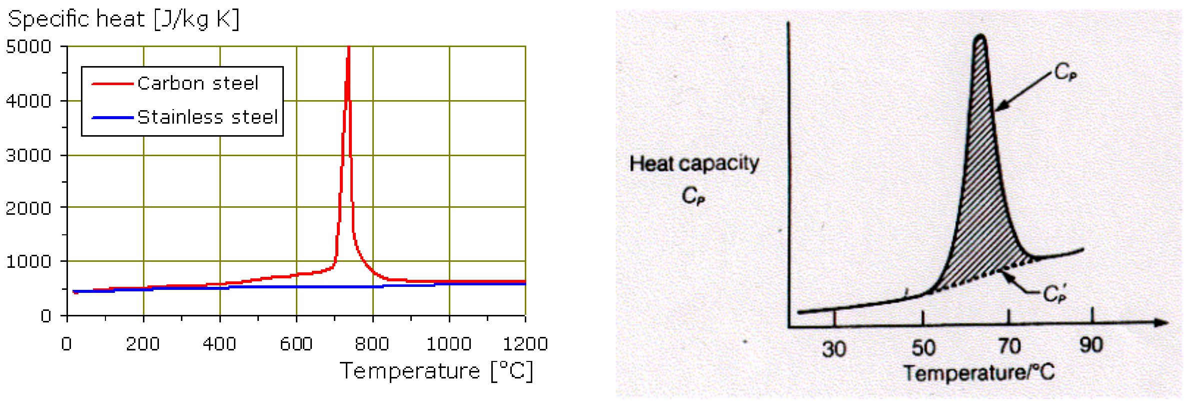

Fig. 4: Peaks in heat capacity resulting from an internal process that absorbs energy without resulting in a higher temperature.
Fig 4a: Carbon steel: transformation from α-iron (body-centered cubic) to γ-iron (face-centered cubic). The transition between these allotropic forms of iron occurs at 727 degree celsius (it is somewhat dependent upon the proportion of carbon contained in the steel). In contrast to carbon steel which contains only iron and carbon, stainless steel also contains a minimum 11% of chromium.
Fig. 4b: Peak in the heat capacity resulting from an unfolding process occurring in a protein.
In the two cases the internal process requires a substantial amount of energy but does not affect the kinetic energy which means that the temperature remains almost constant; this leads to a high heat capacity $C = \Delta E/\Delta T$.
Analysis of internal transformations by the observation of the peaks in heat capacity has led to a technique knowns as "differential scanning calorimetry" (DSC). By observing the difference in heat flow between the sample and reference, differential scanning calorimeters are able to measure the amount of heat absorbed or released and thus can identify specific phase transitions.
Source:
http://www.mace.manchester.ac.uk/project/research/structures/strucfire/materialInFire/Steel/StainlessSteel/thermalProperties.htm
http://www.whatislife.com/reader2/biophysics/Thermodynamics.htm#Molecularinterpretation

- From a theoretical perspective, the equipartition theorem says that each quadratic term in the expression of the energy[22] has an ensemble average of $(1/2)kT$. This applies not only to quadratic terms but also to higher powers. A term q_i^n will lead to a contribution of $(1/n)kT$. The equipartition theorem also applies to interaction terms. The sum of all these contributions must be equal to the average energy of the system which is usually defined by experimental conditions. So we see that a change in interaction can have broad implications.

Effect of intermolecular attraction on pressure

According to the van der Waals equation, the pressure of a gas consisting of inter-

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[22] One must of course remember that the equipartition theorem is a result based on classical mechanics. If quantum effects become important it does no longer apply.

attractive molecules is smaller than the pressure of an ideal gas:

$$p_{\text{attraction}} = p_{\text{ideal}} - a', \quad a' = \frac{a}{V_m^2} \qquad ()$$

where V_m denotes the volume of one mole (in the condition of pression and temperature considered in the equation). a is a parameter which expresses the strength of attraction; for instance for carbon dioxide a is 2.7 times larger than for argon [23]
The difference in pressure for carbon dioxide as compared with argon may be small but here we are interested in the reasoning rather than in numerical values because anyway we intend to apply this argument to living units not to molecules. For small fishes, the velocity is indeed a function of temperature (Shen et al 2011).

Is the velocity a function of interaction strength Tentatively, we can write the molecular velocity of a system of interacting molecules under the form $v = \sqrt{2kT/m} - q(a')$ where $q(a')$ is a (probably positive and increasing) function of the attraction parameter a'. Based on what we said earlier one would expect the term $q(a')$ to be a fairly small correction.

Experiment with intermolecular attraction 1. Case of weak interactions

We fill the container 1 with N molecules of an ideal gas a and the container 2 with N inter-attractive molecules b which, apart from this characteristic, are identical to a in all other respects (e.g. mass or size).
Will the system be in equilibrium?

The presure on side 1 will be higher The situation is somewhat similar to the one considered above in which there were heavier molecules in 2. The equilibrium conditions will be the same as above and equilibrium will be reached when there are equal numbers of molecules of each kind on each side.
Here, however, we are not interested in the evolution toward equilibrium which is fairly trivial. Instead, with some modifications the experiment offers a way to estimate the attraction strength of the molecules b.

This time we put an equal number, N, of inter-attractive molecules on each side. In addition, we assume that the containers are at two different temperatures T_1, T_2. This is the same situation as already considered above except for the fact that the velocity

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[23] Equation () assumes that the ideal and the non-ideal molecules are identical in all other aspects except attraction strength. If one does not make this simplifying assumption the more general equations are as follows:

Ideal gas (e.g. argon): $p = \frac{N_A kT}{V}$, Carbon dioxide: $p = \frac{N_A kT}{V-b} - \frac{a}{V^2}$, $a = 364$ kPa.dm^6/mole^2, $b = 0.043$dm^3/mole

These equations are for one mole (N_A is the Avogadro number). The parameter a describes the attractivity between molecules. If we assume that the two gases have the same b which is indeed almost true for argon and carbon dioxide, then we see that the larger a, the smaller the pressure.

of the molecules is given by:

$$v = \alpha\sqrt{T} - q(a'), \quad \alpha = \sqrt{2k/m}$$

By using the same argument one gets the following formula:

$$\Delta n = \frac{n\left(\sqrt{T_1} - \sqrt{T_2}\right)}{\sqrt{T_1} + \sqrt{T_2} - 2q(a')/\alpha}$$

by solving this relation for $q(a')$ one gets:

$$q(a') = \frac{\alpha}{2}\left(\sqrt{T_1} + \sqrt{T_2}\right)\left[1 - \frac{n}{\Delta n}\frac{\sqrt{T_1} - \sqrt{T_2}}{\sqrt{T_1} + \sqrt{T_2}}\right] \quad (5)$$

In the case of a gas all quantities on the right-hand side can be measured which, at least in principle, would allow to determine the attraction term $q(a')$.

Experiment with intermolecular attraction 2. Case of strong interactions

In the previous experiments with equal temperatures on each side, equilibrium was always reached for an equal number of molecules on each side. However, this remains true only up to a given point. Beyond some critical interaction strength one observes a completely different behavior. This can be illustrated by a few examples.

- Put N red fire ants in container 1 and N others in container 2 and wait. If $N = 100$ you will observe that after some two hours all the ants will be in one of the container (more details can be found in Wang et al 2011, p. 9-10). Such a clustering behavior which eventually leads to symmetry breaking is clearly very different from what we considered so far. However, this kind of aggregation phenomenon is by no means special to living units. It can also be observed in various physical systems.
- Some of the clearest physical examples of aggregation occur with colloids. This is shematically illustrated in Fig. 3.

- As a simple example of aggregation one can consider a solution of oil and balsamic vinegar. As this vinegar has a smaller density than oil, it forms a brown layer on top of the oil.

Now, if the bottle is shaken violently the balsamic vinegar forms dark-brown spherical dropplets of different sizes which begin to move toward the surface. As predicted by Stokes' law the smallest dropplets move slower than the big ones. When two dropplets come in contact they merge into one bigger dropplet. This aggregation process eventually leads back to the layer that existed at the beginning.

The only major difference between this case and the case of colloids is that, because of their small size, the colloids are able to form stable suspensions. They are stable in two different ways: they neither sink nor go up and they do not aggregate. Of

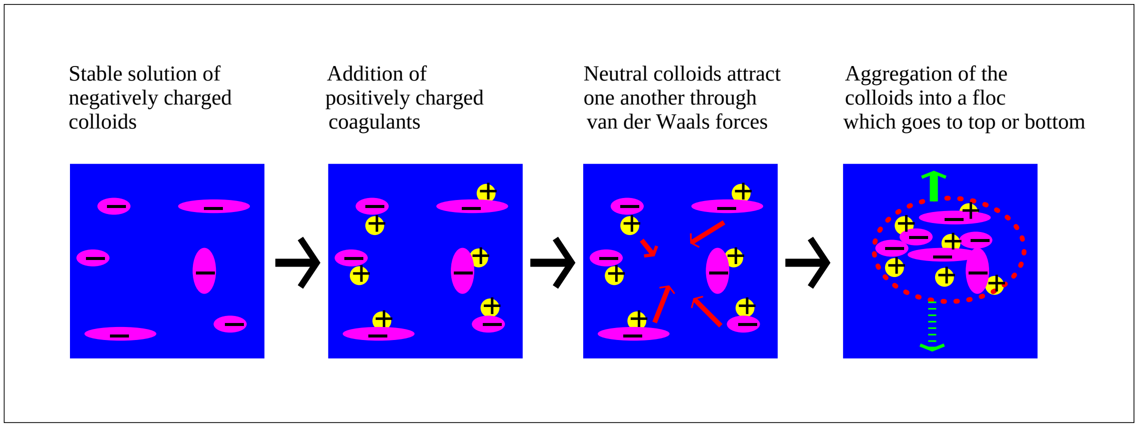

Fig. 3: Aggregation of colloids. Most particles dispersed in water have a negative charge, so they repel each other, at least at short range. As a result they form stable dispersions. Particles with a diameter of less than one micrometer will remain in equilibrium in midwater due to the molecular shocks which are also responsable of the phenomenon of brownian motion. However, once a positively charged coagulant has been added, the particles become neutral and then can attract each other through (weak) van der Waals or London forces. The big particles that they form are called flocs and because of their size they do not remain in equilibrium but, depending on their density, they will drift to the surface or fall to the botton.

course, if for some reason they form aggregates, these bigger particles will move to the surface or to the bottom depending on whether their density is smaller or larger than the density of the liquid.

How can one measure attractions? First proposal

Now, we come to our main question: how can one measure this stronger interaction?

Can one hope to use the method sumarized in Fig. 4.
The question is whether or not the temperature gap will prevent the insects in container 2 of coming to the left. One can propose two arguments.

- If the insects in container 1 quickly form a tight cluster none of them will leave this part. In this case, the higher temperature becomes completely ineffective because it will not bring about any flow from left to right.
- The same argument can be applied to the experiment No 1 of Fig. 4. It leads to the conclusion that in a first phase two different clusters will form on each side without any substantial flow occuring in either direction. Then in the second phase the cluster in container 2 will *collectively* move toward the left[24]. If this representation is correct the temperature gap will be ineffective because it influences only the more or less random movements of individuals not the collective movement of a cluster.

How can one measure attractions? Second proposal

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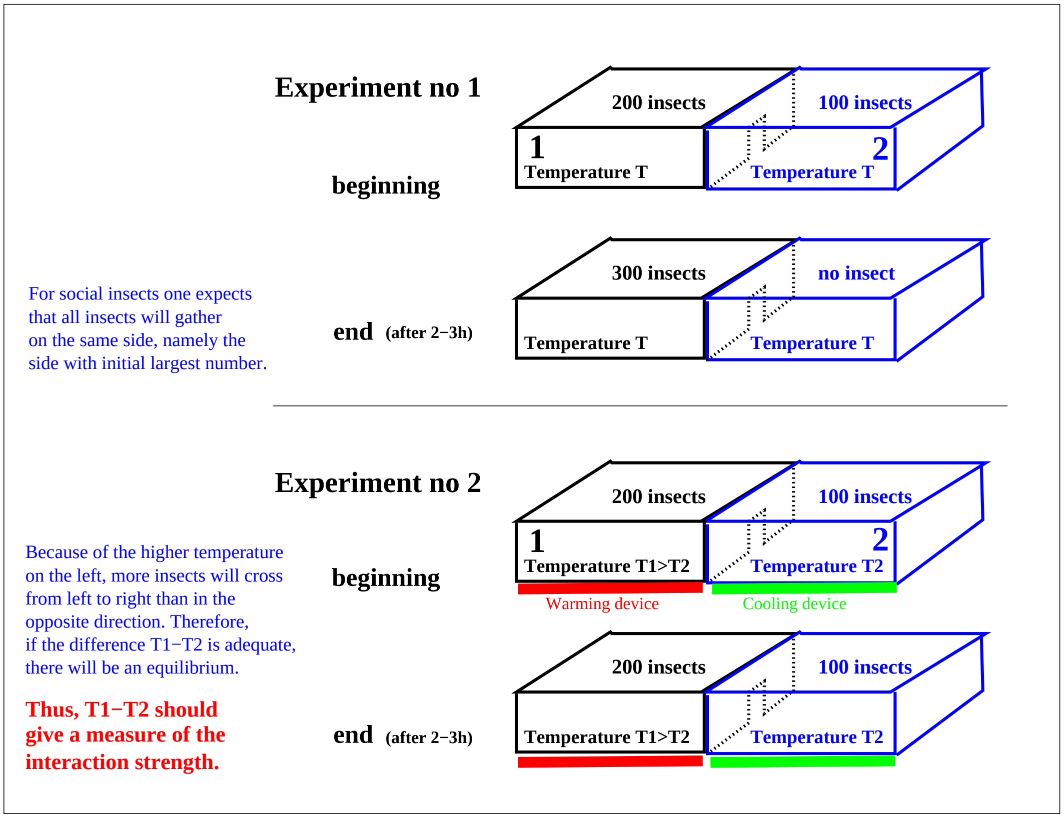
[24] There is of course nothing really mysterious about that. If the force of attraction between two ants is f the force of attraction between two clusters of N ants will be

- Nf if the bulk of the cluster contributes to the attraction
- or $\sqrt{N}f$ if the force is only due to the ants that are at the periphery of each cluster.

This argument suggests that the method of Fig. 4 may perhaps work for small numbers but may fail for large numbers.



For social insects one expects that all insects will gather on the same side, namely the side with initial largest number.

Because of the higher temperature on the left, more insects will cross from left to right than in the opposite direction. Therefore, if the difference T1−T2 is adequate, there will be an equilibrium.

Thus, T1−T2 should give a measure of the interaction strength.

Fig. 4: Proposal No 1 for measuring the attraction between insects. This method is similar to the one explained in the text for the case of weak inter-attractions except that one starts with unequal numbers on each side.
In this experiment there are *two* forces which counter the flow from left to right: (i) The higher density in container 1 (ii) The temperature gap $T_1 - T_2 > 0$. However, these properties have an effect only as long as the insects have more or less random movements. Once clusters have formed they become fairly ineffective.
In other words, we do not yet know whether or not these effects will be sufficient to overcome the attraction exercised by the insects in container 1. The latter is particularly strong for social insects such as bees or ants. Observation will provide an answer to this question.

For colloids, there is a method for measuring the interaction strength; it is called the "Zeta potential" technique. In its principle, it is very simple.
As illustrated in Fig. 3 the attraction strength of colloids is a function of the charges which sit on their surface. If there are substantial charges (whether positive or negative) the colloids will repell each other. On the contrary, if they bear no charges the colloids will attract each another. In short, the problem comes down to measuring this superficial charge. One possible method is to introduce into the liquid an electrode whose sign is opposite to the sign of the charges on the colloids. Thus, the colloids will be attracted toward the electrode. By using various optical or acoustic techniques (e.g. Doppler effect) it is possible to measure the speed of this movement. This speed will give an estimate of the charges carried by the colloids which, as we have seen, is directly related to the strength of attraction.

In the case of insects, the task is more difficult because we do not really know what

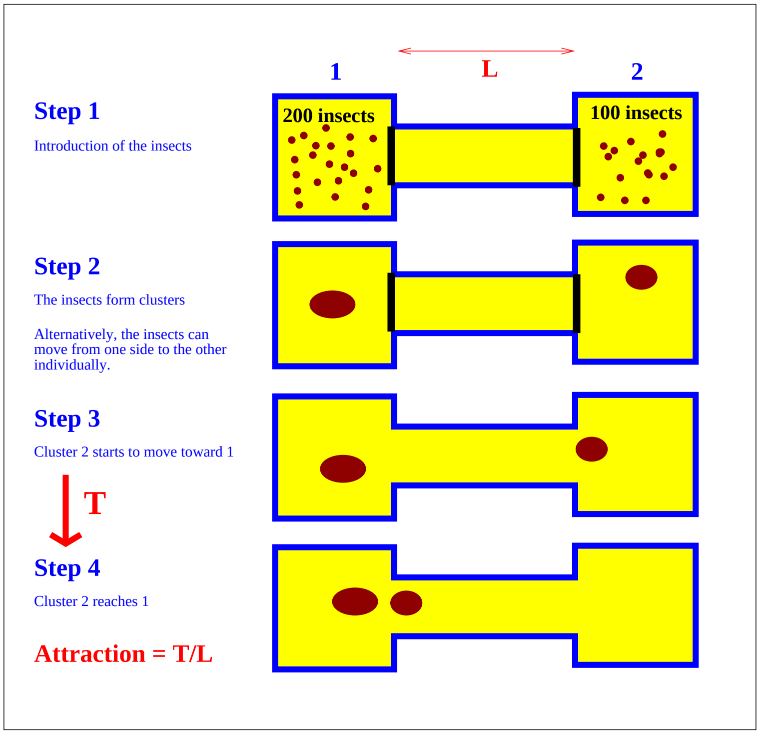


Fig. 5: Proposal No 2 for measuring the attraction strength between social insects. In its principle, this method is similar to the so-called Zeta potential method for colloids. In both cases, one measures the velocity of units under the attraction effect. The higher the velocicy, the higher the attraction.

is the factor which controls the attraction. On on the other hand, however, because ants or bees are much larger than colloids they are easier to observe.

Lattice method for estimating interactions strength

In this section we consider an alternative method for estimating the strength of interactions. which is illustrated in Fig. 6.

First the insects are made motionless by keeping them in carbon dioxide for a few minutes. Then, they are positioned at the vertices of a lattice. When they wake up, their movements are recorded by taking pictures at given time intervals T. Because one does not know the interaction range the data must be analyzed for different in

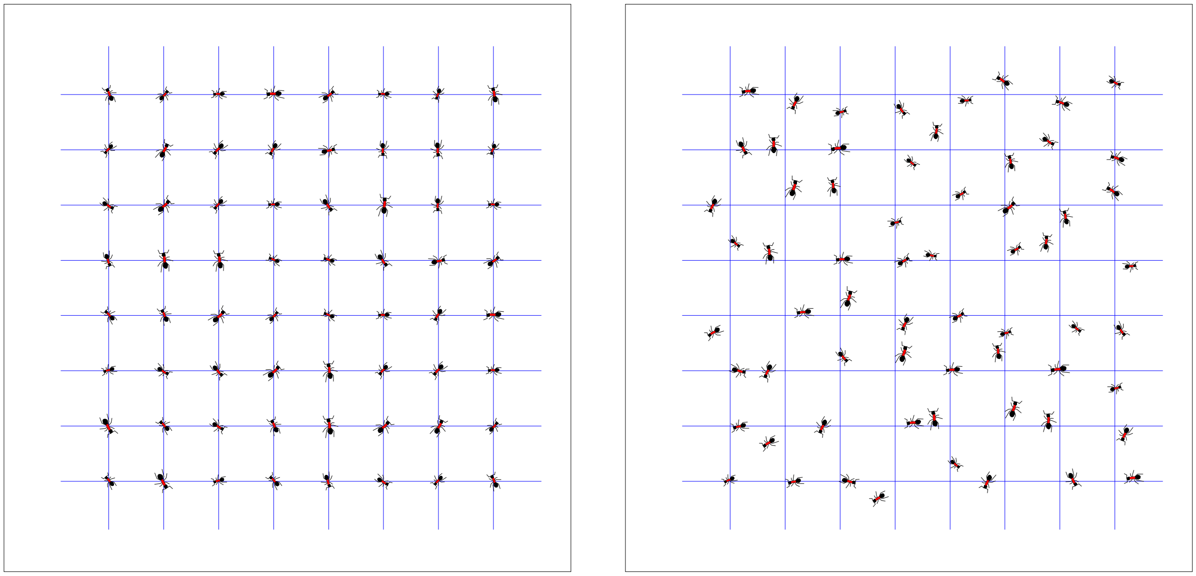


Fig. 6: Lattice method for estimating interaction. After having been made motionless through carbon dioxide, N insects are positioned at the vertices of a square lattice as shown on the left-hand side. In this situation the average distance between them is equal to the spacing L_0 of the lattice. Once they wake up, they may move toward the outside or toward the inside. We denote by $L_r(t)$ the average distance between the insects in a neighborough $V_r(i)$ of radius r:

$$L_{r,i}(t) = (1/\text{number of pairs}) \sum_{j\in V_r(i)} d_{i,j}(t) L_r(t) = \frac{1}{N}\sum_i L_{r,i}(t)$$

where $d_{i,j}(t)$ is the distance between insects i and j. In the first case $L_r(t)$ will become larger than L_0, whereas in the second case it will become smaller.
For a given time interval T, the ratio $A(r) = [L_0 - L_r(T)]/L_0$ will provide an estimate of the interaction at range r. For instance, $L_3(T) = 1.5L_0$ gives $A(3) = -0.5$ and corresponds to a strong repulsion within a range of 3 cm, whereas $L_3(T) = L_0/2$ gives $A(3) = 0.5$ and corresponds to an attraction.

At first sight one may think that when all the insects gather together and form a cluster, $L_r(t)$ cannot become smaller than a lower bound defined by the size of the insects. This is of course true to some extent but one must keep in mind that when bees cluster together they form several layers. Depending on the number of layers $L_r(t)$ can become fairly small.

CHAPTER 3: EXPERIMENTAL RESULTS

Flow rates in escape experiments: definitions

In the present section we continue our investigation of experiments done with the two-container device but we will consider more closely the flow between the two containers. In this respect it will help to draw a clear distinction between the following notions.

- *Total flow $F_T(t)$ versus net flow $F(t)$.* If F_{12} and F_{21} denote the flows from 1 to 2 and 2 to 1 respectively, then the total and net flows will be defined as:

$$\text{Total flow: } F_T(t) = F_{12}(t) + F_{21}(t) \quad \text{Net flow: } F(t) = F_{12}(t) - F_{21}(t)$$

If we think of the containers as representing two countries 1 and 2 the total flow represents the sum of exports and imports (of each of the countries), whereas the net flow will represent the balance of trade.

- *Instantaneous flow* $F(t)$ *versus average flow* $\bar{F}$. The instantaneous flow is the flow at a specific time while $\bar{F}$ is the flow averaged over the duration of the experiment.

$$\text{Duration of experiment: } T \quad \bar{F} = \int_0^T \frac{1}{T} F(t) dt$$

We wrote the definition for the case of the net flow but a similar definition can of course be given for the total flow.

- *Flow* F *versus flow rate* f. If one wishes to compare various experiments performed over different durations and with different numbers of particles one must use flow rates. The passage from flows to flow rates is a normalization operation and this normalization can be performed in various ways depending on the objective of the investigation. In what follows we will mainly use normalization with respect to initial number of particles, duration of the experiment and section of the communication hole.

In what follows, we first present some experimental results. Then, we examine if they can be described by means of an effusion process.

Escape rates for small fishes

Escape experiment with fishes, average flow rate (1)

This experiment was performed in the fall of 2010 at by two students of Beijing Normal University Tian Kai Lan and Zhang Chen Han.

Container 1 and 2 had a total length of 30 cm and contained about 5 liters of water. Container 1 and 2 communicated through a hole which had a diameter of 3 cm. Initially, there were 200 small fishes in container 1. The fishes were so-called zebra fishes (scientific name: Danio rerio) whose length is about 3 cm. In nature, they often live in groups (also called shoals) of about 4 to 30 individuals. The experiment consisted in observing how many would cross into container 2 within a time interval of 4 minutes. Once the 200 fishes were gathered in container 1 the door leading to 2 was opened. After 4 mn it was closed again and the fishes on each side were counted. The experiment was repeated 20 times and averages were computed. The length of compartment 1 was increased successively by a factor 2 and 3 so that the experiment was performed with three different initial densities[25].

Table 1: Escape experiment with 200 zebrafishes

	80 per liter	120 per liter	240 per liter
Average flow rate (expressed in number of fishes per 100 of initial pop, per mn, per sq-cm)	0.55 ± 0.06	0.93 ± 0.03	1.37 ± 0.04

Notes: The numbers in the first row show the initial densities expressed in numbers of fishes per liter. The numbers of fishes that left compartment 1 were recorded after a time interval of 4 mn. The temperature of the water was approximately room temperature that is to say about 20 degree. Each experiment was repeated 20 times. The error bars are confidence intervals for a probability level of 0.95. *Source: Tian and Zhang (2010)*

Escape experiment with fishes: average flow rate (2)

This experiment was done in November 2011 by two students of Beijing Normal University, Cheng Dong and Shi Pei Teng. It was also conducted with zebra fishes. Initially there were 40 fishes and each experiment was repeated 6 times. The experiment was conducted at different temperaures. We will give the results for 10 degrees and 25 degrees, the later one being a biologically optimal temperature for this kind of fishes.

The average flow rate was as follows:

$$\bar{g} = 1.73 \pm 0.7 \text{fishes per 100 initial number, per duration (in mn), per section of hole (in square cm)}$$

Escape experiment with fishes: how cumulative flow rate changes in time

In the previous experiment, in addition to the end result the number of fishes present in container 2 was also recorded every minute. This gave the cumulative net flow rate. The results are given in Table 2.

Time constant in escape experiments

Physical idea behind escape experiments

In an escape experiment one or several units belonging to a group will leave this group. This is a very common phenomenon. It happens in all human organizations:whether school, army or various associations. In the case of schools, the escape rate is called drop-out rate, in the military it is called desertion rate.

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[25] Actually, the experiment was somewhat more complicated in the sense that compartment 1 was in fact in the middle and compartment 2 on each side; this gave the opportunity to observe whwther the fishes went to the left or to the right. Here, however, we will lump together the left and right numbers for we are only interested in the total number of fishes who left compartment 1.

Table 2: Escape experiment with 40 zebrafishes: cumulative escape rate in the course of time

Time (mn)	1	2	3	4	5	6
Cumulative net flow rate (expressed in number of fishes per 100 of initial pop, per mn and per square cm)	2.2	2.0	2.3	1.7	1.4	1.2

Notes: The cumulative net flow rate from container 1 into container 2 corresponds to the number of fishes observed in container 2. As an illustration of the normalization, consider the 2 mn measure: the average number of fishes present in container 2 after 2 mn was 16; this number was divided by 0.4 for the initial population expressed in 100s, by 2 for 2 mn, and by 10 for the 10 square cm section of the communication hole; altogether, it was divided by 8 which gave 2.0.
Source: Chen and Shi (2011)

Obvious physical parallels are the phenomena of evaporation or sublimation. In evaporation, the fatest molecules manage to leave the liquid in spite of the attraction exerted by neighboring molecules. Sublimation is the same phenomenon for solids. As sublimation is a much smaller effect than evaporation, we will mostly discuss evaporation.
When the liquid is contained in a closed container an equilibrium will be established when the molecules leaving the liquid per unit of time are in same number as those which move in the opposite direction.

The proportion of molecules which leave the liquid can be estimated though the so-called *equilibrium vapor pressure* p_e. An approximate model for this pressure is given by the Clausius-Clapeyron formula (Wikipedia article entitled "Equilibrium vapor presure", French version):

$$p_e = p_0 \exp\left[-(ML/R)(\frac{1}{T} - \frac{1}{T_0}\right]$$

where:

- T_0: Boiling temperature at pressure p_0.
- M: Molar mass of the substance expressed in kg/mole
- L: Heat of vaporization expressed in J/kg
- R: Gas constant, $R = 8.31$ J/(K.mol)
- The standard atmospheric pressure is $p_0 = 1013$ mbar.

As an example we apply this formula to water at a temperature of 40 degree Celsius.

$$M = 0.018\,\text{kg/mole},\ L = 2.26\,10^6\ \text{J/kg},\ p_0 = 1013\,\text{mbar},\ T_0 = 373\,\text{K}\ \Rightarrow P = 81.8\,\text{mbar}$$

The pressure observed experimentally is 73.8 mbar which means that the error margin of the Clausius-Clapeyron formula is of the order of 10% (its accuracy becomes better at temperatures closer to the boiling point because the ideal gas assumption which is made in the derivation becomes more valid).

As at given temperature the pressure is proportional to the number of molecules, one sees that the proportion of "escaped molecules" is $81.8/1013 = 8.1\%$. At room temperature of 20 degree Celsius the proportion is about 2%. In short, far from the boiling point only a small proportion of the molecules are in the form of vapor. What is the fundamental reason of this disymmetry? It is due to the difference in strength of interaction between the liquid phase and the vapor phase together with the action of temperature. What are the respective roles of these factors?

- It is reasonable to estimate the strength of inter-molecular attraction through the heat of vaporization because it represents the energy that one must inject to break the bonds between water molecules. It is possible to measure the heat of vaporization at different temperatures just by changing the pressure. Such experiments show that the heat of vaporization decreases when the temperature is increased. However, the decrease is fairly small: only about 10% from 20 to 100 degrees.
- The second effect consists in the fact that at higher temperature the water molecules have a higher kinetic energy which allows more of them to escape. This effect is much stronger than the previous one. Between 20 and 100 degree the average kinetic energy will be multiplied by $T_2/T_1 = 373/293 = 1.27$.

Working together, these effects bring about a multiplication of the proportion of escaped molecules by a factor 50.

Escape experiments are conducted with a container which has two compartments A on the left-hand side and B on the right-hand side. Initially, all N animals are in only one of the two compartments, for instance compartment A. One observes the rate at which they move from this compartment to the other. We denote by $X(t)$ the number of animals in the part (namely B) that was initially empty. $X(t)$ is a random function whose average $E[X(t)]$ over a number of similar experiments will be denoted by $m(t)$. From the initial condition $X(0) = 0$ it follows that $m(0) = E[X(0)] = 0$.

Discussion of the equilibrium situation

If one assumes a perfect symmetry between the two compartments, it may be tempting to conclude that this symmetry will be reflected in the equilibrium situation, which would mean that: $m(\infty) = m^e = N/2$. However, a simple physical argument tells us that this may not necessarily be true.

Suppose that the device is vertical, that compartment A contains water (at 20 degree Celsius) and that B contains air at standard atmospheric pressure. Then, a fraction of water molecules (those whose speed is high enough) will be able to escape from A to B. In B they will form a cloud of vapor. We know that the number of water molecules in B will increase until the pressure of this cloud of vapor becomes equal to the so-called “equilibrium vapor pressure” [26] . In equilibrium the number of water molecules moving from A to B in a time interval Δt is equal to the number of molecules going in the opposite direction. In this case one does *not* have $m^e = N/2$ but rather $m^e \ll N/2$. Why is this so? The reason is that the interaction between water molecules in the vapor phase in which they are in B is much weaker than their interaction in the liquid phase of A. In other words, the geometrical symmetry of the system is broken by the difference in interaction strength in A and B and this difference is brought about merely by a difference in the numbers (and therefore the density) of molecules in each compartment.

In the previous case the argument was fairly easy and convincing because there is a clear difference between water molecules in vapor or liquid form. For animals we do not know how the interaction strength depends upon the density of the animals. For instance we know that if their number is large enough ants and bees can form clusters. One would expect in such clusters the interaction to be stronger than in a state in which the insects are randomly dispersed over a broad area. Bees can form a cluster whenever their number is higher than one hundred. Once a cluster has formed in A only few bees will move to B. This would be a situation similar to the liquid water versus vapor case. What we do not yet know is whether for ants or bees there can be intermediate situations. For instance, if there are 80 bees (not forming a cluster) in A and 50 bees in B, will the interaction be the same in A and B? If it is the same, then there will be no symmetry breaking and $m^e = N/2$. On the contrary, if the interaction is stonger in A, then there will be a symmetry breaking and $m^e < N/2$

During the time interval Δt following the initial time a number Δm of animals will move from A to B. It is natural to assume that Δm is proportional to m. Thus, the simplest equation that one can write for $m(t)$ will be:

$$\frac{dm}{dt} = -pm + q \tag{1}$$

In the equilibrium situation, $dm/dt = 0$ which implies that $-pm^e + q = 0 \Rightarrow q = pm^e$

In (1) p is a function of several physical variables among which one can mention:

- the total number of animals N
- the density ρ of the animals per square centimeter
- the average velocity v of the animals %
- the section s of the communication tube between A and B
- a parameter which defines the interaction between the animals.

---

[26] The equilibrium vapor pressure is given (approximately) by the Clausius-Clapeyron equation.

The inverse τ of p represents the time constant of the system. Therefore, by measuring p one can estimate the relevant interaction parameters (provided all other parameters are unchanged). In other words, the time constant of the system gives insight into the system's interaction strength.

Equation (1) describes a population that fluctuates around its equilibrium. The restoring force is $-pm_1$ and its time constant is $\tau = 1/p$. For the determination of the time constant it is hepful to define a new function $\hat{m} = m - m^e$. The equation which governs $\hat{m}(t)$ is:

$$\frac{d\hat{m}}{dt} = -p\hat{m} \Rightarrow p = -\frac{1}{\hat{m}}\frac{d\hat{m}}{dt} \Rightarrow p = -\frac{d\log|\hat{m}|}{dt} \tag{2}$$

It can be noted that the second expression of (2) tells us that in this model, the time constant $\tau = 1/p$ is equal to the inverse of the relative flow rate

$$\text{Time constant } = \frac{1}{\text{Relative flow rate}} \tag{2'}$$

From the last expression in (2) one can conclude that if the actual process follows this equation, the ratio

$$\frac{\Delta \log \hat{m}}{\Delta t} = \frac{\log(|\hat{m}(t_2)|) - \log(|\hat{m}(t_1)|)}{t_2 - t_1} = \frac{\log\left|\frac{\hat{m}(t_2)}{\hat{m}(t_1)}\right|}{t_2 - t_1} \tag{3}$$

should remain contant in the course of time and equal to $-p$.

If one takes $t_1 = 0, t_2 = t$ relation (3) becomes:

$$p = -\frac{\log\left|\frac{\hat{m}(t)}{\hat{m}(0)}\right|}{t} \tag{4}$$

When $m(0) = 0 \Rightarrow \hat{m}(0) = -m^e$ expression (4) leads to:

$$p = -(1/t)\log\left|\frac{m(t) - m^e}{m^e}\right| = -(1/t)\log\left(\left|1 - \frac{m(t)}{m^e}\right|\right) \tag{5}$$

When $m(t) \ll m^e$ the last expression can be approximated as:

$$p \simeq (1/t)\frac{m(t)}{m^e} \tag{6}$$

The main advantage of the last expression is the fact that one no longer has to care about taking the absolute value when, as a result of random fluctuations, $m(t)$ becomes larger than m^e.

From (6) one sees that a regression $(t, m(t)/m^e)$ will lead to an estimate of p and therefore of $\tau = 1/p$.

This procedure has been carried out in two cases:

(1) The escape experiment for fishes done by Chen and Shi.
(1) The escape experiment for fruit flies done by Wang.

In experiment (1) $m(t)$ is given for $t = 0, 1, \dots, 6$ minutes; therefore it is possible to check whether the relation $(t, m/m^e)$ is indeed linear. As the average correlation turns out to be as high as 0.95, one can conclude that the relation is indeed fairly linear. Therefore it becomes possible to estimate the time constants in a meaningfull way. For the Red Cross fishes one gets the following results.

Temp $= 15, 20, 25$ deg $\rightarrow$ time const (mn): $\tau = 4.8 \pm 0.7, \quad 2.5 \pm 0.8, \quad 2.6 \pm 0.5$

In experiment (2), we do not have several measurements in the course of time. The only available measurementa are the times T_i required to reach a state where the number of flies in the compartment that was initially empty reaches $0.9m^e = 0.9(N/2)$. Therefore we cannot check if the relation $(t, m/m^e)$ is indeed linear but nevertheless, assuming that it is, we can estimate the time constant. For total numbers of fruit flies equal to $N_i = 20, 40, 80, 160$ one observes the following times $T_i = 14, 56, 127, 220$.
From these results one gets the following estimates for the time constants:

$$N = 20, 40, 80, 160 \quad \rightarrow \text{ time constant (mn): } \tau = 6.1, 24, 55, 96$$

Because $e^{-2} = 0.14$ and $e^{-3} = 0.05$, equilibrium is approximately reached after a time interval of the order of 2τ or 3τ; therefore one is not surprised to observe that the estimated time constants are about 2 or 3 times smaller than the total time required to reach an approximate equilibrium state.

Incidentally, it can be observed that the time constant increases linearly with the total number of fruit flies: $\tau[\text{mn}] = 0.63N - 1.7$.

The same kind of technique can be used to estimate the time constants of the clustering processes described in the next section. In the experiments done by Wang, the times T_i required to reach an approximate state of equilibrium (in practice equilibrium minus 10%) were as follows for different total numbers of ants (initially in equal number on each side).

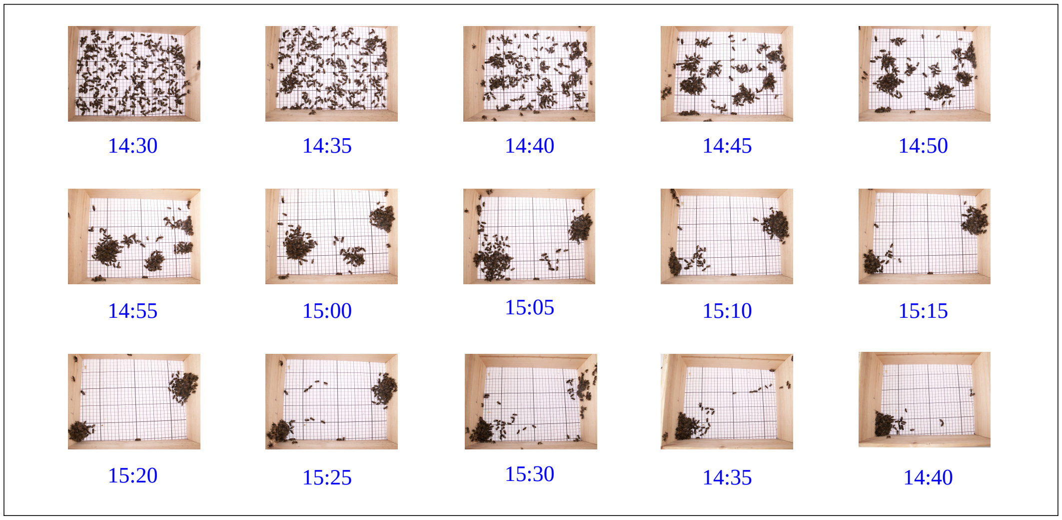
$$N_i = 200, 400, 600, 1000, 1500, 2000 \rightarrow T_i[\text{mn}] = 136, 127, 305, 168, 354, 406$$

One finds again that the time constants are a linear function of the total number of ants: $\tau[\text{mn}] = 0.064N + 50$. The slope is about 10 times smaller than previously. This means that for a given number, ants reach equilibrium 10 times faster than fruit flies. One cannot draw any clear conclusion from such a result because too many factors are different in the two experiments. For instance one can mention the size of the insects, their velocity, the section of the communication tube between the two compartments. All these factors affect the time constant.

Clustering

Some insects (and especially social insects) show a clustering behavior. By this expression, we mean that ants or bees dispersed over a given surface will tend to come together and form one or two clusters in which they touch each other. In the case of bees there will even be clustering in the vertical dimension with successive layers of bees packed on top of each other.

The clustering process is illustrated in the figure.



14:30 14:35 14:40 14:45 14:50
14:55 15:00 15:05 15:10 15:15
15:20 15:25 15:30 14:35 14:40

Fig. xx: Clustering process for bees (Apis mellifera mellifera). Altogether there were about 300 bees. Initially they were put to sleep through 5 minutes in carbon dioxide. *Source: The data are from an experiment done in July 2012 by B. Roehner and J. Darley.*

More details about this process can be found in the paper by Wang et al. (2011).

Flow rates in ant clustering

This experiment is very different from the previous one because instead of spreading over a bigger range, the ants cluster on an area that is smaller than initially.

The results shown on the graph indicate that the flow rate remains roughly constant when the initial number of ants is increased.
Indeed, when the initial number is multiplied by 10 the flow rate changes from about 1 to 0.4 which represents a ratio of 2. In these experiments the distances that the ants must cover in order to move from one side to another does not change when the initial populations are increased. What would one observe in a similar experiment in which the density is kept constant which means that the size of the containers on each side must be increased along with the initial numbers. In this experiment, the ants

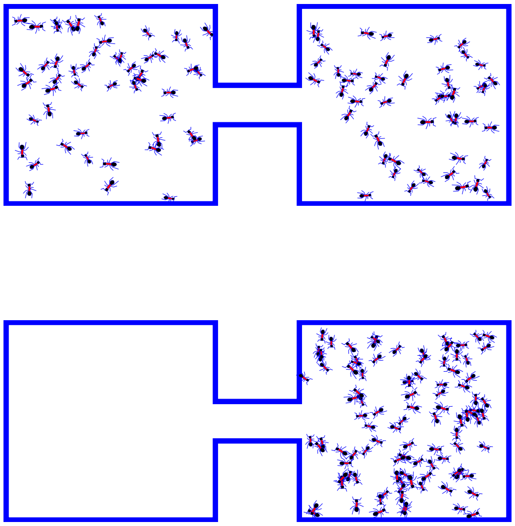


Fig. xx: Flow rates for clustering red fire ants. In contrast to the experiments with fishes, this is not an escape experiment. On the contrary, the ants move from an initial state where they are on separate sides to a state where almost all of them are on the same side. The experiment was done in August 2011 at room temperature that is to say at about 25 degree celsius. It can be seen that the net flow rate does *not* increase when the density becomes higher.

Just to give an order of magnitude of actual traffic in the communication tube, it can be observed that for an initial population of 1,000 the actual flow of ants per minute is $0.4 \times 10 \times 0.78 = 3$. This shows that the section of the communication tube is not in itself a limiting factor. Incidentally, the upward error bars are fairly high because the fluctuations in time occur at the denominator of the flow rate. *Source: The data are from an experiment done by Dr. Lei Wang.*

will have to cover longer distances in order to gather on the same side. Therefore one expects that the clustering will take a longer time. In fact, there may be a threshold above which clustering will no longer occur.

Another question raised by this experiment is the following. The diameter of the communication tube is not, at least in itself, a limiting factor for the movements of the ants. Indeed, even with 1,000 ants initially present on each side, only 3 ants per minute cross on average from one side to another.

However, the small size of the communication tube may hinder the clustering in another way. As all the ants are from the same colony pheronomes should play no role, therefore one would expect that the propensity to cluster depends upon the surface of contact between the two sides. This conjecture can be tested by repeating the experiment with communication tubes of different sizes.

Finally, it can be observed that if one tries the same experiment (that is to say same device, same initial numbers) with drosophila there is no clustering whatsoever. The population on each side remains basically the same except for temporary fluctuations.

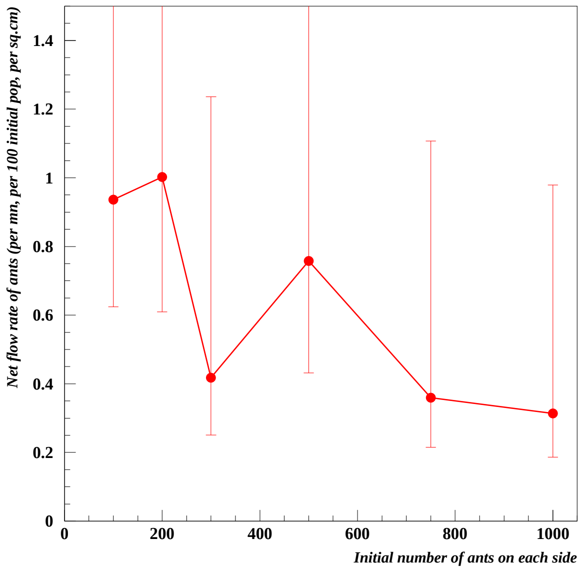


Fig.xx: Flow rate during the process of ant clustering. As in other experiments (e.g. those with fishes) the flow rate is fairly independent of the total number of ants involved. This observation is consistent with the assumption of an individual transition probability which is independendent of the population size. Indeed, under that assumption the number of ants moving from one side to the other in a given time interval would be proportional to the size of the population. *Source: The experiment was performed by Lei Wang in August 2011.*

Distribution of the velocities of small fishes

As one knows the modules V of the velocities of the molecules of a gas have a Maxwell-Boltzmann density function. of the form $f(v) = Av^2 \exp(-mv^2/2kT)$ (where A is a normalization constant). The average velocity is $E(V) = \sqrt{(8/\pi)(kT/m)}$ and the second moment is $E(V^2) = 3kT/m$ (Reif p. 268-269). From these results, it is easy to derive the variance σ^2 and the coefficient of variation $CV = \sigma/E(V)$. One gets:

$$\sigma^2 = E(V^2) - E^2(V) = \left(3 - \frac{8}{pi}\right)\frac{kT}{m} \simeq 0.45\frac{kT}{m} \Rightarrow CV = \frac{0.67/}{\sqrt{8/\pi}} = 42\%$$

Histogram of the velocities of small fishes

Now consider a collection of small fishes. They do not all swim with the same velocity. Will the coefficient of variation of their velocities be smaller or larger than the 42% just obtained for the molecules of a gas? The experiment was done at Beijing Normal University for a group of 30 female guppies (Li et al 2011). The velocities were measured by comparing successive images of a video. Note that the density of the fishes was fairly low so that the distances covered by the fishes during the time interval between two images was smaller than the average distance between the fishes. Therefore, the velocities which were measured were *real* velocities and not diffusion velocities which would have been the case if there had been several "collision" between successive images.

The results obtained (at a temperature of 22 degree celsius) from a set of 145 velocity measurements were as follows: $E(V) = 2.95$ cm/s [27], $\sigma = 1.63$ cm/s. Thus, the coefficient of variation was $CV = 55\%$.

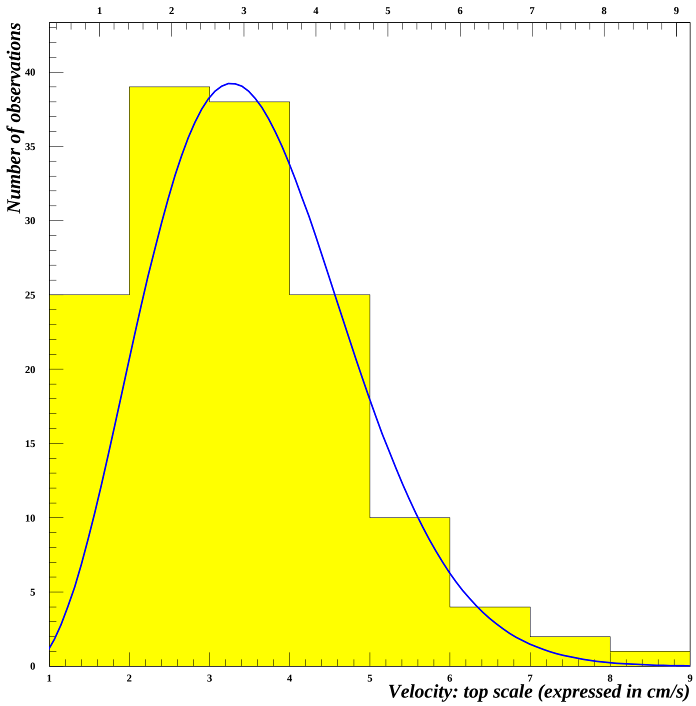


Fig. xx: Histogram of the velocities of small fishes. The fishes are 30 female guppies; the histogram is based on 145 measurements at a temperature of 22 degree Celsius. The blue curve is a Maxwell-Boltzmann distribution of expression: $f(v) = Qv^2 \exp\left(mv^2/(2kT)\right)$ where Q is a normalization factor. The adjustment lead to the following values: $Q = 12,\ m = 2,\ 2kT = 16$. *Source: Li et al. (2011); many thanks to the group leader, Mr. Li, for sending me detailed experimental data.*

In this specific case, it was of the same order of magnitude as for the molecules of a gas. However, this is perhaps no more than a coincidence for the movements of living organisms is temperature dependent

Effect of a change in temperature on the velocity of microorganisms

It is well known that a change in temperature has a marked effect on the speed of the forward movements of micro-organisms. In an article by Schneider
However, the behavior of the fishes depends upon the conditions. For instance at a lower temperature the average velocity of the fishes will be smaller. What about the coeficient of variation? At a temperature of 16 degree one gets the following results:

$$E(V) = 1.0 \text{ cm/s},\ \sigma = 1.45 \text{ cm/s} \ \Rightarrow \quad CV = 72\%$$

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[27] The confidence interval for a probability level of 95% is:
$E(V) = 2.95 \pm 1.96 \times 1.63/\sqrt{145} = 2.95 \pm 0.27$

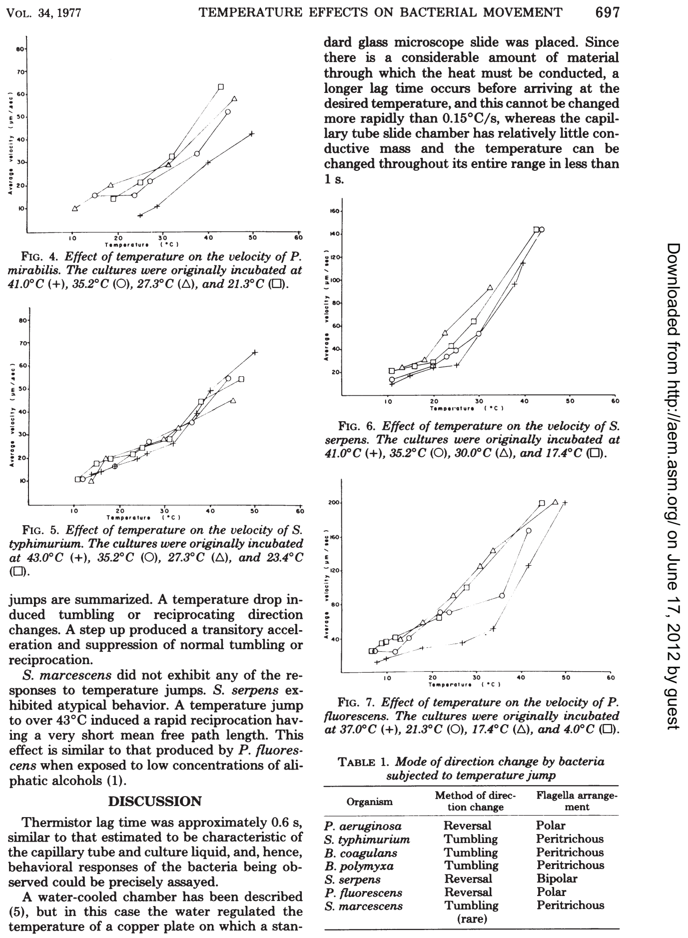

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Fig. 4. *Effect of temperature on the velocity of P. mirabilis. The cultures were originally incubated at 41.0°C* (+), *35.2°C* (○), *27.3°C* (△), *and 21.3°C* (□).

Fig. 5. *Effect of temperature on the velocity of S. typhimurium. The cultures were originally incubated at 43.0°C* (+), *35.2°C* (○), *27.3°C* (△), *and 23.4°C* (□).

jumps are summarized. A temperature drop induced tumbling or reciprocating direction changes. A step up produced a transitory acceleration and suppression of normal tumbling or reciprocation.

S. marcescens did not exhibit any of the responses to temperature jumps. *S. serpens* exhibited atypical behavior. A temperature jump to over 43°C induced a rapid reciprocation having a very short mean free path length. This effect is similar to that produced by *P. fluorescens* when exposed to low concentrations of aliphatic alcohols (1).

DISCUSSION

Thermistor lag time was approximately 0.6 s, similar to that estimated to be characteristic of the capillary tube and culture liquid, and, hence, behavioral responses of the bacteria being observed could be precisely assayed.

A water-cooled chamber has been described (5), but in this case the water regulated the temperature of a copper plate on which a standard glass microscope slide was placed. Since there is a considerable amount of material through which the heat must be conducted, a longer lag time occurs before arriving at the desired temperature, and this cannot be changed more rapidly than 0.15°C/s, whereas the capillary tube slide chamber has relatively little conductive mass and the temperature can be changed throughout its entire range in less than 1 s.

Fig. 6. *Effect of temperature on the velocity of S. serpens. The cultures were originally incubated at 41.0°C* (+), *35.2°C* (○), *30.0°C* (△), *and 17.4°C* (□).

Fig. 7. *Effect of temperature on the velocity of P. fluorescens. The cultures were originally incubated at 37.0°C* (+), *21.3°C* (○), *17.4°C* (△), *and 4.0°C* (□).

Table 1. *Mode of direction change by bacteria subjected to temperature jump*

Organism	Method of direction change	Flagella arrangement
P. aeruginosa	Reversal	Polar
S. typhimurium	Tumbling	Peritrichous
B. coagulans	Tumbling	Peritrichous
B. polymyxa	Tumbling	Peritrichous
S. serpens	Reversal	Bipolar
P. fluorescens	Reversal	Polar
S. marcescens	Tumbling (rare)	Peritrichous

Fig. xx: Effect of temperature on the speed of bacteria. Once the different curves have been normalized so that they all start from 10 micrometer by second, their slopes are close to one. *Source: Schneider and Doetsch (1977, p.).*

On the contrary, a higher temperature seems to reduce the coefficient of variation. At 26 degree, one gets $CV = 36\%$. Intuitively, this is related to the observation that at low temperature many fishes move very little whereas at a higher temperature the proportion of those which do not move is notably reduced.

Histogram of the velocities of ants

Mortality of ant colonies as a function of age

New colonies of ants are started after female ants have been mated in flight. Not surprisingly, only a fairly small percentage of the mated females succeed in starting a viable colony. Based on a comparison between the numbers of reproductives and

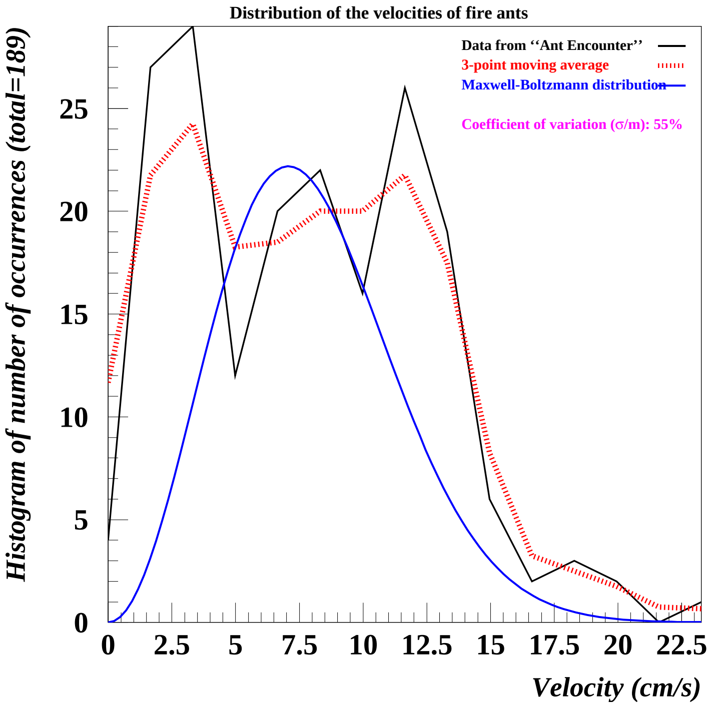

Fig. xx: Histogram of the velocities of red fire ants. The present data are for red fire ants, *Solenopsis invicta*. All parts of the trajectories that involve encounters between ants have been left out to make sure that what we consider are the free velocities and not the self-diffusion velocities. Similar observations performed on other species show that the shape of the distribution is a fairly robust characteristic. The coefficient of variation σ/m is in the interval $(0.40 - 0.55)$. The order of magnitude of the velocities appears fairly high for such small ants as the red fire ants (about 2mm in length). May be there was a mistake in the initial document either in the distance scale or in the figure for the time interval between successive positions. *Source: The data were derived from Fig. 3.1 of Gordon (2010).*

the numbers of new 1-year old colonies found to be in existence the following year, Gordon (2010, p. 79) estimates this proportion to be of the order of 10%.

An annual census of colonies in a given perimeter provides estimates of the survival rate of newly founded colonies. Such results can be summarized by a curve giving the proportion of survivors as a function of age. At this point, one should remember that it is customary to distinguish three types of survivorship curves. This is a fairly empirical classification. There is no real understanding of why humans and drosophila should be in the same group.

Taken in itself, the fact that ant colonies and high-tech corporations both belong to type 2 does not give us a better understanding. However, the fact that there is a fairly robust pattern gives a yardstick. If the colonies of another species are found to belong to another type, one would have good reasons to think that a different mechanism is at work.

It can be observed that for type 2 organisms the mortality rate is basically indepen-

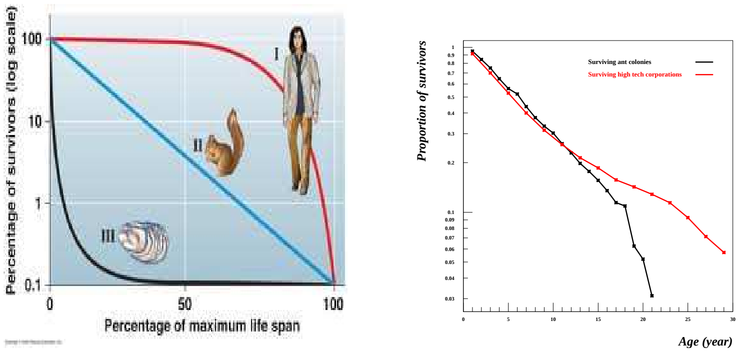

Fig. xx: Survivorship curves. The graph on the left-hand side shows three types of survivorship curves. Humans and drosophila belong to type 1. Both cases are characterized by the fact that after sexual maturity the mortality rate (which is the logarithmic derivative of the survivorship function) grows exponentially with age. Ant colonies and high-tech corporations are of type 2; for this class the mortality rate is basically constant if one forgets the high "infant mortality" of the first and second year. *Source: The ant data were derived from Fig. 4a of Gordon (2013). They refer to about 265 colonies of harvester ants (Pogonomyrmex barbatus) in New Mexico. The data for high-tech corporation mortality were derived from Chart 6 of Luo and Mann (2011, p. 9); they cover the period 1998-2009 in the United States.*

dent of age (except perhaps for one or two years after birth). This can be seen from the fact that the mortality rate is $r = [s(i) - s(i+1)]/s(i)$ where $s(i)$ denotes the proportion of survivors at age i. The ratio r is nothing else than the logarithmic derivative $r = s'/s = d \ln s/di$.
As $\ln s = \alpha i + \beta$ one gets: $r = \alpha$.

For the two other cases one does not know precisely the mathematical shape of the decrease function which means that one cannot state clear results for the behavior of the mortality rate.

Effusion model

Theoretical rates

In this section we model the movements of the fishes as an effusion effect. Our objective is to see whether or not the previous observations are compatible with such a model.

(1) The main characteristic of an effusion model is that the velocity of the particles depends only upon the temperature: $v = \sqrt{2kT/m}$. As the temperature in the two containers is the same it means that the speed of the particles on each side is also the same.

(2) We assume that initially there are N_0 particles all contained in the left-hand side of the tank. The volume of this part is noted V_1 while the volume of the part on the right-hand side is V_2. The hole connecting the two parts has a section s. Our objective is to describe what happens when the particles cross from 1 to 2. At a given moment t, there will be $N_1(t)$ particles in part 1 and $N_2(t)$ in part 2. We denote by small letters the corresponding densities: $n_1(t) = N_1(t)/V_1, \quad n_2(t) = N_2(t)/V_2$.

(2) The particles which will cross from 1 to 2 in the time interval Δt are those which are contained in a cylinder of section s and of length $v\Delta t$ and which in addition have a velocity which is in the appropriate direction. We denote by q the fraction of all the particles whose velocity is appropriate. For the moment we do not need to know q more precisely. Thus, the number of particles crossing from 1 to 2 will be: $q(sv\Delta t)n_1$. Similarly, the number of particles crossing from 2 to 1 will be: $q(sv\Delta t)n_1$.

Consequently, the net flow ΔF from 1 to 2 over the time interval Δt will be:

$$\Delta F = (qvs)(n_1 - n_2)\Delta t$$

(3) The evolution equation for $N_1(t)$ will be: $dN_1 = -dF$. The $-$ sign is due to the fact that N_1 decreases when dF is positive. Dividing by V_1 we get:

$$\frac{dn_1}{dt} = -\alpha(n_1 - n_2) \quad \text{where:} \quad \alpha = \frac{qvs}{V_1}$$

(4) Of course, n_1 and n_2 are not independent. Because the number of particles is conserved, $N_1(t) + N_2(t) = N$, which leads to the following relationship between the densities:

$$n_1(t)V_1 + n_2(t)V_2 = n_0V_1 \Rightarrow n_2(t) = k[n_0 - n_1(t)] \quad \text{where: } k = \frac{V_1}{V_2}$$

This leads to the following evolution equation for $n_1(t)$:

$$\frac{dn_1}{n_1(1+k)-n_0} = -\alpha dt$$

(5) Solving this differential equation leads to:

$$\log[n_1(1+k)-n_0k] = \alpha(1+k)t + C_1 \quad \Rightarrow n_1(1+k)-n_0k = C_2\exp[-\alpha(1+k)t]$$

In this equation C_1, C_2 are two constants. C_2 can be determined from the initial condition $n_1(0) = n_0$. This leads to $C_2 = n_0$. Thus:

$$n_1(t) = \frac{n_0}{1+k}\left[k + \exp(-\beta t)\right] \quad \text{where } \beta = \alpha(1+k)$$

(6) Now we want to compute the average flow rate from 1 to 2, namely: $\Delta f = (1/n_0)(\Delta F/V_1) = (1/n_0)\alpha(n_1 - n_2)dt$. Replacing with the expressions obtained above we get:

$$df = \frac{\Delta F}{n_0V_1} = \frac{1}{n_0}\alpha[n_1(1+k)-n_0k]dt = \alpha\left[k + \exp(-\beta t) - k\right]dt = \alpha\exp(-\beta t)dt$$

The average flow rate over a time interval T will be:

$$\bar{f} = \frac{1}{T}\int_0^T df = \frac{\alpha}{T}\int_0^T \exp(-\beta t)dt$$

Computing the integral one gets:

$$\bar{f} = \frac{\alpha}{\beta}\frac{1-\exp(-\beta T)}{T} = \frac{1}{1+k}\frac{1-\exp(-\beta T)}{T}$$

In order to make contact with the flow rate defined in the experiments the previous flow rate must in addition be normalized with respect to the section s. For the sake of simplicity we keep the same notation.

$$\bar{f} = \frac{\alpha}{s(1+k)}\frac{1-\exp(-\beta T)}{\beta T}$$

How $\bar{f}$ changes with respect to initial density, time, section of communication and velocity

When $T \rightarrow \infty$ the average flow goes to zero as would be expected. In order to get a clearer idea of how $\bar{f}$ depends on the different parameters we develop it to second order:

$$\frac{1-\exp(-\beta T)}{\beta T} \sim 1 - \frac{\beta T}{2} \Rightarrow \bar{f} = \frac{qv}{Vk}\left[1 - \frac{\beta T}{2}\right]$$

If $\beta T \ll 1$ the second term of the development can be neglected. Thus, we see that:

- $\bar{f}$ is constant with respect to the initial density n_o.
- $\bar{f}$ is constant with respect to the section of the communication tunel.
- $\bar{f}$ increases linearly with the velocity v of the particles.

Now, taking into account the second term of the development we see that $\bar{f}$ decreases when T increases.

Is long-range pheromone interaction due to diffusion?

It has been shown that in some cases insects have a very broad interaction range. This has been demonstrated in 1891 by Jean-Henri Fabre (1823-1915) for the case of a species of moth (Great Peacock Moth). Males were able to identify the odor of females or even the odor that a female had left in a cage that she occupied temporarily. Fabre's account (Fabre 1900) of his investigation is a good illustration of how the experimental methodology derived from physics can be applied to other fields. At the end of the 19th century this method was widely used in biology (see the work of Claude Bernard) or in the social sciences (see the work of Emile Durkheim).

Formula

One of the most spectacular examples of the long range of pheromone transmission is provided by the Bombyx butterfly. It is said that males can detect the pheromone emitted by the female over a distance of about one kilometer. If one assumes that the pheromone is dispersed by diffusion[28] the process is described by the diffusion equation whose solution reads (Reignier and Law 1968 p. 549):

$$C(r,t) = \frac{Q}{2D\pi r}\text{erfc}\left[\frac{r}{2\sqrt{Dt}}\right]$$

where:

- $C(r,t)$: concentration at a distance r from the release point and at a time t after the beginning of the release.
- r: distance from the origin where the pheromone is released to the point where it is detected.
- t: time
- Q: emission rate of pheromone by the female expressed in molecules per second.
- D: diffusion constant.

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[28] This assumption is indeed consistent with observations already made by Fabre. He noticed that as the males which manage to reach the female cannot fly against the wind, they must detect the pheromone diffusing toward them in a direction *opposite* to the wind. But is it really true that they cannot fly against the wind? Probably they can provided that the wind is not too strong.

For spherical particles this constant is given by the Stokes-Einstein formula:

$$D = kT/(6\pi\eta a)$$

where:
$k =$ Boltzman constant, $k = 1.4 \times 10^{-23}$m^2 kg s^{-2} K^{-1}
$T =$ Kelvin temperature
$\eta =$ viscosity, more precisely dynamic viscosity expressed in Pa.s (for air at 15 degree Celsius.
$\eta = 1.8 \times 10^5$ Pa.s $a =$ radius of the particles; pheromone molecules usually are more elongated than spherical; for instance the length of a molecule of $C_{11}H_{24}$ is about 2.5 nm, while its width is of the order of 0.1 nm; nevertheless as we will focus only on orders of magnitude, we will consider that pheromone molecules can be described as spheres with a radius around $a = 0.25$ nm.

- erfc is the complementary error function; for values of the variable larger than 3 (which is the range in which we will work here), this function is well approximated by the following asymptotic formula:

$$\text{For } x > 3 : \quad \text{erfc}(x) \simeq \exp(-x^2)/\sqrt{\pi}x$$

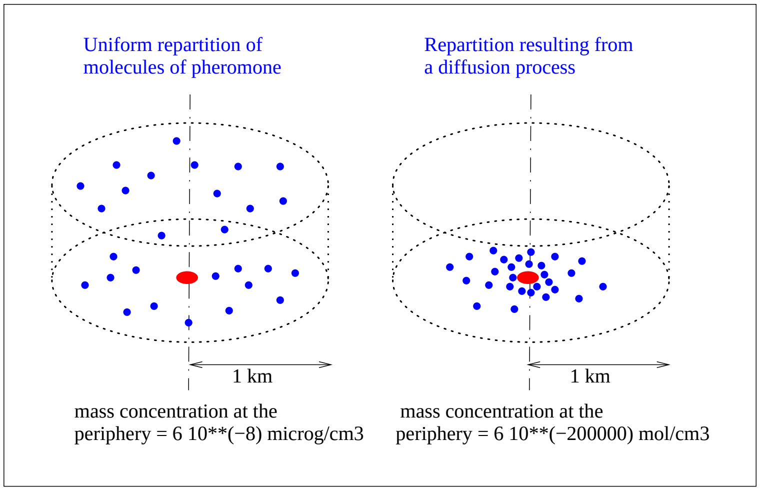

Fig. 5: Pheromone distribution. The female (e.g. a Bombyx mori) is located at the centre of the circular area while the male is supposed to be at the periphery. In our calculation we assumed that the female has been releasing her pheromone during 24 hours before the male tries to detect it.
The figure shows two different assumptions (i) The (apparently) unrealistic but simple assumption of a uniform repartition. In this case the pheromone has a concentration which can indeed be detected by the male (the smallest detectable concentration is about $10^{-12}\mu$g/cm^3). (ii) The hypothesis of a repartition resulting from a diffusion process. In this case the concentration in completely undetectable. There is a third possible assumption, namely a repartition by convection due to the wind. It should be a breeze rather than a strong wind for otherwise the average butterfly would not be able to fly against it. Slow flying butterflies can fly at a speed of 8 km/h; the fastest have a velocity of 40 km/h which corresponds to a fairly strong wind.

Uniform repartition

Before using the previous formula, we start with the simple assumption that the repartition of the pheromone is uniform. We assume that the female has been releasing her pheromone during a time $T = 24$ hours before the male tries to detect it. We suppose that the male is at a distance of 1 km of the female. The emission rate is conditioned by the evaporation rate of the pheromone. An experiment described in Traniello (1980, p. 183) gives an emission rate of $Q = 2.7 \times 10^{15}$ molecules per second. The total quantity of pheromone released during the time t is therefore $N = Qt$.

To get the volume V of the pheromone layer, one must estimate its thickness h in the vertical direction. We assume that h is of the order of the diffusion length $L_d = 2\sqrt{Dt}$. Which is of the order of one meter because (as will be seen below) beyond a few times the diffusion length the concentration is reduced to almost nothing because the decrease is exponential.
From the volume V and the number N one gets the concentration $c = N/v$. The calculation gives: $c = 75 \times 10^6$ molecules/cm^3.

The molecular weight of bombykol, the pheromone used by Bombyx more, is 475 g/mole (Regnier and Law 1968 p. 543). Thus, with the previous molecular concentration one gets a mass concentration of $c_m = 6 \times 10^{-8} \mu\text{g}/\text{cm}^3$. Observations have shown that detectable levels of sex attractant pheromones are of the order of $10^{-12} \mu\text{g}/\text{cm}^3$. Thus, detection can occur.

At first sight the present calculation may seem completely unrealistic. However, if there the air is not still but presents movements and turbulence (which is particularly important at ground level due to the many obstacles) this may well result in a fairly uniform repartition at least in the direction in which the air is moving. This will work even if the air is moving very slowly, say with speeds of the order of 1 km/h.

Diffusion

If the air is *completely* still the pheromone will only propagate by diffusion but the calculation shows that diffusion does not lead to a detectable concentration beyond a distance of a few times the diffusion length L_d[29]. The diffusion length $L_d = 2\sqrt{Dt}$ can be computed from the diffusion constant . The diffusion constant can be computed through the Stokes-Einstein formula or can be estimated from experiments (Traniello 1980, p. 183). The two methods lead to results which differ (only) by a

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[29] This results immediately from the asymptotic formula given above:

$$\text{erfc}(x/L_d) \sim \exp[-(x/L_d)^2]$$

which means that beyond a few times L_d the concentration almost vanishes.

factor of 100.

$$D_{\text{th}} = 5 \times 10^{-8}\text{m}^2/s, \quad D_{\text{exp}} = 6 \times 10^{-6}\text{m}^2/s$$

Due to the square root which occurs in its expression, the two diffusion lengths will differ only by a factor of 10. One gets $L_d = 0.1$ m and $L_d = 1.4$ m, respectively.

These values show that beyond a radius of 10 meters the concentration will be almost zero. A distance of 10 times the diffusion length leads to a factor $\exp(-10^2) \sim 10^{-44}$.

Basic preliminary experiments

In the second part of this report we delineated a number of possible experiments aimed at measuring inter-attractivity strength. However, before doing such experiments it is appropriate to perform a number of preliminary tests in order to determine the main characteristics and parameters of the living organisms under investigation.

The distribution of velocities is obviously an important characteristic of the species under consideration; as it can be measured fairly easily (see the figure) it is a good idea to be start with that. If the time interval $\Delta t = t_2 - t_1$ is small enough (for instance the image by image time intervals of a video are of the order of $1/20$ of a second) it is the real velocity which will be measured. For a longer time interval (of the order of one minute or more) it is the diffusion velocity which will be measured.

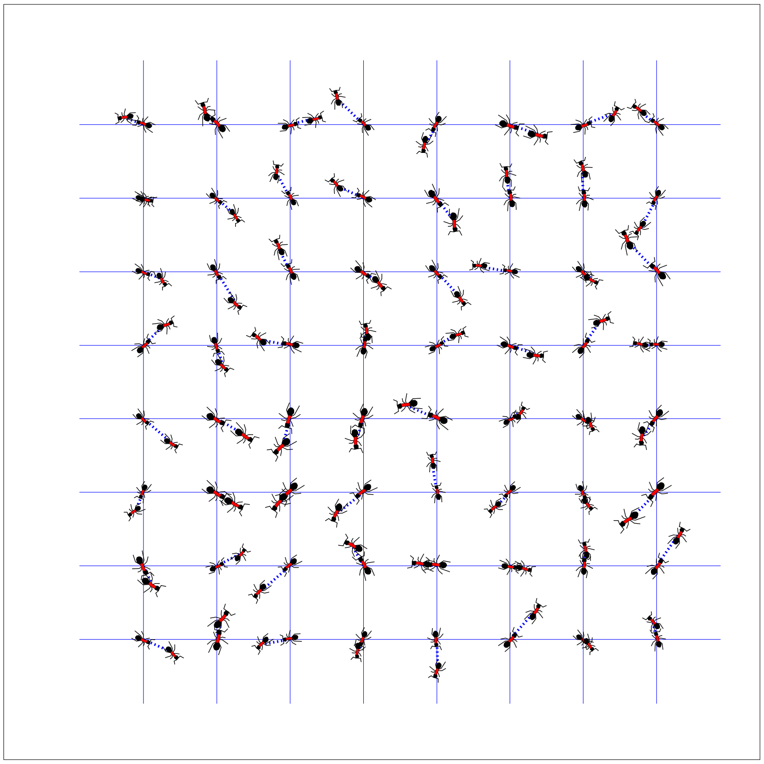

Fig. xx: Measuring the velocities of living organisms. The figure shows the superposition of two pictures taken at successive times t_1, t_2. If one denotes by d_i the distances represented by the blue broken lines, the distribution of the velocities will be given by the histogram of the numbers $v_i = d_i/(t_2 - t_1)$.

Once the diffusion velocity has been determined, it may be useful to perform a consistency check by doing the diffusion experiment shown in the figure.

An escape experiment will already give a crude idea of the inter-attractivity. Thus, there is a clear difference between the behavior of social organisms which tend to cluster in the same side of the container and non-social organisms for which the behavior is more similar to that of a gas.

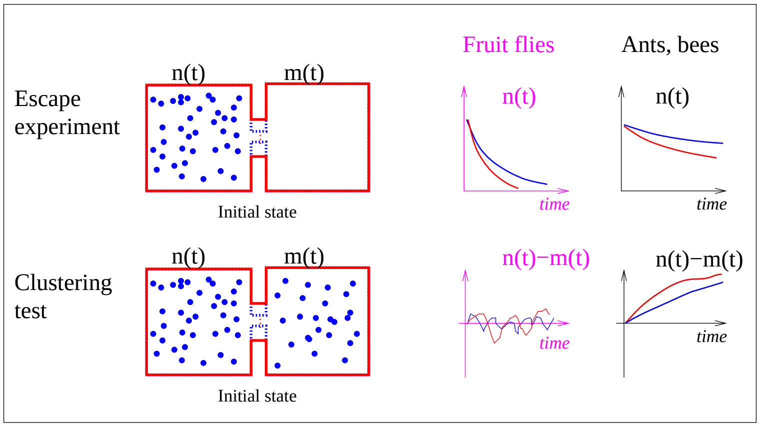

Fig. xx: Two basic tests.

Introduction

How can one formalize the question?

We want to solve the following problem.

One suspects that the elements (which in practice will be ants, bees, fishes, and so on) belonging to a group (of size n) are interdependent and one wants to characterize this inter-dependence quantitatively. To do that one must first formalize the interdependence through a specific criterion which will associate a number to each level of interdependence. Several formalizations can be proposed. One method which seems fairly natural is to describe each element i by a random variable X_i; then our question conists in measuring the degree of interdependence between the n variables X_i.

Two classes of models

One simple way to espress such an interdependence is first to compute the inter-correlations ρ_{ij} between all the pairs (X_i, X_j); then the global interdependence can be defined as the average:

$$\bar{r} = \frac{1}{n(n-1)/2} \sum_{i<j} r_{ij}$$

In this perspective, one must find a procedure which allows us to compute $\bar{r}$.

Another possible approach is to set up a full-fledged model in which the interactions between the X_i are described by a specific mechanism (e.g. interaction between nearest neighbors, global interaction and so on). This is a more risky approach for if the model's assumptions are incorrect the estimated parameters will turn out to be wrong.

Let us emphasize that the the models that will be built are not an end in themselves. They are merely tools. As a matter of fact, it would be possible to construct many models that would be appropriate enough to be adjusted to observed data in a "meaningful" way. The main purpose of the proposed models is to allow us to estimate interaction strength. Typically, parameters describing the strength of the interactions will be defined in the models and by adjusting them to experimental data we will be able to get estimates which will give an idea not only of the interaction strength but also of the characteristics of the interaction such as range and time constant.

Nedless to say, the quality of the estimates that we will get is as much (or even more) dependent on the experiments as on the model. The less noise in the experimental data, the cleaner our estimates.

In the first section we propose a fairly broad model which does not make specific assumptions about the form of the interaction. In this model the interaction is described as a global average correlation. The more positive the correlation, the stronger the attraction between the living organisms.

The second section describes a model that is more detailed in two ways.

- It is a time dependent model which will allow us to estimate time constants.
- The interactions are described in a more detailed way than in the previous model. In particular, this model allows separate estimates of the various factors which contribute to the observed behavior, such as the noise component (that is to say the analog of temperature), the attraction, the response to external shocks and so on.

Both models are analytical models.

Before describing these models we give some basic background information regarding the question of interaction strength measurements.

Background information about interaction strength

Physics methodology cannot be used for systems of living organisms

In physics it is possible to estimate interaction strength by measuring the input energy required to break up the links between molecules and atoms. Unfortunately, for living organisms this kind of method does not seem practicable. Why?
When one puts more energy into a liquid it will eventually become a gas. The gas has the interesting property of still being composed of the same molecules but with almost no interaction between them. If we raise the temperature of the liquid even more there will be a point where the molecules begin to break up into individual atoms. For water vapor for instance, whereas at room temperature only about one molecule in 10^{14} is decomposed into hydrogen and oxygen, the proportion becomes 3% at 2,200 degree Celsius and 50% at 3,000 degree. In other words, if one wants to estimate intermolecular interaction in liquid water one must measure the amount of energy necessary to transform the water into vapor at a temperature between 100 and (say) 2,200 degree. Above this temperature the molecules will be replaced by atoms in ever increasing proportion.

Is there a similar phenomenon for living organisms? First it can be observed that the greater molecular agitation at higher temperature also occurs in populations of living organisms. Indeed, as described in a previous section, the average velocity of fishes increases with the temperature of the water. However, this effect is limited to a narrow temperature interval, basically between 10 and 25 degrees. Outside this interval the physiology of the fishes is affected. When the temperature becomes too high they will die thus releasing the separate molecules which compose them in a phenomenon which is similar to the decomposition of the molecules into atoms discussed above.

Ultimately, what makes the method very effective in physics is the existence of two different states, liquid with fairly strong interaction and vapor with almost no interaction. Is there something similar in systems of living organisms?
As an analog of a liquid one can think of a cluster of bees or ants. So, the methology used in physics leads us to ask what happens when the temperature of such a cluster is increased? Is there a specific temperature (below the threshold above which the physiology of the individuals is affected) at which clusters break up into separate individuals? Answering this question is made more difficult by the fact that even at a fairly low temperature of 25 degrees, a cluster of bees has a limited duration. So, the question is less clearly defined than for water and vapor.

Apart from the breaking up methodology another possible method is to derive interaction strength estimates just by observing the behavior of a system in certain conditions. Naturally, in order to achieve a good (or at leat a reasonable) accuracy we will try to choose these conditions so as to minimize the background noise. The main challenge will be the following.
Once we behavior of the system has been documented trough a set of observations, we want to know what part of this behavior is due to interaction forces. In other words, we need to know what would be the behavior of a similar system whose elements would be independent. Such a system will serve as a means of comparison in the same way as vapor is used in physical systems.
Most often such an hypothetical system of independent elements will be defined and analyzed through theoretical arguments. That is why it is important to set up fairly simple experiments. In what follows we will mainly rely on experiments in which the elements can be in only *two states*.

More specifically, these two states will be two spatial locations. The domain containing the elements will be divided into 2 parts of same area, 1 and 2. Thus, an element i of the system will be in state 1 when it is located in part 1 and in state 2 when it is in part 2. With this definition the behavior of the system will be summarized in the number $x(t)$ of elements contained in part 1. For a specific experiment, any such function $x(t)$ will be a realization of a a *random function* $X(t)$ and our task is to derive information about the interaction strength from the properties of this function.

As one knows, the main characteristics of a random function are the following:

- Its mean: $m(t) = E[X(t)]$

- Its variance: $\sigma^2(t) = E\left[(X - m(t))^2\right]$ which represents the magnitude of the fluctuations of $X(t)$ around its mean.
- Its autocorrelation function:

$$\rho(t, r) = \frac{E\left[(X(t+r) - m(t+r))\,(X(t) - m(t))\right]}{\sigma_2(t)}$$

The autocorrelation characterizes the more or less erratic behavior of $X(t)$ in the course of time. If $X(t)$ is very erratic in the sense that the values $X(t_1), X(t_2)$ that it takes at two successive times t_1, t_2 are almost uncorrelated, then $\rho(t_2 - t_1)$ will be small. On the contrary, if these values are strongly correlated, $\rho(t_2 - t_1)$ will be close to 1.

When the mean is constant in the course of time, that is $m(t) \equiv m$, the function $X(t)$ is said to be stationary with respect to the mean.
Similarly, one can also define stationarity with respect to the two other characteristics.

- When the standard deviation is constant in the course of time, $\sigma(t) \equiv \sigma$, the function $X(t)$ will be said to be stationary with respect to the variance and standard deviation.
- When $\rho(t, r)$ depends only upon the lag r and not upon t, that is to say $\rho(t, r) \equiv \rho(r)$, the function $X(t)$ will be said to be stationary with respect to the autocorrelation.

In what follows, our interest will more particularly be focused on two aspects:

(1) The standard deviation σ
(2) The time constant τ.

We need to define more precisely what is the time constant of a system.

Definition of the time constant of a system?

Anytime that the properties of a system in the course of time are defined by an exponential function, it is possible to define the tome constant of the system. For instance, when the size $y(t)$ of a population is ruled by $y(t) = y_0 \exp(t/\tau)$, one will say that τ is the time constant of the system. This definition becomes quite natural if we consider the differential equation of which $y(t)$ is the solution.

$$\frac{dy}{dt} = \alpha x \Rightarrow \frac{dy}{d(\alpha t)} = x \Rightarrow \tau = 1/\alpha,\ t' = \alpha t = t/\tau,\ \frac{dy}{dt'} = x$$

In the last expression, α (and τ) have been absorbed into a rescaling of the time variable.

This can be seen as a fairly trivial definition and one may wonder why it is important. After all, the differential equation $dy/dt = \alpha x$ is too simple to adequately describe

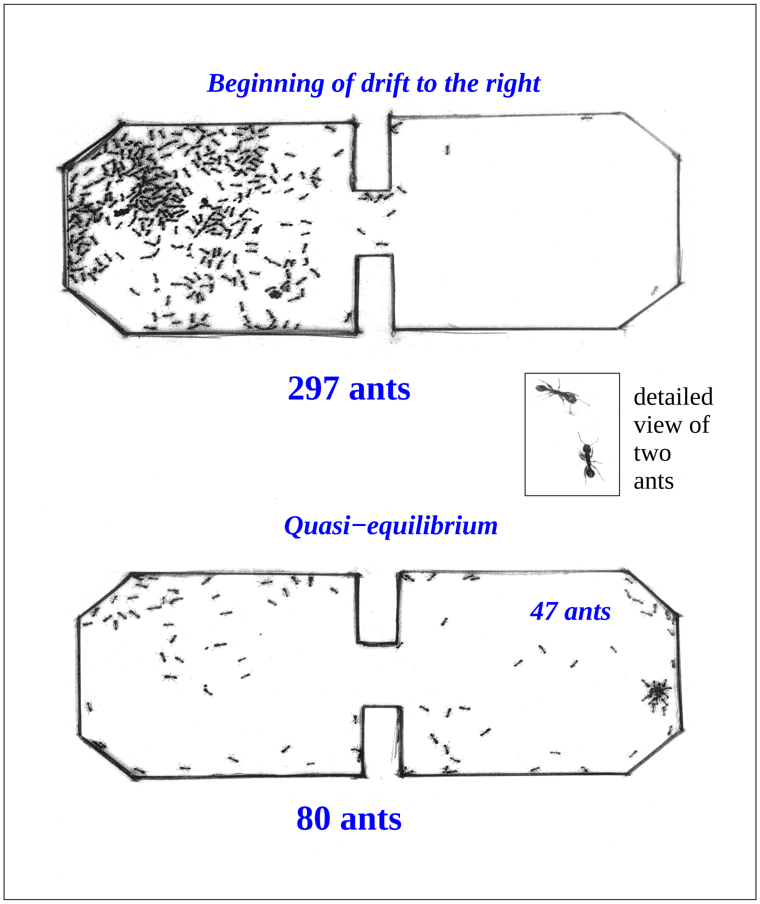

Fig. xx: Experiments with ants in a two-compartment device In the first picture, one starts with an out of-equilibrium situation. It is similar to water in a cup with no vapor molecules over it. In the course of time, some of the ants will move from left to right. Recording this process in the course of time gives a way to estimate the time constant of the system.

In the second picture there are almost as many ants on each side. However, this is not necessarily a stable equilibrium. On the right-hand side one can notice a small cluster. Such clusters appear frequently. Sometimes they grow, sometimes they do not.

any real system. Nevertheless, the importance of the notion of time constant is underlined by the two following observations.

- The notion of time constant is closely related to the notion of eigenvalue of a system. If $L(d/dx)$ denotes a differential operator, a function y_{s_i} which satisfies $L(d/dx)y_{s_i} = s_i y$ will be called an eigenfunction [30] of $L(d/dx)$ associated with the eigenvalue s_i. In the context of time dependent systems, the importance of this notion comes from the fact that the solutions of the partial differential equation $L(d/dx)y = \partial y/\partial t$ are of the form

$$y(x,t) = \sum_i c_i y_i(x) \exp(s_i t)$$

where the constants c_i will be determined from some initial condition $y(x,0) = y_0(x)$.

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[30] The terms eigenvalue and eigenfunction are built with the prefix “eigen”, a German word which means “its own” or “characteristic of”.

The expression of $y(x,t)$ shows that it has a whole set of time constants $\tau_i = 1/s_i$. However, the behavior of the system is largely controled by only a few of the τ_i. In order to prevent $y(x,t)$ from going to infinity for $t \rightarrow \infty$, the s_i must be negative or zero: $s_i = -s'_i,\ s'_i \geq 0$.
The term with $s_0 = 0$ gives the limit of $y(x,t)$ for large t. Clearly, due to the factor $\exp(-s'_i t)$, the terms containing large s'_i will decay very quickly when t increases . Thus, only the smallest values of s'_i (which correspond to the longest time constants) will have a significant contribution.
In short, the behavior of the system will be mostly controlled by the longest time constant; shorter ones can be treated as corrections.

- Even if a system does not exactly follow the previous equation, it may nevertheless be characterized by a time constant that can be obtained through the following procedure.

First, we extract τ from the expression of $y(t)$.

$$y(t) = y_0 \exp(t/\tau) \Rightarrow t/\tau = \log(y(t)/y_0)$$

Thus, the graph $(t, \log(y(t)/y_0))$ should be a straight line whose slope is $1/\tau$.
Now, suppose one has made several observations of the system at times t_k, and that the points $(t_k, \log(y_k/y_0))$ are more or less aligned along a straight line, then the coefficient of the regression line through these points will describe the time constant of the system. This procedure may work even for systems which are stochastic rather than deterministic. It is important to realize that it provides both a test of whether or not the system has a time constant and (if the test is positive) an estimate of this time constant.

- The function $y(t) = y_0 \exp(t/\tau)$ is a monotonic function. However, it is possible to define a time constant even for functions which are far from being monotonic. For instance, the number of elements in compartment 1 that we considered above may fluctuate around an equilibrium value y_e. In spite of the fact that such a function will have many ups and downs it is possible to compute its time constant.

One procedure that one can think of is to collect all monotonic parts, to apply the previous procedure to all of them and to take the average of the resulting estimates of τ. However, this procedure does not work because when $y(t)$ is close to y_e the restoring force due to the equation is small and therefore one cannot neglect the effect of the noise. Unfortunately, in practice the noise is unknown.

There is an alternative procedure which relies on the fact that the time constant of the autocorelation function (usually) is the same as the time constant of the process $X(t)$ itself. Intuitively, this makes sense as can be seen by considering two opposed situations.

- White noise on the one hand. In this case all successive fluctuations are uncorrelated which means that the curve of $y(t)$ has a great number of short fluctuations. In other words, everytime the system is displaced away from equilibrium it returns to it very quickly, a behavior which characterizes a system with short time constant. As one knows, for white noise the autocorrelation function $\rho(r)$ is equal to 1 for $r = 0$, then falls off to zero very quickly because even a small time lag shift will result in a vanishing correlation.
- On the contrary a case where $y(t)$ shows wide hills and troughs corresponds to a system with a long time constant. The autocorrelation function will decrease slowly because for the correlation between $y(t)$ and $y(t+r)$ to become small the time lag r must be larger than the average duration of the hills and troughs that is to say larger than the time constant τ.

This procedure will involve the following steps.

(1) One must select a time interval during which the series is approximately stationary for otherwise the values taken by the autocorrelation will be much affected by the trend of $y(t)$.

(2) One computes the autocorrelation for different time lags r_i.

(3) If the present model applies then the graph of $(r, \log(\rho(r)))$ should be (more or less) a straight line. The inverse of the absolute value of the slope of this line is the time constant τ of the system.

Effect of interaction strength on σ and τ

As the standard deviation σ and the time constant τ are two basic characteristics of any process, it would be useful to have an idea about how they are affected by the interaction strength. This is not an easy question. Intuition tells us very little about that. It would be desirable to rely on experimental evidence; for that purpose one would need a system whose interaction strength can be changed at will and whose standard deviation and time constant can be measured. So far, we were not able to find an appropriate case. This leaves the possibility of examining the question on models but even at this level there are few cases of analytically solvable systems with interaction. One of them, which has been studied extensively by physicists is the so-called Ising model[31]

In the Ising model, one considers n random variables σ_i which are called spins and can take only two values -1 and 1. For our purpose, we will interpret these values in the following way:

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[31] The model is named after the German-American physicist Ernst Ising (1900-1998). Under the direction of Wilhelm Lenz he studied chains of coupled magnetic moments. Because of his Jewish origin, he lost his position in 1933. Surprisingly, however, he spent the whole war in Germany and emigrated to the United States only in 1947. Until his retirement in 1976 he was a physics professor at Bradley University in Illinois. In this position, he devoted himself mostly to teaching and did not write any new research paper.

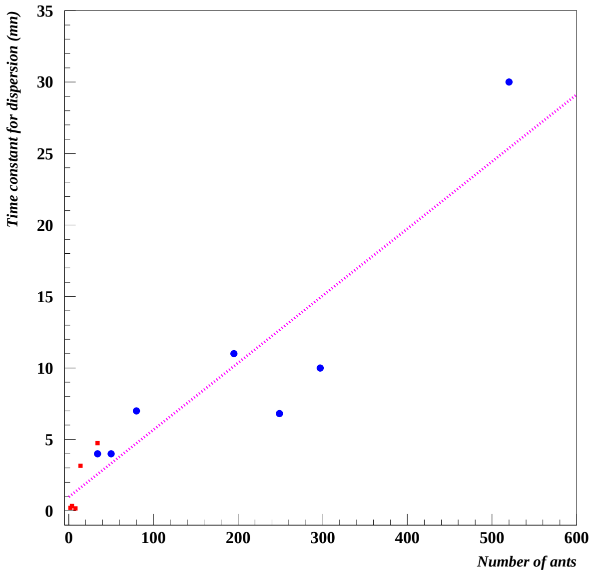

Fig. xx: Time constant of ants. In all experiments with more than 20 ants, one part of the device was initially empty. In the course of time, during a first phase ants moved into this compartment until it contained about one half of the number, then in a second phase the numbers on each side fluctuated in a fairly stationary way. The blue points are estimates based on the regression of $log(1 - y(t)/y_e)$ against time over the first phase. The red squares are estimates based on the autocorrelation function computed from the (more or less) stationary regime of the second phase.
Sometimes, especially for large populations the stationary process of phase 2 lasted only shortly and was followed by the formation of a cluster in one of the compartments. The time constants of this clustering process are given in the next graph.

> The domain available to n living organisms is divided into two parts 1 and 2. $\sigma_i = 1$ means that element i is in part 1, whereas $\sigma_i = -1$ means that it is in part 2.

If one denotes by n_1 the number of the σ_i which are equal to 1, the sum $S(n) = \sigma_1 + \ldots + \sigma_n$ will be equal to $n_1 - (n - n_1) = 2n_1 - n$. Thus, the sum of the spins is closely related to the number of elements in part 1; the later can be easily measured in our experiments
The transition probability of element i during the time interval Δt is assumed to be given by (Glauber 1963 p. 296)

$$w_i \Delta t, \text{ where } w_i = \frac{\alpha}{2}\left[1 - \frac{\gamma\sigma_i}{2}(\sigma_{i-1} + \sigma_{i+1}\right]$$

Thus, when $sigma_{i-1} = \sigma_{i+1} = 1$ (which means that both elements are in part 1) the probability for element i to move to the other part is:

- $\frac{\alpha}{2}(1 - \gamma)$ if $\sigma_i = 1$
- $\frac{\alpha}{2}(1 + \gamma)$ if $\sigma_i = -1$

We see that if $\gamma > 0$, i has a low probability to leave part 1 if it is already in part 1

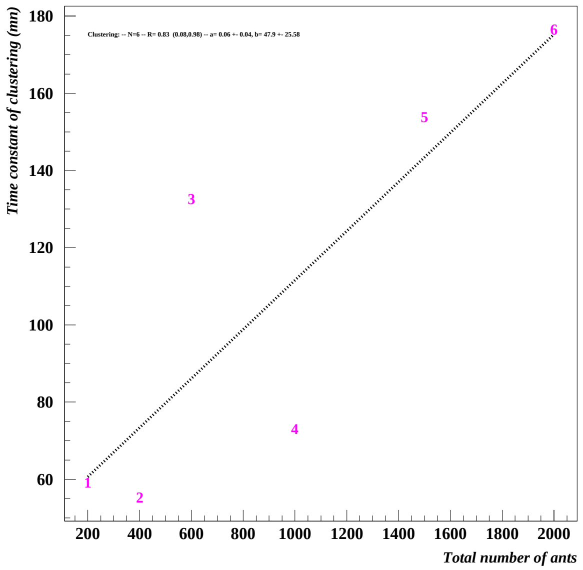

Fig. xx: Time constant as a function of the population size n for a clustering process. Initially, there were equal numbers of ants (red fire ants) in the two compartments. In the course of time a clustering process took place through which they gathered into one compartment leaving the other one almost empty (in practice compartment with a population of less than 10% of initial size).
Each data point is an average over 5 repetitions.
Comparison with the previous graph shows that time constants for dispersion are longer than time constants for dispersion. However, before drawing any conclusion one should make sure that all other conditions were similar, particularly the section of the communication channel between part 1 and 2. *Source: The measurements were made by Wang Lei in August 2011.*

but a high probability to move to part 1 if it is in part 2. it is in this sense that γ can be considered as representing the attraction strength.
The factor α controls the frequency rate of the transitions. The higher α the more transitions in a given time interval.

The formulas giving the standard deviation and the time constant as a function of γ are as follows (Glauber 1963 p. 299-301).

$$g^2 = \frac{\sigma^2\left(S(n)\right)}{\sigma^2\left(S_{\text{ind}}(n)\right)} = \frac{1+\eta}{1-\eta}, \qquad \eta = \frac{1-\sqrt{1-\gamma^2}}{\gamma}$$

$$h = \frac{\tau}{\tau_{hboxind}} = \frac{1}{1-\gamma}$$

$S_{\text{ind}}(n)$ represents the expression of $S(n)$ for independent elements, that is to say for $\gamma = 0$. Similarly, $\tau_{hboxind}$ represents the expression of τ when $\gamma = 0$.

As can be seen on the graph, both g and h increase with the attraction strength and tend toward ∞ when $\gamma \rightarrow 1$.

Can one understand intuitively why the time constant of the system increases along with the interaction strength?

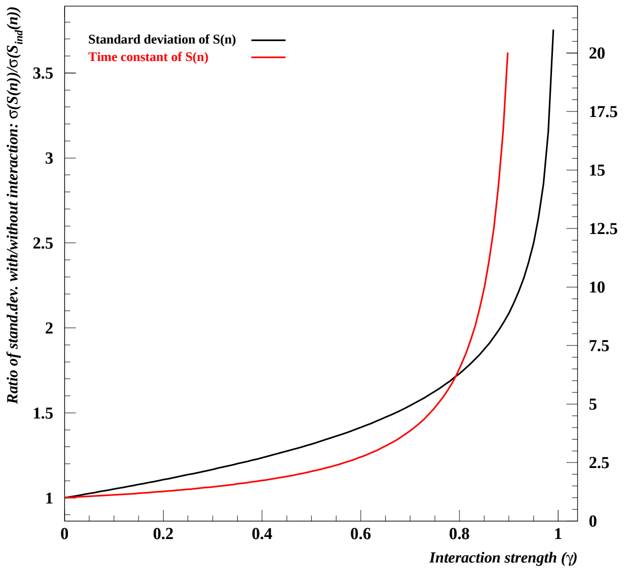

Fig. xx: Effect of changing interaction strength in the Ising model. In the Ising model the elements are supposed to form a linear chain. The parameter γ represents the interaction strength between element i and its two neighbors $i-1$ and $i+1$. For $\gamma > 0$ element i has a propensity to imitate its two neighbors. In physics, such a disposition is referred to as ferromagnetism. The graph shows the standard deviation of the sum $S(n) = \sigma_1 \ldots \sigma_n$ relative to its value when $\gamma = 0$. The inverse of the time constant is the coefficient of time in the exponential decrease of $S(n)$. It can be seen that both the standard deviation and the time constant increase with the interaction strength.

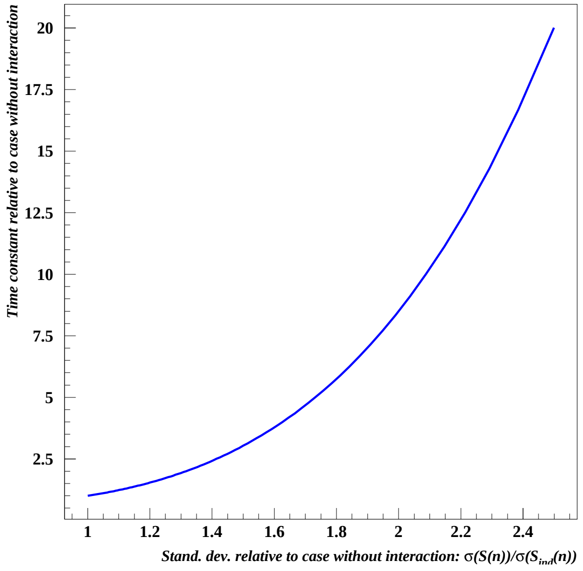

Fig. xx: Relation between the time constant and standard deviation in an Ising model. It is interesting to observe that one has a very similar relationship between the time constant and standard deviation of a first-order auto-regressive process (that is to say a discrete finite difference equation with a noise term in the right-hand side) in spite of the fact that this equation has a completely different origin and meaning. In other words, this relationship seems to have a fairly broad range of validity.

At least one can easily understand why for independent elements the time constant of the system will be independed of its size. Consider the sum $S(t) = X_1(t) +$

$\ldots + X_n(t)$ and suppose that initially all elements are in part 1. This means that initially all ants are on the same side number 1. $S(0) = n$. How long will it take for the system to return to its quasi-equilibrium state $S_e \simeq n/2$? If the ants move independently from one another and independently of their initial position, during the first time interval Δt each ant will select completely randomly the compartment in which it will be at the end of time Δt. As one knows, the sum $S(1)$ will follow the binomial distribution which means that at the end of the first step with a high probability we will have $S(1) \simeq n/2$. The larger n the closer $S(1)$ will be to $n/2$ in relative terms. In short, the time constant will be just one step and this result will hold independently of the value of n.

As will be seen below, the fact that there is a cross-correlation between the X_i does not change the result of the previous argument.

Cross-correlation model

We will introduce this models by steps. First we explain the idea of the model, then we discuss how it should be used for the purpose of estimating the average cross-correlation.

General idea of the model

Consider a container which contains n ants. In this container we define a subset A and we count in the course of time the number $n_A(t)$ of ants that are found in A . For instance, we can record these numbers every 15 seconds over a period of one hour which will give $60 \times 4 = 240$ numbers. From these numbers we can compute their average m and their standard deviation σ [32].

The question is: can we learn something about the interaction between the ants from the values of m and σ?
Intuitively one would expect that if the n elements are highly correlated the standard deviation will be higher than when they are not correlated at all. Why?

If the elements are completely correlated they will move all together into A or out of A. Thus, $n_A(t)$ will make big jumps as seen in the graph below. On the contrary, if the elements are not correlated at all, $n_A(t)$ will change by small steps of $0, 1, 2, \ldots$ as shown in the picture. A jump of 9 can happen but it will be an exceptional event. Indeed, it will have the same likelihood as obtaining 9 heads by throwing 9 coins.
In other words, one expects that the correlation between the elements will be more or less proportional to the standard deviation. The higher the standard deviation,

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[32] The average and the standard deviation will be fairly independent of the time interval between successive observations because changing this interval amounts to changing the sampling time of the function $n_A(t)$. If $n_A(t)$ is fairly stationary, m and σ will also be fairly independent of the total length of the record.

the higher the correlation. In other words, by measuring the standard deviation of $n_A(t)$ we can estimate the correlation which is itself a measure of the inter-attraction between the ants.

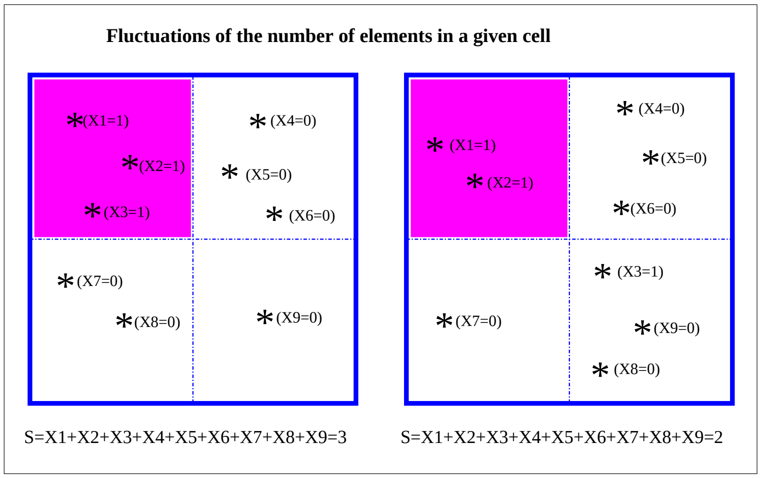

Fig. xx: Fluctuation of the number of elements in a subset A (magenta colored) of the whole domain. Each star represents an element. To each of them one can associate a random variable which will be equal to 1 when the element belongs to A and to 0 otherwise. With this definition the sum S will count the number of elements in A and the fluctuations of the random variable S will represent the fluctuations of the number of elements counted in A in the course of time.

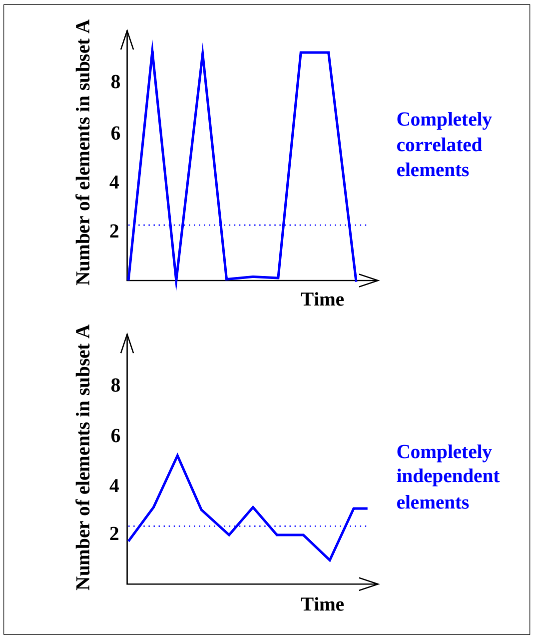

Fig. xx: Fluctuations of the number $n_A(t)$ of elements in a subset A of the whole domain in two special cases. When the movements of the elements are completely correlated all 9 will move to A or out of A at the same time which will result in big fluctuations. On the contrary, when the elements are completely independent from one another, the fluctuations of $n_A(t)$ will be fairly small.

Main formula

More precisely, the method relies on the following proposition.

Proposition 1: Standard deviation of a sum of cross-correlated variables. We consider a sum S_n of n identically distributed random variables X_i of mean m and standard deviation σ. We assume that between $X_i, X_j, i \neq j$ there is a cross-correlation r_{ij}. The average of all cross-correlations is denoted by $\overline{r}$:

$$\overline{r} = \frac{1}{[n(n-1)/2]} \sum_{i \neq j}^{n} r_{ij}$$

Then, the variance of $S_n = X_1 + \ldots + X_n$ is given by:

$$\sigma^2(S_n) = n\sigma^2[1 + (n-1)\overline{r}]$$

Proof

We proceed in several steps.

For the sake of simplicity we first consider the average of a sum of three correlated random variables X_1, X_2, X_3 of mean m and identical standard deviation σ. Our objective is to compute the standard deviation of:

$$S_3 \quad S_3 = X_1 + X_2 + X_3$$

By definition of the variance one gets: one gets:

$$\sigma^2(S_3) = E\left[(S_3 - E(S_3))^2\right]$$

One knows that the expectation of a sum of random variables is always equal to the sum of the expectations, whether the variables are correlated or not. Thus: $E(S_3) = E(X_1) + E(X_2) + E(X_3)$. Consequently:

$$\sigma^2(S_3) = E\left[(\sum_{i=1}^{3} \hat{X}_i)^2\right], \quad \text{where: } \hat{X}_i = X_i - E(X_i)$$

The mean of the variable $\hat{X}_i$ is equal to zero and it has the same standard deviation σ as X_i. Thus,

$$\sigma^2(S_3) = \sum_{i=1}^{3} E(\hat{X}_i^2) + 2\left[E(\hat{X}_2\hat{X}_3) + E(\hat{X}_3\hat{X}_1) + E(\hat{X}_1\hat{X}_2)\right]$$

We express the expectations of the products by introducing the coefficient of correlation of the X_i:

$$r_{12} = \frac{E\left[(X_1 - E(X_1))\,(X_2 - E(X_2))\right]}{\sigma(X_1)\sigma(X_2)} = \frac{E(\hat{X}_1\hat{X}_2)}{\sigma^2}$$

Thus:

$$\sigma^2(S_3) = 3\sigma^2 + 2\sigma^2(r_{23} + r_{31} + r_{12})$$

Introducing the mean of the r_{ij}, $\overline{r} = (r_{23} + r_{31} + r_{12})/3$
we obtain:

$$\sigma^2(S_3) = 3\sigma^2[1 + 2\overline{r}]$$

This formula has an obvious generalization to an arbitrary number n of random variables:

$$\sigma^2(S_n) = n\sigma^2 g^2 \quad g = \sqrt{1 + (n-1)\overline{r}} \tag{3.1b}$$

where:

$$\overline{r} = \frac{1}{[n(n-1)/2]} \sum_{i \neq j}^{n} r_{ij}$$

Interpretation of the coefficient g

What is the significance of the coefficient g?
Under the assumption that the X_i are independent (which means that they are also uncorrelated) the variance of S_n would be n times the variance of X_i that is to say $\sigma_i^2(S_n) = n\sigma^2$. In other words, g is the ratio of the standard deviation of correlated variables to the standard deviation of uncorrelated variables:

$$g = \frac{\sigma(S_n)}{\sigma_i(S_n)}$$

It can be noted that if $\overline{r} < 0$, the standard deviation of the correlated variables will be *smaller* than the standard deviation of the independent variables. To what practical situation would this correspond?

To get a better insight let us assume that there are only two living organisms ($n = 2$) that the total area has been divided into only two parts ($p = 1/2$) and that $\overline{r} = r_{12} = -1$. The fact that the correlation is -1 means that when the variables X_1 and X_2 will always take "opposite" values[33]. In other words, when 1 is in A, 2 will be outside A and when 1 leaves A element 2 will enter A. Such a behavior corresponds to a situation in which the two elements do not wish to be together. One can think of a prey-predator situation in which the prey tries to avoid the predator.

As our main objective is to estimate attraction forces which correspond to $\overline{r} > 0$, we will not be concerned with the case $\overline{r} < 0$.

Special cases

It is enlightening to apply the previous formula to a number of special cases.

(1) When the r_{ij} are all equal to zero $g = 1$ and we get $\sigma^2(S_n) = n\sigma^2$ which is the standard result for independent variables. Indeed, as is well known, in the case of independent variables the variance of a sum is the sum of the variances.

(2) On the other hand, $\overline{r} = 1$ implies that *all* the r_{ij} are equal to 1. In this case the three variables are identical (with probability 1) and one gets: $\sigma(S_3) = 3\sigma(X_1) = 3\sigma$ in agreement with the above result.

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[33] The values assumed by X_1, X_2 are 0 and 1 which means that they are not really opposite in the arithmetical sense. If we define $X_i' = X_i - 1/2$, then X_i' will take on the opposite values $-1/2$ and $1/2$. However, in this case $S = X_1' + \ldots X_n'$ will no longer count the number of living organisms which are in A but will be proportional to the difference of those in A and those not in A.

(3) The previous formula apply in a general way to any random variables X_i. For the analysis of experiments with living organisms, the variables X_i have a specific meaning which gives them the following characteristics:

$$E(X_i) = P\{i \in A\}1 + P\{i \notin A\}0 = p$$

$$\sigma = E(X_i^2) - E^2(X_i) = P\{i \in A\}1^2 + P\{i \notin A\}0^2 - p^2 = p - p^2 == pq, \quad \text{where} q = 1 - p$$

Thus, the expression of $\sigma^2(S_n)$ leads to:

$$\sigma^2(S_n) = npq[(n-1)\overline{r} + 1]$$

As an illustration let us apply this formula to the case corresponding to the top graph in the previous figure. With $\overline{r} = 1$ one gets:

$$\sigma^2(S_n) = n^2 pq \Rightarrow \sigma(S_n) = n\sqrt{pq}$$

The result is reasonable because when $\overline{r} = 1$ all the variables X_i are identical (with probability 1) and $S_n = nX_1$ from which results that $\sigma(S_n) = n\sigma(X_1) = n\sqrt{(}pq)$. With $n = 9$ and $p = 1/4$ one gets: $\sigma(S_9) = (9/4)\sqrt{3} \simeq 3.9$

Alternatively $\sigma^2(S_n)$ can also be written:

$$\frac{\sigma^2(S_n)}{npq} = (n-1)\overline{r} + 1$$

This expression leads to a methodology for estimating the average cross-corelation which is described in the following proposition.

Experimental methodology

Proposition 2: How to estimate the average cross-correlation The average cross-correlation $\overline{r}$ can be estimated by taking the following steps:
1) One defines an area A which is a fraction p of the whole domain occupied by n living organisms.
2) One counts in the course of time the numbers $n_A(t)$ of living organisms which are in A and one computes the experimental values of the mean m_e and variance σ_e^2 of $n_A(t)$.
3) Under the assumptions of the cross-correlation model the numbers $n_A(t)$ are represented by the random variable S_n.; thus, σ_e^2 will be represented by $\sigma^2(S_n)$.
4) Consequently, if one repeats these measurements for various numbers n_k of living organisms, the variance of $n_A(t)$ should follow the following expression:

$$\frac{\sigma^2(S_{n_k})}{n_k pq} = (n_k - 1)\overline{r} + 1$$

which means that $\overline{r}$ will be the slope of the regression $n-1, \sigma_e^2)/npq)$.
5) Similarly, for given n one repeats these measurements for areas of various sizes for which the fraction p takes the values p_k the variance of $n_A(t)$ should follow the following expression:

$$\overline{r} = \frac{\sigma^2(S_n)}{n(n-1)p_k q_k - \frac{1}{n-1}}$$

which means that $\overline{r}$ will be the average of the quantity on the right-hand side.

Implication of asymmetric observations?

It can be noticed that so far we did not make use of the mean m_e of the observations $n_A(t)$. The reason is very simple. According to the present model the mean should always be given by: $m_e = E(S_n) = nE(X_1) = n/p$. For instance, if $n = 200$ and if the whole domain occupied by the living organisms has been divided in only 2 parts so that $p = 1/2$, one should have $m_e = 100$. Needless to say, m_e will never be exactly equal to 50 because of inevitable statistical fluctuations. However, such fluctuations should remain compatible with the order of magnitude of σ_e. This is not always the case.

As an illustration, let us mention the following observation recorded with ants: $n = 195$, $m_e = 58$, $\sigma_e = 12$. In this example, $n/2 - m_e = 195/2 - 58 = 39 = 3.3\sigma_e$. For variables which have a gaussian distribution (as is implied by our model), a fluctuation of 3.3σ has a probablity as low as 10^{-3}. Here, however, it is not a fluctuation which reaches this value but the mean itself. Clearly, such an observation is not compatible with the assumptions of our model. Unfortunately, this kind of observation is the rule rather than the exception. How can this be understood?

Before discussing this point in greater detail, it is important to emphasize that this asymmetry seriously affects the determination of $\overline{r}$. Why?

The standard deviation of a random variable depends on the frequency and amplitude of the fluctuations but the most basic factor is its very order of magnitude. What we mean is that, except in exceptional circumstances, the standard deviation of a variable which flutuates around 100 is usually higher than the one of a variable which fluctuates around 1. In other words, an abnormally low mean will artificially reduce the standard deviation σ_e which will result in underestimating g and thus $\overline{r}$. On the contrary, an abnormally high mean will lead to an overestimated $\overline{r}$. So, this issue regarding the mean is quite an essential point.

Simulation

In order to illustrate how the present model is supposed to work we present results provided by a simulation. This simulation involved the following steps.

(1) First we need to built a set of interdependent random variables. To this end we start with a set of independent random variables Z_i and we define new variables X_i as linear combinations of the Z_i. We have been using the Choleski procedure to produce variables whose cross-correlations are all equal. In this case $r_{ij} = r$ for all pairs. As an illustration we give the matrix form of these linear combinations for $n = 2$ and $n = 3$.

$$\begin{pmatrix} X_1 \\ X_2 \\ X_3 \end{pmatrix} = \begin{pmatrix} 1 & 0 & 0 \\ r & \sqrt{1-r^2} & 0 \\ r & r\sqrt{\frac{1-r}{1+r}} & \sqrt{1-\frac{2r^2}{1+r}} \end{pmatrix} \begin{pmatrix} Z_1 \\ Z_2 \\ Z_3 \end{pmatrix}$$

For the purpose of the simulation the random variables which appear in these expressions will be replaced by m-dimensional vectors. As a result, this step gives a set of n correlated vectors each of dimension m:

$$X_i(t),\ i = 1, \dots, n, \quad t = 1, \dots, m,\ i \neq j : \text{cor}(X_i, X_j) = r$$

(2) The second step consists in checking if the random variables X_i have the properties that one expects. This is done in the following graphs. The first set of graphs shows the trajectories of each element. One can see that when r is close to one the trajectories are fairly parallel. On the contrary, when r is close to zero they are almost independent. In practice, the trajectories of individual elements cannot be observed for that would require a different marker on each and every element. The second set of graphs shows what can actually be observed, namely a set of successive pictures of the whole population.

(3) Now we come to the methodology for measuring r. As explained earlier, the methodology that we suggest is to measure the fluctuations of the number of elements in a subset A of the whole container.

The following table shows the estimates obtained in this way. It can be seen that the ratio g^2 defined previously increases with the number of elements.

It is true that in the present case the estimates are fairly imprecise but one must keep in mind that these estimates were obtained through a regression on only 4 points. Two interesting conclusions can be drawn. (i) It is important that the time-series defining the variables X_i are as long as possible. Here we have taken $m = 500$; for smaller values of m the imprecision would be even higher. (ii) the weaker the correlation the more difficult it is to to measure r because in such cases the effects of the cross-correlation are buried in the noise-background.

(4) A more direct procedure would be to compute the correlations between all pairs of trajectories. As already said, in practice it is in fact not possible to observe

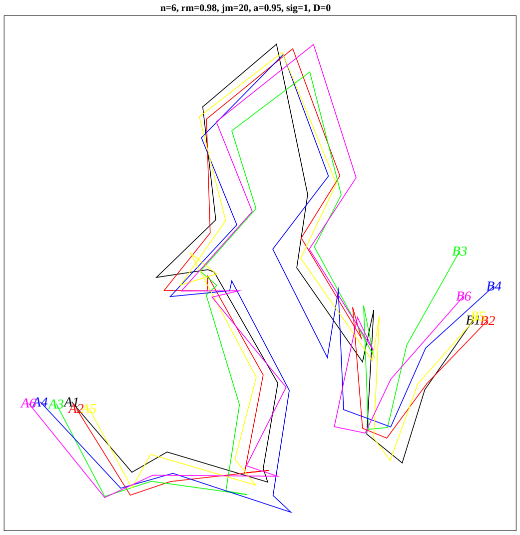

Fig. xx: Simulation of a process with high cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.98. The $A_i,\ i = 1, \ldots 6$ designate the starting points of the trajectories while the $B_i,\ i = 1, \ldots 6$ are the end points.

For this graph as well as for the following graphs the trajectory of each of the 8 elements follows an autoregressive process $X(t) = aX(t-1) + B(t)$ where $B(t)$ is a random variable which represents the noise; $a = 0.95$ which implies that the process has a fairly large time constant (that is to say a long memory).

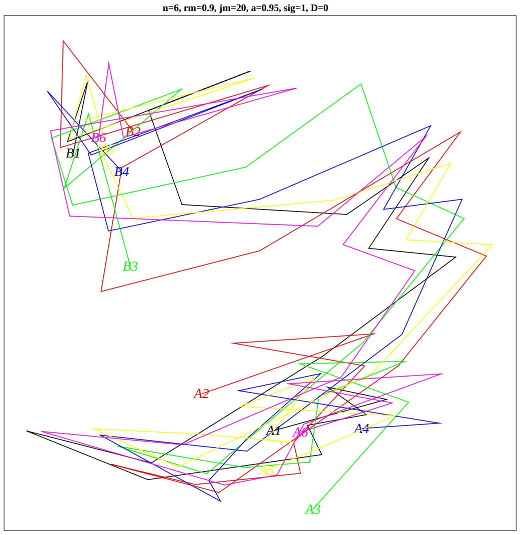

Fig. xx: Simulation of a process with medium cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.90.

these trajectories. However, in the simulation the individual trajectories are well defined which makes it possible to test this procedure. Naturally, as this method uses a much greater amount of information one expects a better accuracy. One gets the following estimates:

$$r = 0.90 : x \text{ variables } r_{\text{x-est}} = 0.91 y \text{ variables } r_{\text{y-est}} = 0.88, \quad r_{\text{xy-est}} = 0.89$$

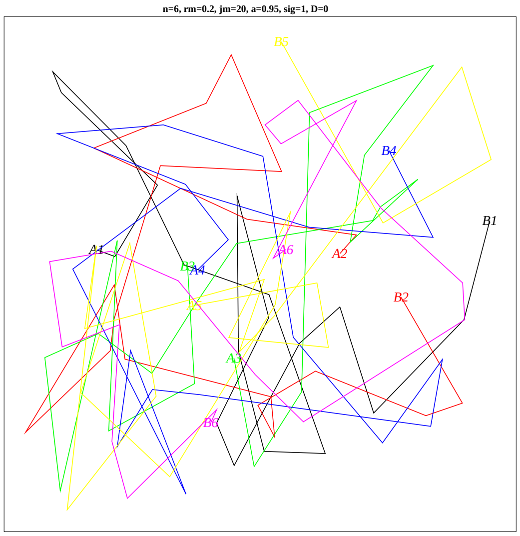

Fig. xx: Simulation of a process with low cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.20.

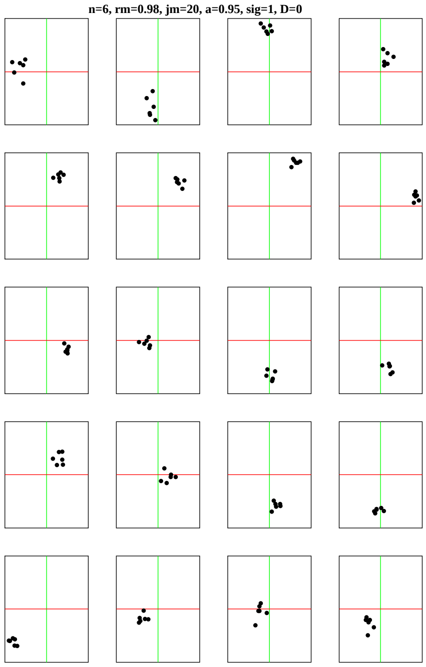

Fig. xx: Simulation of a process with high cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.98.

$$r = 0.60 : x \text{ variables } r_{\text{x-est}} = 0.64 y \text{ variables } r_{\text{y-est}} = 0.63, \quad r_{\text{xy-est}} = 0.63$$

$$r = 0.20 : x \text{ variables } r_{\text{x-est}} = 0.33 y \text{ variables } r_{\text{y-est}} = 0.17, \quad r_{\text{xy-est}} = 0.25$$

It can be seen that the accuracy is indeed much better.

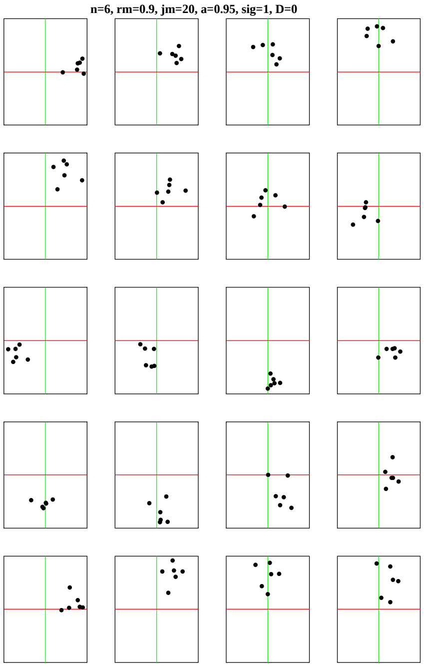

Fig. xx: Simulation of a process with medium cross-correlation. The cross-correlation between the 6 elements is 0.90. This figure (as well as the following ones) picture their positions on 20 successive time steps.

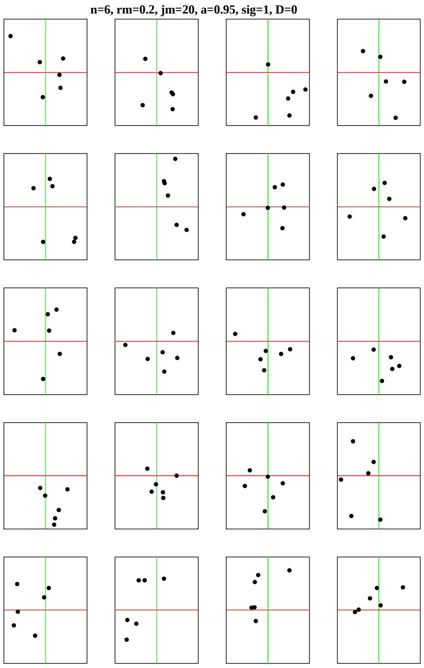

Fig. xx: Simulation of a process with low cross-correlation. The cross-correlation between the 6 elements is 0.2.

How to deal with asymmetric observations: first method

The description given by our model implies that if the total area is divided into two parts A_1, A_2. none is favored. This means that the probablity to be in A_1 should be

Table Estimates of the cross-correlation based on simulated data

Cross-correlation r_{exact}	n	g^2 method 1	g^2 method 2	Slopes of regression lines r_{est}
0.90	3	2.48	2.90	
	4	2.91	4.52	
	5	4.16	5.32	
	6	4.45	4.53	
				$0.72 \pm 0.25,\ 0.57 \pm 0.75$
0.60	3	1.75	1.89	
	4	2.24	2.46	
	5	2.91	3.30	
	6	3.71	4.39	
				$0.65 \pm 0.10,\ 0.83 \pm 0.16$
0.20	3	1.24	1.69	
	4	1.75	2.18	
	5	1.62	1.79	
	6	1.47	1.90	
				$0.056 \pm 0.2,\ 0.02 \pm 0.2$

Notes: n is the number of elements in the population. g^2 is the ratio of the observed variance to the variance for uncorrelated variables. Method 1 refers to the method in which it is the probability p which is adjusted before g^2 is computed, whereas in method 2 it is the number of active elements which is adjusted prior to computing g^2. The column "Slopes of regression line" refers to the regression $(n-1, g^2)$; the first and second numbers are the slopes for method 1 and 2 respectively.

the same as the probability to be in A_2. If it is not the case, there must be some kind of asymmetry. One can think of (at least) two possible causes of asymmetry.

(1) If the number counted in A_1 is much larger than $n/2$, it may be because for some reason(s) (usually unknown to us) the ants prefer to be in A_1. For instance, if there is a dead ant in A_2 this part may be avoided[34]. If this is the case, it means that if A represents a fraction p of the total area, the probability to be in A should not be taken as equal to p but rather as equal to $p' = m_e/n$. For instance, in the previous example where $n = 195$ and $p = 0.5$, one gets $p'n = m_e = 58 \Rightarrow p' = 58/195 = 0.30$.

In short, in this methodology the theoretical variable p will be replaced in all the formulas of Proposition 2 by the adjusted parameter $p' = m_e/n$.

(2) A second possible cause is the fact that some individuals just do not move. One can say that they are "frozen". It is to this case that we turn now.

How to deal with asymmetric observations: second method (frozen elements)

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[34] It should be noted that at this point this remains a fairly hypothetical reason. We did not try to test it by putting several dead ants on one side. In fact, we did not wish to engage in such a direction because it seems a hopeless task to try to find out what are the parameters which rule the behavior of the ants. Moreover, the "frozen ant" mechanism that we discuss later on seems simpler and more satisfactory anyway.

On using the previous method one does not have to care about the cause of the asymmetry. However, observations show that a fairly common cause is simply the fact that some of the living organisms remain motionless. If they were in subset A initially, they will remain there during the whole duration of the observation. Similarly, if they were not in A initially, they will remain outside of A all along. As they never change side, these elements can be said to be "frozen". On the contrary, the elements which move in and out of A will be called active elements.

If one assumes that there are n' active elements, the sum S can be written as follows:

$$S_n = S_{n'} + f_A, \text{ where: } S'_n = X_1 + \dots X'_n, \quad f_A = X_{n'+1} + \dots X_n$$

Whereas S' is a random variable, f_A is a deterministic constant which is equal to the number of frozen elements located in A. Thus, the variance of S_n becomes:

$$\sigma^2(S_n) = E\left[(S_n - E(S_n))^2\right] = E\left[(S_{n'} + f_A - E(S_{n'}) - f_A)^2\right] = \sigma^2(S'_n)$$

which shows that our previous calculation applies here as well provided n is replaced by n'.

$$\sigma^2(S_n) = n'\sigma g^2, \quad g = \sqrt{1 + (n'-1)\overline{r}}$$

So, the only question which remains is how to determine n'. In fact, there are 3 unknown numbers: n', the number of frozen elements in A that we have denoted by f_A, and the number of frozen elements that are not in A which will be denoted by $f_{\bar{A}}$. Although we only need n', this number can only be found together with the two other unknown numbers.
At first one might think that there can be a way to determine these numbers from evidence based on the means in A and $\bar{A}$. This is not the case, however, for a reason which is explained below.

As the question cannot be solved in a general way we will be content with examining two special cases which are of special practical significance. For the sake of simplicity, in the following discussion it will be assumed that $p = 1/2$.
(1) One major cause of frozen elements occurs when ants or bees cluster together. If the cluster is formed in A this will result in a big f_A. As $S_n = S_{n'} + f_A$ we see that this will result in the fact that m_e (which is the observed value of $E(S_n)$) will be fairly large and in particlar larger than $n/2$, the expected value in the absence of any frozen element. Consequently, we will consider the fact that $m_e > n/2$ as indicating that a cluster has formed in A and none outside A. In such a case almost all the frozen elements are in A which means that $f_A \simeq n - n'$. Thus one gets:

$$E(S_n) = E(S'_n) + f_A \simeq E(S'_n) + (n-n')1 \Rightarrow m_e = n'/2 + n - n' \Rightarrow n' = 2(n - m_e)$$

In the general case, the last result would take on the form: $n' = (n - m_e)/(1-p)$ and this case will be signaled by the fact that m_e is substantially larger than np.

(2) On the contrary, if the cluster is formed outside of A then almost none of the $n-n'$ frozen elements will be in A which means that

$$S_n == E(S'_n) + f_A \simeq S_{n'} + (n-n')0 \Rightarrow m_e = n'/2 \Rightarrow n' = 2m_e$$

In the general case, the last result would take on the form: $n' = pm_e$ and this case will be characterized by the fact that m_e is substantially smaller than np

(3) Finally, one must consider the intermediate case in which the number of frozen elements is approximately the same in A and outside of A. This may happen when there are two clusters, one A and the other in $\overline{A}$. It can also happen in the absence of any cluster when the individuals which are frozen (or at least somewhat "sleepy") are distributed uniformly in the whole population. Under that fairly natural assumption: it makes sense to assume that the sleepy elements are neraly in equal number in the two parts. In such a situation:

$$S_n = S_{n'} + \frac{n-n'}{2}1 \Rightarrow m_e = n'/2 + \frac{n-n'}{2} = n/2$$

We see that m_e, the average population in A, will be the same as without frozen individuals[35]. This result could of course have been expected in advance. Indeed, if the frozen elements are distributed in the same way as the rest of the population the mean will not be affected. For instance, if for $n = 200$ there are 198 frozen elements and just 2 non-frozen elements and if the 198 elements are distributed uniformly between A and $\overline{A}$, one will have $m_e = (0 \text{ or } 1) + 99 \simeq n/2$. In other words, the mean is the same as without any frozen elements In contrast, the variances will be very different:

- With 198 frozen elements: $\sigma^2(S_{200}) = \sigma^2$.
- Without any frozen elements: $\sigma^2(S_{200} = 200\sigma^2$.

Conclusions The previous discussion shows that:

(1) A problem due to frozen elements can be detected (and corrected) if m_e the time-averaged population in A is substantially different from np.

(2) If $m_e \simeq np$ but there are nevertheless frozen elements, this problem can neither be detected nor corrected and it will lead to *under-estimating* the variance and therefore also the average cross-correlation $\overline{r}$.

Remark Frozen elements can of course be detected by individual visual inspection of the living organisms. However, when their number reaches several hundreds this becomes an almost impossible task.

Example of application of the previous methodology

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[35] The same argument holds in the general case when the area A is a fraction p of the total area.

We consider the following case which corresponds to a real observation performed on ants

$$n = 520,\ p = 1/2\ m_e = 212,\ \sigma_e = 47$$

and we apply successively the two previous methods.

Method 1 (asymmetrical preference for some unknown reason)
The adjusted probability is

$$p' = m_e/n = 0.41 \Rightarrow q' = 1{-}p' = 0.59 \Rightarrow \sigma^2(S_1) = pq = 0.24 \Rightarrow \sigma_i^2(S_n) = npq = 126$$

As a result:

$$g^2 = \frac{\sigma_e^2}{\sigma_i^2(S_n)} = \frac{47^2}{126} = 17 \Rightarrow \overline{r} = \frac{g^2 - 1}{n-1} = 0.032$$

Method 2 (frozen elements)
Here we are in the case where $m_e = 212$ is substantially lower than $np = 520/2 = 260$. Hence we get the adjusted number of active elements n' through the formula:

$$n' = \frac{m_e}{p} = 2 \times 212 = 424$$

Then we determine $\overline{r}$ by using the standard formula with n replaced by n'.

$$= n'pqg^2 = \frac{\sigma_e^2}{n'pq} = \frac{47^2}{424 \times (1/4)} = 21 \Rightarrow \overline{r} = \frac{g^2-1}{n'-1} = \frac{21-1}{423} = 0.047$$

As can be seen the two methods lead to average cross-correlations of the same order of magnitude (they differ by 32%). Here, just for the sake of ilustration, we have computed $\overline{r}$ from a single experimental result. One should observe that the right method for determining $\overline{r}$ is not to compute it from individual results but to get it as the slope of the regression line determined by several results (in fact, as many results as possible).

For a given σ_e, the average correlation $\overline{r}$ is completely determined by g^2. However, in computing the regression line it is not only g^2 which matters but also the value of n' because the x-variable of the regression is the number of *active* elements. For instance, $p = 1/2$ and $m_e = n/20$ implies $n' = n/10$. The fact that n' is much smaller than n makes a big difference in the regression. This is illustrated in the following graph which summarizes 11 experiments carried out with various number of ants.
At first sight it may seem surprising that the estimated cross-correlation is as low as 0.04. In the next section we explain why this is so.

Why is the estimated cross-correlation so small?

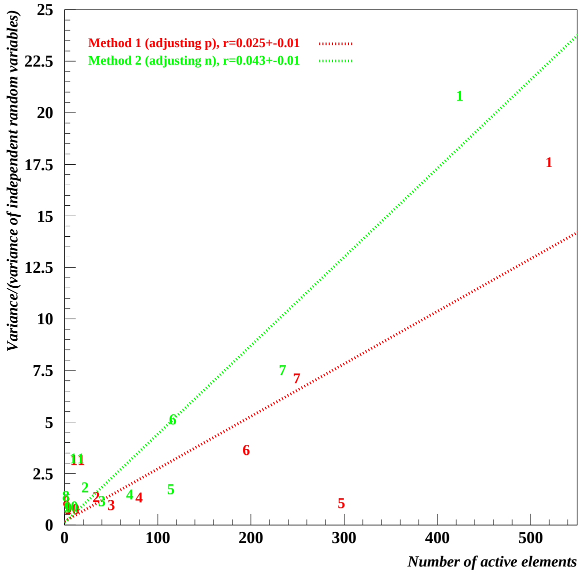

Fig. xx: Comparison of two estimation methods of the average cross-correlation of a population of ants. The cross-correlation is a way of expressing the average interaction strength between the ants. The correlation of the set of 11 points (not to be confused with the estimated cross-correlation which is the slope of the regression line) is 0.84 for the first method and 0.95 for the second. In the second method the frozen elements are left out and do not contribute. The present results suggest that at least in this case the second method does a better job. The error bars of $\overline{r}$ represent a confidence interval for a confidence level of 0.95.

First of all, it is necessary to make an important distinction. Suppose that by computing the correlation of a set of data $(x_i, y_i) \quad 1 \leq i \leq n$ one gets a correlation as low as 0.04. Such a low correlation would almost always mean that the correlation is not significant in the sense that the confidence interval contains the correlation zero[36]

Here, however, the correlation $\overline{r}$ is obtained in a completely different way, namely as the slope of a regression line. From the errors bars given in the caption of the figure it can be seen that this estimate is quite significan in the sense that the confidence interval of $\overline{r}$ does *not* include 0.

However important, this distinction does not explain why we get such a low correlation. This is what we wish to understand now.
The formula $\sigma_e^2 = npq\left[1 + (n-1)\overline{r}\right]$ shows that if $\overline{r} \simeq 1$, the observed standard deviation is proportional to the total number of elements: $\sigma_e \simeq n\sqrt{pq}$. What does that mean in practice?

Can the cross-correlation model explain the increase of the time constant with population size?

The time constant of a population of ants, bees or flies can be measured through their relaxation time from an out-of-equilibrium condition toward equilibrium or quasi

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[36] The only exception to this rule may occur when the number n of pairs is very large (say several thousands) so that the confidence interval becomes smaller than 0.04.

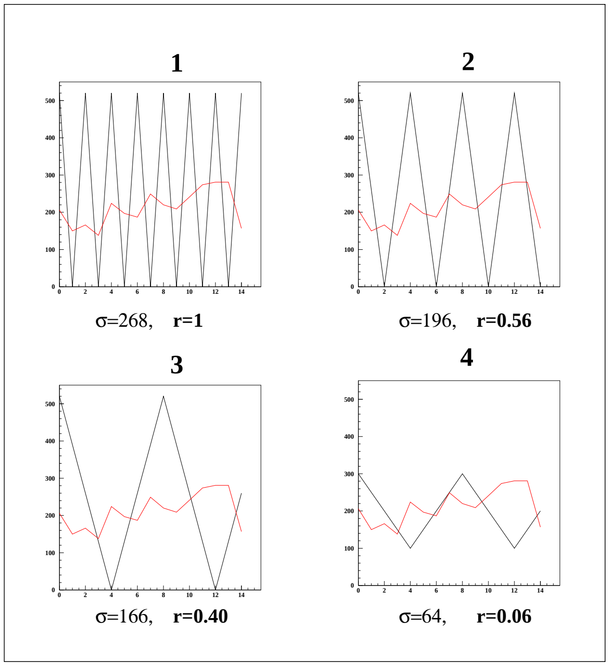

Fig. xx: Relation between the fluctuations of $n_1(t)$ and the values of $\overline{r}$. We suppose that the whole domain which contains the ants has been divided into two parts and we observe the fluctuations $n_1(t)$ of the number of ants in part 1. The black curve corresponds to an hypothetical curve while the red curve is the one that was actually observed. The numbers given under the graph are the standard deviation and the (corresponding) correlation for the black curves. For thered curve these numbers are 47 and about 0.04 respectively.
The first graph corresponds to the greatest possible standard deviation in the sense that each time step all the ants move from part 1 to part 2 or vice versa; in this case the average cross-correlation is almost equal to 1. In the second case the same move occurs in two time steps, while in the third it occurs in 4 time steps. As in the actual experiment one time step was 5 mn, in this last case all ants would change side within 20 minutes. Finally, the last graph corresponds to a case in which the variance of the simulated curve is similar to the variance of the observed curve.

equilibrium. Some results of this kind are summarized in the graphs below.
In the next sections we will see that adding together random functions that have the same time constant results in a sum that has also the same time constant. This result could be expected in so far as the addition of variables *taken at the same moment* is not likely to affect the time structure. This result will be shown first for uncorrelated random functions and then for correlated random functions.

Time constant of a sum of uncorrelated random functions

For the sake of simplicity we will consider the sum of only two random functions. The same argument can be easily extended to a sum of n random functions.

We consider two stationary random functions $X_1(t), X_2(t)$ which have the same distribution (their expectation is supposed to be equal to zero for the sake of simplicity) and the same autocorrelation function $\rho_X(r)$ and we want to compute the autocorrelation function $\rho_S(r)$ of the sum $S(t) = X_1(t) + X_2(t)$.

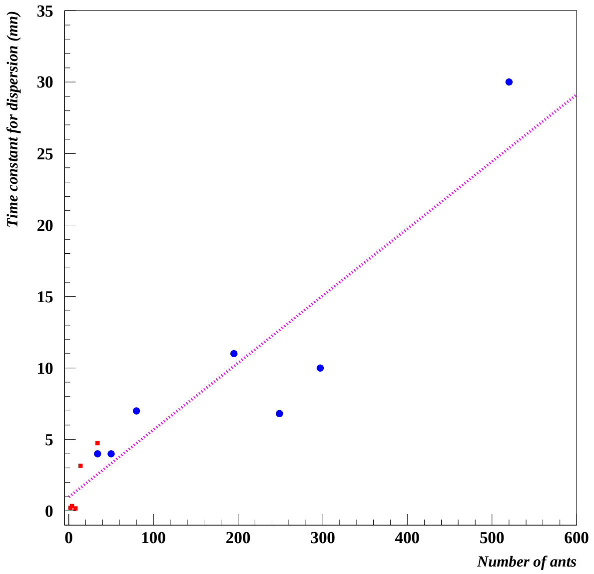

Fig. xx: Time constant as a function of the population size n. Initially, all ants were in one compartment, say 1. In the course of time a process of dispersion took place through which they occupied the two compartments in approximately equal numbers. This process comprised two phases. In the first phase the number of ants in compartment 2, $n_2(t)$ increased quickly, then after a quasi-equilibrium has been reached there was a stationary process during which $n_2(t)$ fluctuated around $n/2$.
The data corresponding to the blue dots were measured during the first phase whereas those for the red squares were measured during the second phase through the autocorrelation method. Sometimes, especially for large populations the stationary process of phase 2 lasted only shortly and was followed by the formation of a cluster in one of the compartments. The time constants of this clustering process are given in the next graph.

The calculation is straightforward.

$$\rho_S(r) = \frac{E\left[S(t)S(t-r)\right]}{\sigma_S^2}$$

$$E\left[S(t)S(t-r)\right] = E\left[\left(X_1(t)+X_2(t)\right)\left(X_1(t-r)+X_2(t-r)\right)\right]$$

$$E\left[S(t)S(t-r)\right] = 2\rho_X(r)\sigma_X^2 + E\left[X_1(t)X_2(t-r)\right] + E\left[X_2(t)X_1(t-r)\right]$$

Because $X_1(t)$ and $X_2(t)$ are supposed uncorrelated,

$$E\left[X_1(t)X_2(t-r)\right] = E\left[X_1(t)\right]E\left[X_2(t-r)\right] = 0$$

Thus:

$$E\left[S(t)S(t-r)\right] = 2\rho_X(r)\sigma_X^2$$

As the variance σ_S^2 of S is equal to twice the variance of the $X_i(t)$, one gets:

$$\rho_S(r) = \frac{2\rho_X(r)\sigma_X^2}{2\sigma_X^2} = \rho_X(r)$$

.

Thus, the sum $S(t)$ will have the same time constant as each of the X_i.

Next, we examine what must be changed in this calculation when the $X_i(t)$ are correlated.

Time constant of a sum of correlated random functions

The assumption are the same as in the previous sub-section except that the $X_i(t)$ are correlated. Such a correlation, ρ, can be introduced explicitely by defining the $X_i(t)$ in the following way:

$$X_1(t) = Z_1(t), \quad X_2(t) = \rho Z_1(t) + \sqrt{1-\rho^2} Z_2(t)$$

where the $Z_i(t)$ are two uncorrelated random functions which have same autocorrelation function $\rho_Z(r)$ With these definitions,

$$\sigma^2_{X_1} = \sigma^2_Z, \; \sigma^2_{X_2} = (\rho^2 + 1 - \rho^2)\sigma^2_Z = \sigma^2_Z$$

It can also be seen that the autocorrelation function of X_2 is $\rho_Z(r)$. The calculation is the same as previously except for the two factors ρ and $\sqrt{1-\rho^2}$. One gets:

$$E\left[X_2(t)X_2(t-r)\right] = (\rho^2 + 1 - \rho^2)\rho(r)\sigma^2_Z$$

Taking into account that the variance of the X_i is equal to the variance of the Z_i, it follows that $\rho_X(r) = \rho_Z(r)$.

The sum $S(t)$ of the $X_i(t)$ becomes:

$$S(t) = aZ_1(t) + bZ_2(t), \; a = 1 + \rho, \; b = \sqrt{1-\rho^2}$$

Thus:

$$E\left[S(t)S(t-r)\right] = (a^2+b^2)\sigma^2_Z\rho_Z(r) + abE\left[Z_1(t)Z_2(t-r)\right] + abE\left[Z_2(t)Z_1(t-r)\right]$$

As the $Z_i(t)$ are uncorrelated, the terms $E\left[Z_1(t)Z_1(t-r)\right]$ and $E\left[Z_1(t)Z_2(t-r)\right]$ are equal to zero. The left-hand side can be written: $\rho_S(r)\sigma^2_S$ and the variance of S will be expressed in terms of the variance of the X_i in the way seen earlier: $\sigma^2_S = 2\sigma^2_X(1+\rho)$. Thus one gets:

$$\rho_S(r)2\sigma^2_X(1+\rho) = (a^2 + b^2)\sigma^2_Z\rho_Z(r)$$

Taking into account that $a^2 + b^2 = 2(1+\rho)$, that $\sigma^2_Z = \sigma^2_X$ and that $\rho_Z(r) = \rho_X(r)$ one gets:

$$\rho_S(r) = \rho_X(r)$$

In conclusion, one sees that with this model it is impossible to describe changes in the time constant. That is hardly surprising for a model such as the present one which is basically time independent.

MEASURING INTERACTION STRENGTH BETWEEN LIVING ORGANISMS

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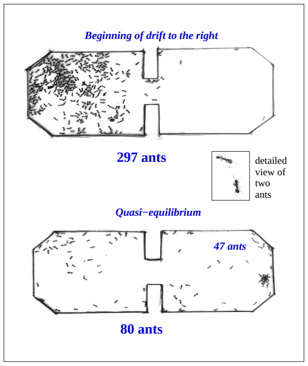
Lecture given at Tokyo University on 28 November 2012, 4:40 pm, Department of Economics (3rd seminar room, 12th floor of the Economics Research Building)

Abstract

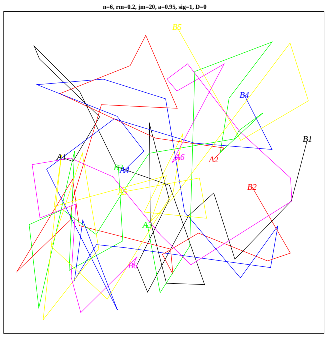
In economics as in other fields one would like to derive the properties of macro-systems from the characteristics of individual elements. In physics, this problem was solved by statistical mechanics at least in principle and provided the system is in equilibrium. So a natural question is how to adapt the concepts and methods of statistical mechanics to non-physical systems.
A first question that we will address (albeit only briefly) is how to make sure that physical concepts, e.g. the notion of temperature, can be used in non-physical systems in a *consistent* and *fruitful* way.
In statistical physics a system is described by the knowledge of its energy function H(also called Hamiltonian). It takes the following form:

$$H = H_{\text{free particles}} + H_{\text{interactions}} + H_{\text{external factors}}$$

The term $H_{\text{interactions}}$ describes inter-individual interactions. Unless we can assume that the system is composed only of free particles which is a fairly trivial case, in order to use statistical mechanics we need to know (quantitatively) the interactions within the system. Most of the methods that physicists use for measuring interactions cannot be used in non-physical systems, for instance because they lead to the dislocation of the system (as for instance in melting, boiling or evaporation). Thus, if we want to extend statistical mechanics to non-physical systems it is important to define methods through which one can measure interaction strength in non-physical systems.
As a first step, we attempt such measurements for systems of living organisms such as groups of insects. Such systems are closer to physical systems than are social systems because the notions of distance, velocity or energy can be defined in the very much the same way as in physics. It is our hope that such methods will also prove useful for social systems.
In one of the methods that we propose, one divides the available space into two parts A and B and one records in the course of time the numbers $n_A(t)$ of individuals located in part A.



Experiments with ants in a two-compartment device



Simulation with crosscorrelation equal to 0.2.

We then use a probabilistic model that allows us to derive the (average) cross-correlation between individual organisms from the standard deviation of the function $n_A(t)$.

Content

(1) Why do we need to know interaction strength?
(2) What can be learned from physics about interaction testing?
(3) Panorama of methods and experimental devices
(4) Presentation of the cross-correlation method
(5) Discussion

Role of interaction in physical and social systems

In statistical physics

In statistical physics the properties of macroscopic systems are derived from the characteristics of molecules (or atoms or electrons). One crucial characteristic specifies how these molecules interact.
As an illustration for a real gas (as opposed to an ideal gas for which interactions are supposed to be negligible), the energy function may take the following form:

$$H = H_{\text{free particles}} + H_{\text{interactions}}, \quad H_{\text{free particles}} = \sum_i \frac{mv_i^2}{2}, \; H_{\text{interactions}} = \sum_{i>j} \frac{k}{(r_i - r_j)^6}$$

This expression focuses on one specific form of interaction, but in fact several forms of interaction are at work simulateously.

In trying to apply a similar approach to economics, the molecules will be replaced by economic units which can be traders in financial markets, companies, economic sectors or the economies of different countries. Needless to say, all these economic units interact in one way or another. In order to apply the methods of statistical physics to economic systems we need to know the ways and strength of these interactions.

However, even if we do not intent to use the formalism of statistical mechanics, estimates of interaction may turn out to give useful insight into the economic systems under consideration. Let me explain why.

In physical chemistry

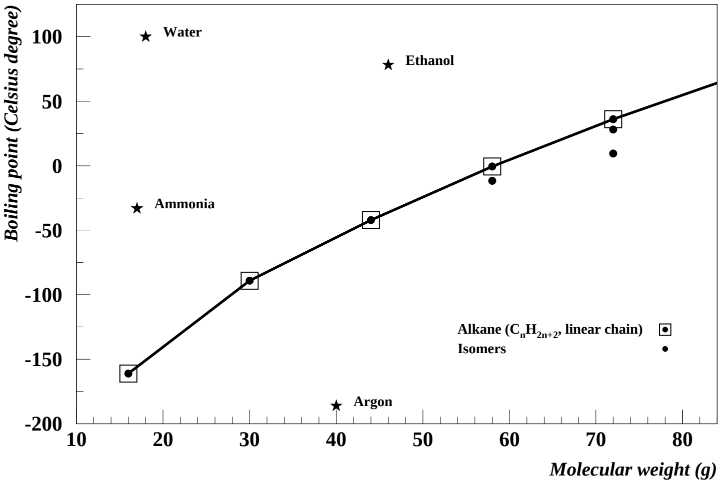
Although the objective of physical chemistry is also to explain the properties of macroscopic systems in terms of molecular interactions, there are two main differences with the approach of statistical mechanics.

- First, physical chemistry considers a broad range of molecules rather than just the simplest ones as is done in physics. Thus, because many cases are being considered it becomes a necessity to adopt a comparative perspective: why is the melting point of argon lower than the melting point of water? Why is the equilibrium vapor pressure higher for ethanol than for water? Why is the boiling temperature higher for decane than for methane? And so on and so forth.
- Because to propose full-fledged models for all these cases would be an almost impossible task, physical chemistry will rather resort to qualitative arguments.

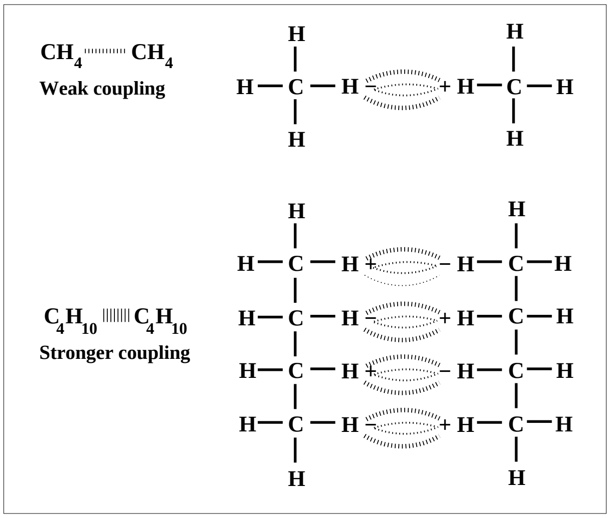
Implications of interactions for macroscopic properties

Physical properties

Most of the properties of physical systems are closely connected to the interaction strength.



Boiling point as a function of molecular weight, i.e. interaction strength.



Attraction between alkane molecules.

One can mention:

- State of matter: solid, liquid or gas (see below)
- Equation of state of gases connecting density, pressure, temperature (ideal gas versus van der Wall gas)
- Boiling temperature (illustrated in graph)
- Heat of vaporization
- Surface tension (energy to take a molecule to the surface)
- Equilibrium vapor pressure
- Rate of evaporation (escape experiment)
- Viscosity

- Velocity of sound (ex: diamond)

States of matter

Among the properties that can be (more or less) predicted when one knows the strength of interaction between molecules there is one basic property which is of particular importance, namely the system's state of matter.

Physics distinguishes 3 states of matter: gas, liquid and solid[37].

Solid-like systems versus gas-like systems

An obvious question is whether the previous distinction has a parallel in non-physical systems. For the sake of simplicity, we consider only the two extreme cases of solid-like versus gas-like systems.

One distinctive property of gases is that when put together two gas systems will form a new system identical to the former ones except for its volume. On the contrary, two solid systems put together will remain separate.
In physical terms this property will be expressed by the fact that for gases the diffusion constant D is *much* larger than for solids. For hydrogen (at zero degree) $D = 6\ 10^4\ \text{m}^2/\text{s}$, whereas for copper at 600 degree $D = 3\ 10^{-8}\ \text{m}^2/\text{s}$.
(the source is http://web.mit.edu/3.091/www/WittNotes/Notes_9.pdf)

What about non-physical systems? If we put together two living organisms, they will *not* form a new living organism but will remain separate. Thus, we can say that living organisms are solid-like systems, in other words they have strong interactions.
On the contrary, when put together two groups of people who speak the same language will form a new group. Thus, we can say that they are gas-like systems in which interaction is fairly low.

At this point it is important to realize that the ability for two systems A and B to form a new system does not only depend on the strength of interaction within the A and B components but also upon the interaction that the elements of A can have with the elements of B. This can be illustrated by our previous example.

- If all people in group A speak the same language L_A that is different from the language L_B spoken in group B, then it will be difficult for the reunion of A and B to form a stable group because the group $A \cup B$ will tend to split into its initial components.

This is the situation for two groups of immigrants freshly arrived in a country. As a result, these groups will form separate clusters in the city in which they arrive. This is what can be seen in New York with the areas of "Little Italy" or "Chinatown". In

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[37] A 4th state would be plasma which is a high-tempertaure gas in which the atoms have lost their electrons. Although plasma has specific properties, for the issue we are considering here it does not differ significantly from gases. That is why we will limit ourselves to the three other states of matter.

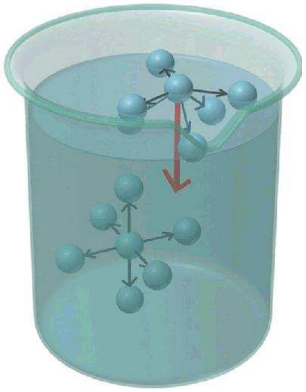
short, immediately after their arrival such groups of immigrants are solid-like.

- If, apart from their own languages, the people in the two groups are able to speak (even if imperfectly) a common language L_C, then their ability to form a reunion $A \cup B$ will be increased.

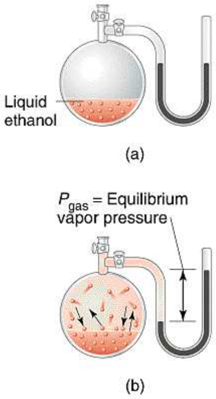
This is what happened when the immigrants in “Little Italy” and “Chinatown” little by little learned to speak English. From solid-like such groups will become gas-like.

As another illustration, one can mention the following cases. Two neighboring colonies of the *same species* often fight one another. On the contrary, a colony of ants may contain ants of a *different* species with which it lives in symbiosis. To explain such cases in terms of interactions will require a detailed study. However, there are similar cases in physics. Why does hydrogen (and only hydrogen) diffuse very quickly in palladium (and only in palladium)? This shows that we should not expect any universal rules but satisfy ourselves with broad, qualitative rules (even if these rules are plagged with a few exceptions).

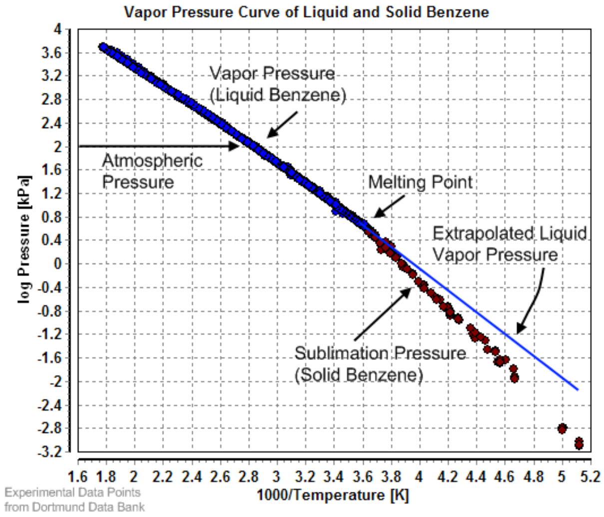
Parallel of surface tension in social systems: separatism



Forces on bulk versus surface molecules.



Equilibrium vapor pressure.



Experimental Data Points
from Dortmund Data Bank

Relation between the equilibrium vapor pressure and temperature. It can be noted that the vapor pressure for the solid follows almost the same law as for the liquid.

When two states of matter are in contact, they share a surface called an interface. Whereas bulk molecules have neighbors in all directions, at an interface, molecules have neighbors of same kind only on one side. Thus, surface molecules are different from those in the bulk.

It takes energy to create a new surface of a solid or liquid because one must move a molecule from the bulk to a site at the surface and this takes energy. The amount of energy it takes to create one unit of area of new surface is called the surface tension. It is expressed in Joule/square meter. The surface tension reflects fairly well the strength of interaction in a system. For instance, at 20 degree the surface tension at a water-air interface is 73 mJ/(square meter) whereas the surface tension at a mercury-air interface is 472 mJ/(square meter).

If one reviews separatist movements one quickly finds that almost all of them are located near border or coast lines. This characteristic is agravated whenever such places are separated from the rest of the country by mountain ranges with poor means of transportation.
Many illustrative examples are described in “Separatism and Integration” (Roehner and Rahilly 2002)

Parallels of equilibrium vapor pressure in non-physical systems: dropout and escape rates

Among the molecules which are near the interface those which have the highest velocity are the most likely to be able to escape. For a given average velocity (that is to say for a given temperature) the number of molecules which will escape is conditioned by the interaction strength in the liquid. Thus, one is not surprised that there is a close connection between the number of escaped molecules (that can be measured by the equilibrium vapor pressure) and the interaction strength. In other words, the equilibrium vapor pressure is a good indicator of the interaction strength.

How can this be applied to non-physical systems?
For any organization such as school, army, church, political party or club the number of people who leave the organization in a given time interval refects the attraction force of the organization. In most of these cases the persons who drop out are absorbed by the society in which the organization is established and few will come back. In other words, we are not in a situation where the volume above the liquid is closed but rather in a situation in which the liquid is in open air. In this case it is the rate of evaporation which replaces the vapor pressure as interaction indicator.

Some 4 years ago,
I tried to collect dropout data for various clubs such as musical associations, card-player clubs, sport clubs and so on, in the hope that they may give estimates of the

interaction strength inside these organizations. At first, this could appear as a promising approach for indeed in all developed countries there are thousands of clubs and associations of all kinds. There were many obstacles, however.

- It was difficult to make a clear distinction between real participants and those who registered but did not really participate. This problem was particularly serious which clubs which charged no or minimal entrance fee.
- The dropout (as well as the registrations) do not only reflect the attraction of the club but also the influence of various other possible occupations between which a person may share its free time.
- One obvious bias comes from the persons whose dropout is due to their death. This bias becomes all the more serious in clubs in which many members are retired persons.

For all these reasons, this approach was eventually dropped and instead we started to do experiments with insects. Here are some pictures which illustrate some practical aspects of this approach. Their main objective is to show that such experiments can be done with fairly modest equipment.

Phase transitions

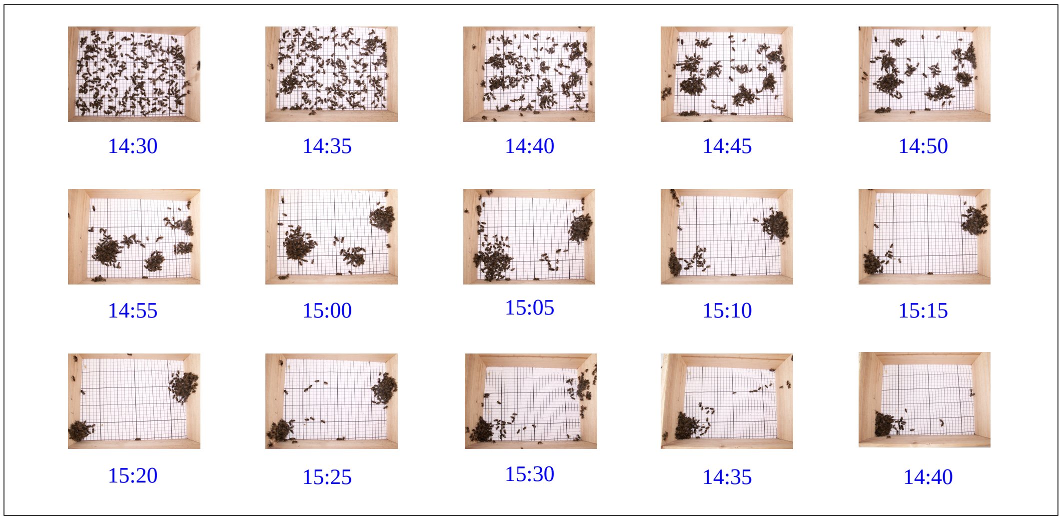
As an example let us consider water. The three states will be ice, liquid water and vapor water. Whether in the solid, liquid or gas state, the interaction mechanisms of water molecules are basically the same but the coupling strength will be stronger in ice, than in liquid (and stronger in liquid than in gas) because the average distance between the molecules is smaller in a solid than in a liquid (and smaller in a liquid than in a gas). As most of the interactions are decreasing with increasing distance (as are the power laws in the formula given above), larger average inter-molecular distance means weaker interaction. In other words, in order to move from gas to liquid or from liquid to solid one has to reduce inter-molecular distance. This can be done in two ways.

(1) One can reduce the volume of the container containing the system. This will bring the elements closer together.

(2) Reducing the translational momentum of the elements will allow the inter-attraction bring them closer together. Ideally, if the molecules were completely steady, even a small inter-attraction would bring them together.

Presentation of methods and experimental devices

Methods



Clustering process for bees (Apis mellifera mellifera). Altogether there were about 300 bees. Initially they were put to sleep through 5 minutes in carbon dioxide. *Source: The data are from an experiment done in July 2012 by J. Darley and B. Roehner.*

Which method to use?

1) Is there clustering?

Yes → How fast? Proportion of outliers not in cluster?

No → Use *Cross-correlation method*, or *Expansion rate method*.

2) Cross-correlation method

In order to know if this method will give reliable results, one must answer the following questions.

- What is the proportion of elements moving from left to right versus from right to left?
- What is the number of "frozen elements" i.e. those elements that do not move?

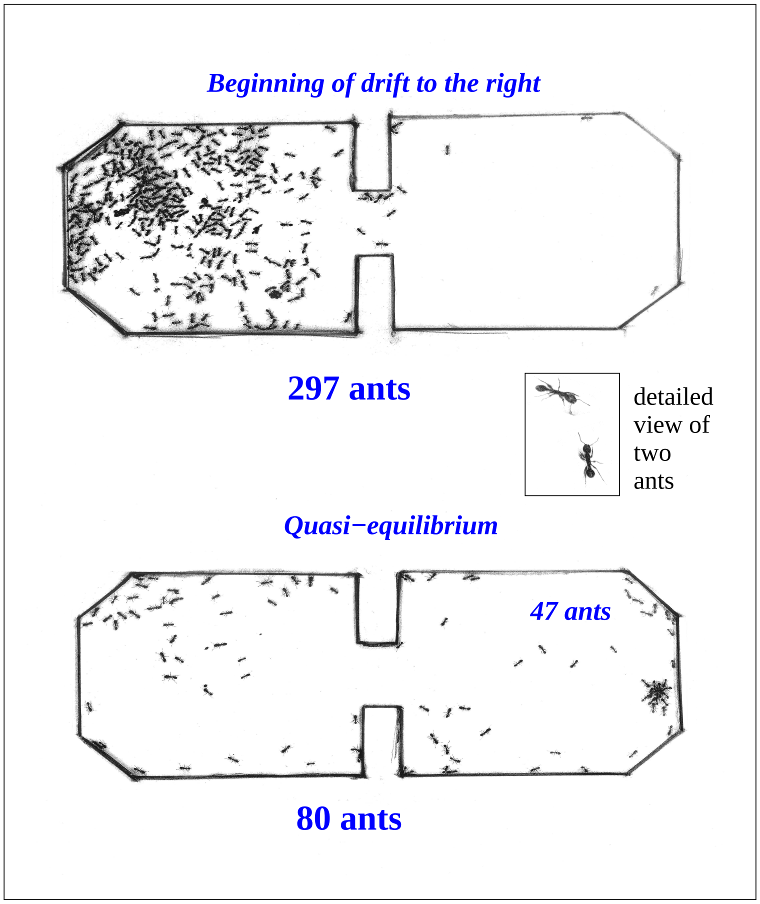
3) Expansion method (remains to be tested)

Presentation of some useful experimental devices

To be eventually successful this approach needs to be explored by *several* research groups. This is the way physics has been working in the past three centuries. All experiments were tried, retried and checked by many physicists. It is through the comparison of their results that a better understanding of the experimental conditions necessary for the experiment to succeed could eventually be gained.
Such a collective exploration process is even more important here because, due to the very nature of these experiments, the fluctuations are fairly large.

Ants and drosophiles On the left: collecting ants. The white Bristol board was left a few centimeters from the exit hole of a colony for about half an hour. The brown product is chesnut cream with a few drops of water. On the right: a tube containing drosophila as prepared by a research laboratory in population genetics.

Carbon dioxide gas cylinder. As compressed carbon dioxide is necessary in many activities, small cylinders similar to the one shown on the picture can be bought fairly easily and at low cost. The one represented here is used for the production of sparkling water, it weighs only one kilogramme and costs about 20 euros (10 euros for the empty bottle and 8 euros for a refill).



Container with weighing device on one side (2). Here most of the beetles have formed a cluster in one of the corners. The weight is 375 mg which, when divided by 19 mg, gives a total of 20 beetles.

In showing some of the experimental devices my purpose is to convince the audience that it is possible to do this kind of experiments with fairly little sophisticated equipment.

Basically, the needs can be summarized as follows:

- First one needs to get the *living organisms*: ants can be easily collected (see picture), drosophila can be obtained from biology laboratories, fruit flies can be bought in the form for worms (larvae) destined for fishermen or for big aquarium fishes, small fishes are sold as preys and foodstuff for bigger fishes, bettles can also be bought in the form of worms.

- Secondly, in many cases, one needs a small bottle of carbon dioxide to make them sleep in order to be able to handle them easily. Carbon dioxide has an almost instantaneous anesthesic effect on all these insects. According to a paper published in the Journal of Experimental biology (Ribbands 1950) anaesthesia through carbon dioxide does not infer a memory loss and changes only slightly the behavior of bees. It is probably safe to assume that the effect on the other insects mentioned above is similar.
- Next one needs an appropriate container. A simple solution is to cut it into a piece of flexible plastic (such as PVC) of adequate thickness (3 to 5mm is usually enough). This is illustrated in one of the pictures.
- Finally, one needs a counting device. Taking pictures and counting by hand is a simple solution but not always satisfactory especially for counting the elements in a cluster. For this reason we have developed a weighing method (illustrated in one of the pictures).

Next we describe one of the methods that we have developed for computing the average correlation between interdependent elements of a system.

Cross-correlation method

The main advantages of this method are the following.

(1) Contrary to the dropout model, the cross-correlation model can be used whether or not there is a clustering process.

(2) The (usually) few non-clustering elements considered in the dropout model present high fluctuations. On the contrary, the cross-correlation model relies on data for the relatively large number of elements which cross from one side to the other. As a result, one expects a smaller dispersion of the results.

(3) As cross-correlation measurements take only about half an hour this method can be used to follow the interaction of a system in the course of time. This is not possible with the dropout model because one must wait until the clustering process is completed.

We will introduce this models by steps. First we explain the idea of the model, then we discuss how it should be used for the purpose of estimating the average cross-correlation.

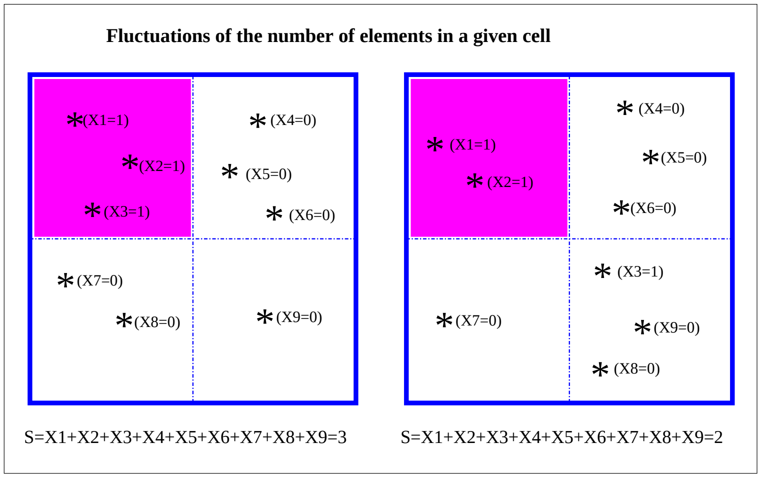
General idea of the model

Consider a container which contains n ants. In this container we define a subset A

and we count in the course of time the number $n_A(t)$ of ants that are found in A . For instance, we can record these numbers every 15 seconds over a period of one hour which will give $60 \times 4 = 240$ numbers. From these numbers we can compute their average m and their standard deviation σ [38].

The question is: can we learn something about the interaction between the ants from the values of m and σ?
Intuitively one would expect that if the n elements are highly correlated the standard deviation will be higher than when they are not correlated at all. Why?

If the elements are completely correlated they will move all together into A or out of A. Thus, $n_A(t)$ will make big jumps as seen in the graph below. On the contrary, if the elements are not correlated at all, $n_A(t)$ will change by small steps of $0, 1, 2, \ldots$ as shown in the picture. A jump of 9 can happen but it will be an exceptional event. Indeed, it will have the same likelihood as obtaining 9 heads by throwing 9 coins.
In other words, one expects that the correlation between the elements will be more or less proportional to the standard deviation. The higher the standard deviation, the higher the correlation. In other words, by measuring the standard deviation of $n_A(t)$ we can estimate the correlation which is itself a measure of the inter-attraction between the ants.



Fluctuation of the number of elements in a subset A (magenta colored) of the whole domain. Each star represents an element. To each of them one can associate a random variable which will be equal to 1 when the element belongs to A and to 0 otherwise. With this definition the sum S will count the number of elements in A and the fluctuations of the random variable S will represent the fluctuations of the number of elements counted in A in the course of time.

Main formula

The method relies on the following proposition.

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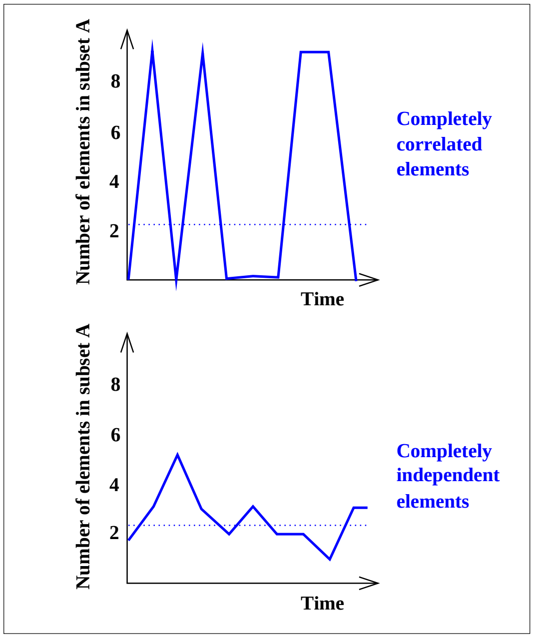
[38] The average and the standard deviation will be fairly independent of the time interval between successive observations because changing this interval amounts to changing the sampling time of the function $n_A(t)$. If $n_A(t)$ is fairly stationary, m and σ will also be fairly independent of the total length of the record.



Fluctuations of the number $n_A(t)$ of elements in a subset A of the whole domain in two special cases. When the movements of the elements are completely correlated all 9 will move to A or out of A at the same time which will result in big fluctuations. On the contrary, when the elements are completely independent from one another, the fluctuations of $n_A(t)$ will be fairly small.

Proposition: Standard deviation of a sum of cross-correlated variables. We consider a sum S_n of n identically distributed random variables X_i of mean m and standard deviation σ. We assume that between $X_i, X_j, i \neq j$ there is a cross-correlation r_{ij}. The average of all cross-correlations is denoted by $\overline{r}$: $\overline{r} = \frac{1}{[n(n-1)/2]} \sum_{i \neq j}^{n} r_{ij}$. Then, the variance of $S_n = X_1 + \ldots + X_n$ is given by:

$$\sigma^2(S_n) = n\sigma^2 \left[(n-1)\overline{r} + 1\right] \Rightarrow g^2 \equiv \frac{\sigma^2(S_n)}{n\sigma^2} = (n-1)\overline{r} + 1$$

$n\sigma^2$ is the variance of the sum S_n when the X_i are uncorrelated.

Proof

We proceed in several steps.

For the sake of simplicity we first consider the average of a sum of three correlated random variables X_1, X_2, X_3 of mean m and identical standard deviation σ. Our objective is to compute the standard deviation of:

$$S_3 \quad S_3 = X_1 + X_2 + X_3$$

By definition of the variance one gets: one gets:

$$\sigma^2(S_3) = E\left[(S_3 - E(S_3))^2\right]$$

One knows that the expectation of a sum of random variables is always equal to the sum of the expectations, whether the variables are correlated or not. Thus: $E(S_3) = E(X_1) + E(X_2) + E(X_3)$. Consequently:

$$\sigma^2(S_3) = E\left[(\sum_{i=1}^{3} \hat{X}_i)^2\right], \quad \text{where: } \hat{X}_i = X_i - E(X_i)$$

The mean of the variable $\hat{X}_i$ is equal to zero and it has the same standard deviation σ as X_i. Thus,

$$\sigma^2(S_3) = \sum_{i=1}^{3} E(\hat{X}_i^2) + 2\left[E(\hat{X}_2\hat{X}_3) + E(\hat{X}_3\hat{X}_1) + E(\hat{X}_1\hat{X}_2)\right]$$

We express the expectations of the products by introducing the coefficient of correlation of the X_i:

$$r_{12} = \frac{E\left[(X_1 - E(X_1))\,(X_2 - E(X_2))\right]}{\sigma(X_1)\sigma(X_2)} = \frac{E(\hat{X}_1\hat{X}_2)}{\sigma^2}$$

Thus:

$$\sigma^2(S_3) = 3\sigma^2 + 2\sigma^2(r_{23} + r_{31} + r_{12})$$

Introducing the mean of the r_{ij}, $\overline{r} = (r_{23} + r_{31} + r_{12})/3$
we obtain:

$$\sigma^2(S_3) = 3\sigma^2[1 + 2\overline{r}]$$

This formula has an obvious generalization to an arbitrary number n of random variables:

$$\sigma^2(S_n) = n\sigma^2 g^2 \qquad g = \sqrt{1 + (n-1)\overline{r}} \tag{3.1b}$$

where:

$$\overline{r} = \frac{1}{[n(n-1)/2]} \sum_{i \neq j}^{n} r_{ij}$$

Interpretation of the coefficient g

What is the significance of the coefficient g?
Under the assumption that the X_i are independent (which means that they are also uncorrelated) the variance of S_n would be n times the variance of X_i that is to say $\sigma_i^2(S_n) = n\sigma^2$. In other words, g is the ratio of the standard deviation of correlated variables to the standard deviation of uncorrelated variables:

$$g = \frac{\sigma(S_n)}{\sigma_i(S_n)}$$

It can be noted that if $\overline{r} < 0$, the standard deviation of the correlated variables will be *smaller* than the standard deviation of the independent variables. To what practical situation would this correspond?

To get a better insight let us assume that there are only two living organisms ($n = 2$) that the total area has been divided into only two parts ($p = 1/2$) and that $\overline{r} = r_{12} = -1$. The fact that the correlation is -1 means that when the variables X_1 and X_2 will always take “opposite” values[39]. In other words, when 1 is in A, 2 will be outside

---

[39] The values assumed by X_1, X_2 are 0 and 1 which means that they are not really opposite in the arithmetical sense. If we define $X_i' = X_i - 1/2$, then X_i' will take on the opposite values $-1/2$ and $1/2$. However, in this case $S = X_1' + \dots X_n'$ will no longer count the number of living organisms which are in A but will be proportional to the difference of those in A and those not in A.

A and when 1 leaves A element 2 will enter A. Such a behavior corresponds to a situation in which the two elements do not wish to be together. One can think of a prey-predator situation in which the prey tries to avoid the predator.

As our main objective is to estimate attraction forces which correspond to $\overline{r} > 0$, we will not be concerned with the case $\overline{r} < 0$.

Special cases

It is enlightening to apply the previous formula to a number of special cases.

(1) When the r_{ij} are all equal to zero $g = 1$ and we get $\sigma^2(S_n) = n\sigma^2$ which is the standard result for independent variables. Indeed, as is well known, in the case of independent variables the variance of a sum is the sum of the variances.

(2) On the other hand, $\overline{r} = 1$ implies that *all* the r_{ij} are equal to 1. In this case the three variables are identical (with probability 1) and one gets: $\sigma(S_3) = 3\sigma(X_1) = 3\sigma$ in agreement with the above result.

(3) The previous formula apply in a general way to any random variables X_i. For the analysis of experiments with living organisms, the variables X_i have a specific meaning which gives them the following characteristics:

$$E(X_i) = P\{i \in A\}1 + P\{i \notin A\}0 = p$$

$$\sigma = E(X_i^2) - E^2(X_i) = P\{i \in A\}1^2 + P\{i \notin A\}0^2 - p^2 = p - p^2 == pq, \quad \text{where} q = 1 - p$$

Thus, the expression of $\sigma^2(S_n)$ leads to:

$$\sigma^2(S_n) = npq[(n-1)\overline{r} + 1]$$

As an illustration let us apply this formula to the case corresponding to the top graph in the previous figure. With $\overline{r} = 1$ one gets:

$$\sigma^2(S_n) = n^2 pq \Rightarrow \sigma(S_n) = n\sqrt{pq}$$

The result is reasonable because when $\overline{r} = 1$ all the variables X_i are identical (with probability 1) and $S_n = nX_1$ from which results that $\sigma(S_n) = n\sigma(X_1) = n\sqrt{(}pq)$. With $n = 9$ and $p = 1/4$ one gets: $\sigma(S_9) = (9/4)\sqrt{3} \simeq 3.9$

Alternatively $\sigma^2(S_n)$ can also be written:

$$\frac{\sigma^2(S_n)}{npq} = (n-1)\overline{r} + 1$$

This expression leads to a methodology for estimating the average cross-corelation which is described in the following proposition.

Experimental methodology

Proposition 2: How to estimate the average cross-correlation The average cross-correlation $\overline{r}$ can be estimated by taking the following steps:
1) One defines an area A which is a fraction p of the whole domain occupied by n living organisms.
2) One counts in the course of time the numbers $n_A(t)$ of living organisms which are in A and one computes the experimental values of the mean m_e and variance σ_e^2 of $n_A(t)$.
3) Under the assumptions of the cross-correlation model the numbers $n_A(t)$ are represented by the random variable S_n.; thus, σ_e^2 will be represented by $\sigma^2(S_n)$.
4) Consequently, if one repeats these measurements for various numbers n_k of living organisms, the variance of $n_A(t)$ should follow the following expression:

$$\frac{\sigma^2(S_{n_k})}{n_k pq} = (n_k - 1)\overline{r} + 1$$

which means that $\overline{r}$ will be the slope of the regression $(n-1, \sigma_e^2/npq)$.
5) Similarly, if for given n one repeats these measurements for areas of various sizes for which the fraction p takes the values p_k, then the variance of $n_A(t)$ should follow the following expression:

$$\overline{r} = \frac{\sigma^2(S_n)}{n(n-1)p_k q_k - \frac{1}{n-1}}$$

which means that $\overline{r}$ will be the average of the quantity on the right-hand side.

Dealing with asymmetric observations

It can be noticed that so far we did not make use of the mean m_e of the observations $n_A(t)$. The reason is very simple. According to the present model the mean should always be given by: $m_e = E(S_n) = nE(X_1) = n/p$. For instance, if $n = 200$ and if the whole domain occupied by the living organisms has been divided in only 2 parts so that $p = 1/2$, one should have $m_e = 100$. Needless to say, m_e will never be exactly equal to 50 because of inevitable statistical fluctuations. However, such fluctuations should remain compatible with the order of magnitude of σ_e. This is not always the case.

As an illustration, let us mention the following observation recorded with ants: $n = 195,\ m_e = 58,\ \sigma_e = 12$. In this example, $n/2 - m_e = 195/2 - 58 = 39 = 3.3\sigma_e$. For variables which have a gaussian distribution (as is implied by our model), a fluctuation of 3.3σ has a probablity as low as 10^{-3}. Here, however, it is not a fluctuation which reaches this value but the mean itself. Clearly, such an observation is not compatible with the assumptions of our model. Unfortunately, this kind of observation is the rule rather than the exception. How can this be understood?

Before discussing this point in greater detail, it is important to emphasize that this asymmetry seriously affects the determination of $\overline{r}$. Why?

The standard deviation of a random variable depends on the frequency and amplitude of the fluctuations but the most basic factor is its very order of magnitude. What we mean is that, except in exceptional circumstances, the standard deviation of a variable which flutuates around 100 is usually higher than the one of a variable which fluctuates around 1. In other words, an abnormally low or high mean will result in an abnormally low or high standard deviation σ_e which in turn will affect g and the estimate of $\overline{r}$. So, the issue regarding the mean is quite an essential point.

Simulation

In order to illustrate how the present model is supposed to work we present results provided by a simulation. This simulation involved the following steps.

(1) First we need to built a set of interdependent random variables. To this end we start with a set of independent random variables Z_i and we define new variables X_i as linear combinations of the Z_i. We have been using the Choleski procedure to produce variables whose cross-correlations are all equal. In this case $r_{ij} = r$ for all pairs. As an illustration we give the matrix form of these linear combinations for $n = 2$ and $n = 3$.

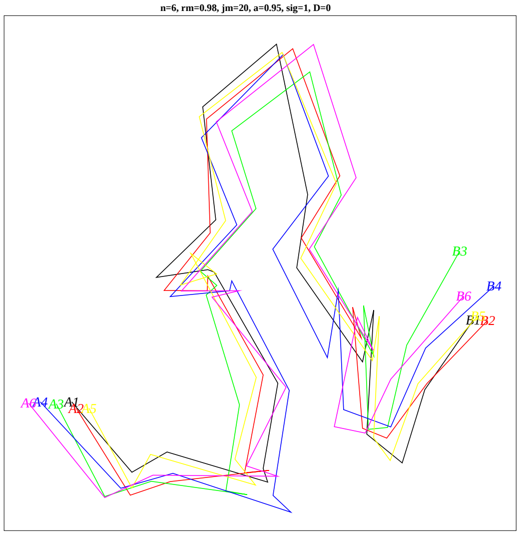
$$\begin{pmatrix} X_1 \\ X_2 \\ X_3 \end{pmatrix} = \begin{pmatrix} 1 & 0 & 0 \\ r & \sqrt{1-r^2} & 0 \\ r & r\sqrt{\frac{1-r}{1+r}} & \sqrt{1-\frac{2r^2}{1+r}} \end{pmatrix} \begin{pmatrix} Z_1 \\ Z_2 \\ Z_3 \end{pmatrix}$$

For the purpose of the simulation the random variables which appear in these expressions will be replaced by m-dimensional vectors. As a result, this step gives a set of n correlated vectors each of dimension m:

$$X_i(t),\ i = 1, \dots, n, \quad t = 1, \dots, m,\ i \neq j : \mathrm{cor}(X_i, X_j) = r$$

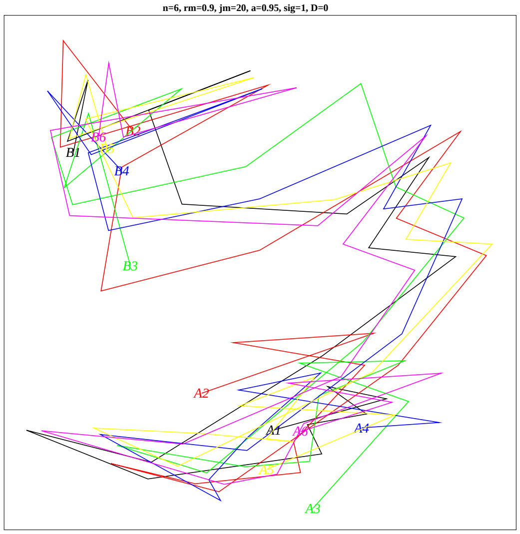
(2) The second step consists in checking if the random variables X_i have the properties that one expects. This is done in the following graphs. The first set of graphs shows the trajectories of each element. One can see that when r is close to one the trajectories are fairly parallel. On the contrary, when r is close to zero they are almost independent. In practice, the trajectories of individual elements cannot be observed for that would require a different marker on each and every element. The second set of graphs shows what can actually be observed, namely a set of successive pictures of the whole population.

(3) Now we come to the methodology for measuring r. As explained earlier, the methodology that we suggest is to measure the fluctuations of the number of elements in a subset A of the whole container.



Simulation of a process with high cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.98. The $A_i,\ i = 1, \dots 6$ designate the starting points of the trajectories while the $B_i,\ i = 1, \dots 6$ are the end points.

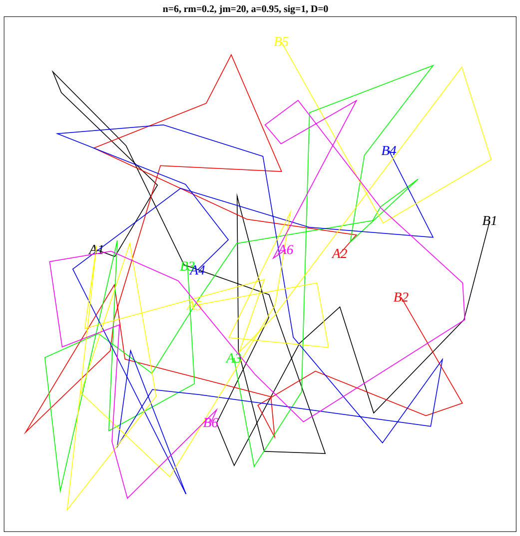
For this graph as well as for the following graphs the trajectory of each of the 8 elements follows an autoregressive process $X(t) = aX(t-1) + B(t)$ where $B(t)$ is a random variable which represents the noise; $a = 0.95$ which implies that the process has a fairly large time constant (that is to say a long memory).



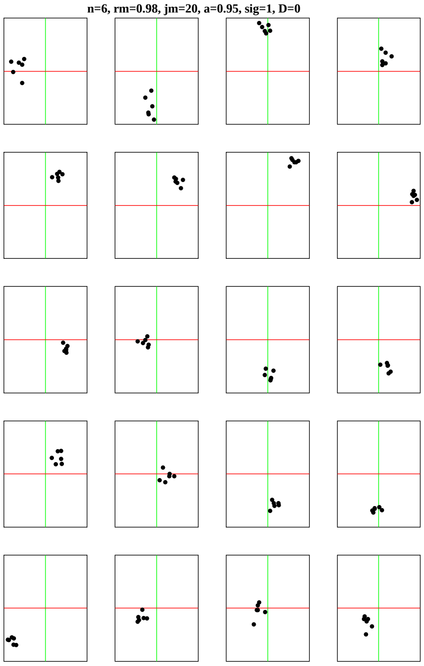
Simulation of a process with medium cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.90.

The following table shows the estimates obtained in this way. It can be seen that the ratio g^2 defined previously increases with the number of elements.

It is true that in the present case the estimates are fairly imprecise but one must keep in mind that these estimates were obtained through a regression on only 4 points. Two interesting conclusions can be drawn. (i) It is important that the time-series defining the variables X_i are as long as possible. Here we have taken $m = 500$;



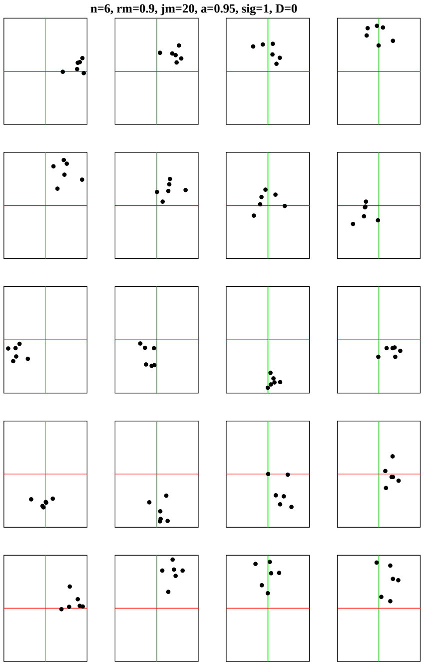
Simulation of a process with low cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.20.



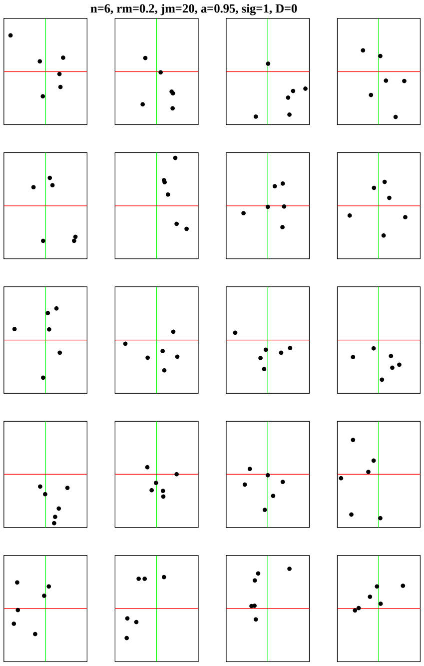
Simulation of a process with high cross-correlation. The cross-correlation between the trajectories of the 6 elements is 0.98.

for smaller values of m the imprecision would be even higher. (ii) the weaker the correlation the more difficult it is to to measure r because in such cases the effects of the cross-correlation are buried in the noise-background.

(4) A more direct procedure would be to compute the correlations between all pairs of trajectories. As already said, in practice it is in fact not possible to observe



Simulation of a process with medium cross-correlation. The cross-correlation between the 6 elements is 0.90. This figure (as well as the following ones) picture their positions on 20 successive time steps.



Simulation of a process with low cross-correlation. The cross-correlation between the 6 elements is 0.2.

these trajectories. However, in the simulation the individual trajectories are well defined which makes it possible to test this procedure. Naturally, as this method uses a much greater amount of information one expects a better accuracy. One gets the following estimates:

Estimates of the cross-correlation based on simulated data

Cross-correlation r_{exact}	n	g^2 method 1	g^2 method 2	Slopes of regression lines r_{est}
0.90	3	2.48	2.90	
	4	2.91	4.52	
	5	4.16	5.32	
	6	4.45	4.53	
				$0.72 \pm 0.25,\ 0.57 \pm 0.75$
0.60	3	1.75	1.89	
	4	2.24	2.46	
	5	2.91	3.30	
	6	3.71	4.39	
				$0.65 \pm 0.10,\ 0.83 \pm 0.16$
0.20	3	1.24	1.69	
	4	1.75	2.18	
	5	1.62	1.79	
	6	1.47	1.90	
				$0.056 \pm 0.2,\ 0.02 \pm 0.2$

Notes: n is the number of elements in the population. g^2 is the ratio of the observed variance to the variance for uncorrelated variables. Method 1 refers to the method in which it is the probability p which is adjusted before g^2 is computed, whereas in method 2 it is the number of active elements which is adjusted prior to computing g^2. The column "Slopes of regression line" refers to the regression $(n-1, g^2)$; the first and second numbers are the slopes for method 1 and 2 respectively.

Regression on every position of the ants

$r = 0.90:$ x variables $\rightarrow r_{\text{x-est}} = 0.91$ y variables $\rightarrow r_{\text{y-est}} = 0.88,$ $r_{\text{xy-est}} = 0.89$

$r = 0.60:$ x variables $\rightarrow r_{\text{x-est}} = 0.64$ y variables $\rightarrow r_{\text{y-est}} = 0.63,$ $r_{\text{xy-est}} = 0.63$

$r = 0.20:$ x variables $\rightarrow r_{\text{x-est}} = 0.33$ y variables $\rightarrow r_{\text{y-est}} = 0.17,$ $r_{\text{xy-est}} = 0.25$

It can be seen that the accuracy is indeed better than for the results given in the table especially for low r.

How to deal with asymmetric observations: first method

The description given by our model implies that if the total area is divided into two parts A_1, A_2. none is favored. This means that the probablity to be in A_1 should be the same as the probability to be in A_2. If it is not the case, there must be some kind of asymmetry. One can think of (at least) two possible causes of asymmetry.

(1) If the number counted in A_1 is much larger than $n/2$, it may be because for some reason(s) (usually unknown to us) the ants prefer to be in A_1. For instance, if

there is a dead ant in A_2 this part may be avoided[40]. If this is the case, it means that if A represents a fraction p of the total area, the probability to be in A should not be taken as equal to p but rather as equal to $p' = m_e/n$. For instance, in the previous example where $n = 195$ and $p = 0.5$, one gets $p'n = m_e = 58 \Rightarrow p' = 58/195 = 0.30$.

In short, in this methodology the theoretical variable p will be replaced in all the formulas of Proposition 2 by the adjusted parameter $p' = m_e/n$.

(2) A second possible cause is the fact that some individuals just do not move. One can say that they are "frozen". It is to this case that we turn now.

How to deal with asymmetric observations: second method (frozen elements)

On using the previous method one does not have to care about the cause of the asymmetry. However, observations show that a fairly common cause is simply the fact that some of the living organisms remain motionless. If they were in subset A initially, they will remain there during the whole duration of the observation. Similarly, if they were not in A initially, they will remain outside of A all along. As they never change side, these elements can be said to be "frozen". On the contrary, the elements which move in and out of A will be called active elements.

If one assumes that there are n' active elements, the sum S can be written as follows:

$$S_n = S_{n'} + f_A, \text{ where: } S'_n = X_1 + \dots X'_n, \quad f_A = X_{n'+1} + \dots X_n$$

Whereas S' is a random variable, f_A is a deterministic constant which is equal to the number of frozen elements located in A. Thus, the variance of S_n becomes:

$$\sigma^2(S_n) = E\left[(S_n - E(S_n))^2\right] = E\left[(S_{n'} + f_A - E(S_{n'}) - f_A)^2\right] = \sigma^2(S'_n)$$

which shows that our previous calculation applies here as well provided n is replaced by n'.

$$\sigma^2(S_n) = n'\sigma g^2, \quad g = \sqrt{1 + (n'-1)\overline{r}}$$

So, the only question which remains is how to determine n'. In fact, there are 3 unknown numbers: n', the number of frozen elements in A that we have denoted by f_A, and the number of frozen elements that are not in A which will be denoted by $f_{\bar{A}}$. Although we only need n', this number can only be found together with the two other unknown numbers.

At first one might think that there can be a way to determine these numbers from

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[40] It should be noted that at this point this remains a fairly hypothetical reason. We did not try to test it by putting several dead ants on one side. In fact, we did not wish to engage in such a direction because it seems a hopeless task to try to find out what are the parameters which rule the behavior of the ants. Moreover, the "frozen ant" mechanism that we discuss later on seems simpler and more satisfactory anyway.

evidence based on the means in A and $\bar{A}$. This is not the case, however, for a reason which is explained below.

As the question cannot be solved in a general way we will be content with examining two special cases which are of special practical significance. For the sake of simplicity, in the following discussion it will be assumed that $p = 1/2$.

(1) One major cause of frozen elements occurs when ants or bees cluster together. If the cluster is formed in A this will result in a big f_A. As $S_n = S_{n'} + f_A$ we see that this will result in the fact that m_e (which is the observed value of $E(S_n)$) will be fairly large and in particlar larger than $n/2$, the expected value in the absence of any frozen element. Consequently, we will consider the fact that $m_e > n/2$ as indicating that a cluster has formed in A and none outside A. In such a case almost all the frozen elements are in A which means that $f_A \simeq n - n'$. Thus one gets:

$$E(S_n) = E(S'_n) + f_A \simeq E(S'_n) + (n - n')1 \Rightarrow m_e = n'/2 + n - n' \Rightarrow n' = 2(n - m_e)$$

In the general case, the last result would take on the form: $n' = (n - m_e)/(1 - p)$ and this case will be signaled by the fact that m_e is substantially larger than np.

(2) On the contrary, if the cluster is formed outside of A then almost none of the $n - n'$ frozen elements will be in A which means that

$$S_n == E(S'_n) + f_A \simeq S_{n'} + (n - n')0 \Rightarrow m_e = n'/2 \Rightarrow n' = 2m_e$$

In the general case, the last result would take on the form: $n' = pm_e$ and this case will be characterized by the fact that m_e is substantially smaller than np

(3) Finally, one must consider the intermediate case in which the number of frozen elements is approximately the same in A and outside of A. This may happen when there are two clusters, one A and the other in $\overline{A}$. It can also happen in the absence of any cluster when the individuals which are frozen (or at least somewhat "sleepy") are distributed uniformly in the whole population. Under that fairly natural assumption: it makes sense to assume that the sleepy elements are neraly in equal number in the two parts. In such a situation:

$$S_n = S_{n'} + \frac{n - n'}{2}1 \Rightarrow m_e = n'/2 + \frac{n - n'}{2} = n/2$$

We see that m_e, the average population in A, will be the same as without frozen individuals[41]. This result could of course have been expected in advance. Indeed, if the frozen elements are distributed in the same way as the rest of the population the mean will not be affected. For instance, if for $n = 200$ there are 198 frozen elements and just 2 non-frozen elements and if the 198 elements are distributed uniformly

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[41] The same argument holds in the general case when the area A is a fraction p of the total area.

between A and $\overline{A}$, one will have $m_e = (0 \text{ or } 1) + 99 \simeq n/2$. In other words, the mean is the same as without any frozen elements.
In contrast, the variances will be very different:

- With 198 frozen elements: $\sigma^2(S_{200}) = \sigma^2$.
- Without any frozen element: $\sigma^2(S_{200}) = 200\sigma^2$.

Conclusions The previous discussion shows that:

(1) A problem due to frozen elements can be detected (and corrected) if m_e, the time-averaged population in A, is substantially different from np.

(2) If $m_e \simeq np$ but there are nevertheless frozen elements, this problem can neither be detected nor corrected and it will lead to *under-estimating* the variance and to a biased estimate for the average cross-correlation $\overline{r}$.

Remark Frozen elements can of course be detected by individual visual inspection of the living organisms. However, when their number reaches several hundreds this becomes fairly difficult.

Example of application of the previous methodology

We consider the following case which corresponds to a real observation performed on ants

$$n = 520,\ p = 1/2\ m_e = 212,\ \sigma_e = 47$$

and we apply successively the two previous methods.

Method 1 (asymmetrical preference for some unknown reason)
The adjusted probability is

$$p' = m_e/n = 0.41 \Rightarrow q' = 1 - p' = 0.59 \Rightarrow \sigma^2(S_1) = pq = 0.24 \Rightarrow \sigma_i^2(S_n) = npq = 126$$

As a result:

$$g^2 = \frac{\sigma_e^2}{\sigma_i^2(S_n)} = \frac{47^2}{126} = 17 \Rightarrow \overline{r} = \frac{g^2 - 1}{n - 1} = 0.032$$

Method 2 (frozen elements)
Here we are in the case where $m_e = 212$ is substantially lower than $np = 520/2 = 260$. Hence we get the adjusted number of active elements n' through the formula:

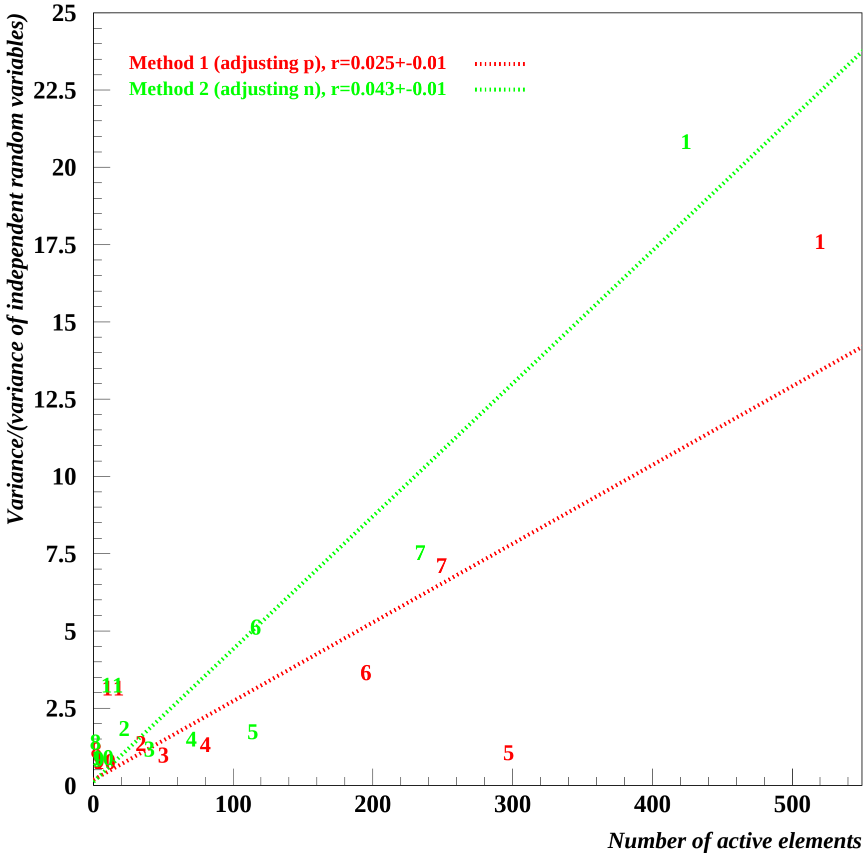
$$n' = \frac{m_e}{p} = 2 \times 212 = 424$$

Then we determine $\overline{r}$ by using the standard formula with n replaced by n'.

$$= n'pqg^2 = \frac{\sigma_e^2}{n'pq} = \frac{47^2}{424 \times (1/4)} = 21 \Rightarrow \overline{r} = \frac{g^2 - 1}{n' - 1} = \frac{21 - 1}{423} = 0.047$$

As can be seen the two methods lead to average cross-correlations of the same order of magnitude (they differ by 32%). Here, just for the sake of ilustration, we have computed $\overline{r}$ from a single experimental result. One should observe that the right method for determining $\overline{r}$ is not to compute it from individual results but to get it as the slope of the regression line determined by several results (in fact, as many results as possible).

For a given σ_e, the average correlation $\overline{r}$ is completely determined by g^2. However, in computing the regression line it is not only g^2 which matters but also the value of n' because the x-variable of the regression is the number of *active* elements. For instance, $p = 1/2$ and $m_e = n/20$ implies $n' = n/10$. The fact that n' is much smaller than n makes a big difference in the regression. This is illustrated in the following graph which summarizes 11 experiments carried out with various number of ants.



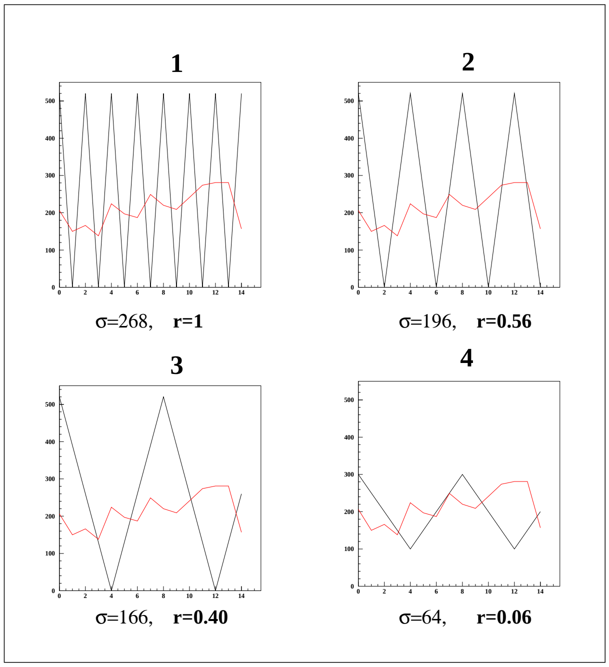
Comparison of two estimation methods of the average cross-correlation of a population of ants. The cross-correlation is a way of expressing the average interaction strength between the ants. The correlation of the set of 11 points (not to be confused with the estimated cross-correlation which is the slope of the regression line) is 0.84 for the first method and 0.95 for the second. In the second method the frozen elements are left out and do not contribute. The present results suggest that at least in this case the second method does a better job. The error bars of $\overline{r}$ represent a confidence interval for a confidence level of 0.95.

At first sight it may seem surprising that the estimated cross-correlation is as low as 0.04. In the next section we explain why this is so.

Why is the estimated cross-correlation so small?

First of all, it is necessary to make an important distinction. Suppose that by computing the correlation of a set of data $(x_i, y_i) \quad 1 \leq i \leq n$ one gets a correlation as low as 0.04. Such a low correlation would almost always mean that the correlation is not significant in the sense that the confidence interval contains the correlation zero[42].

Here, however, the correlation $\overline{r}$ is obtained in a different way, namely as the slope of a regression line. From the errors bars given in the caption of the figure it can be seen that this estimate is quite significan in the sense that the confidence interval of $\overline{r}$ does *not* include 0.



Relation between the fluctuations of $n_1(t)$ and the values of $\overline{r}$. We suppose that the whole domain which contains the ants has been divided into two parts and we observe the fluctuations $n_1(t)$ of the number of ants in part 1. The black curves correspond to different hypothetical curves while the red curve is what was actually observed in the experiment with ants considered above. The numbers given under the graph are the standard deviation and the (corresponding) correlation for the black curves. For the red curve these numbers are 47 and about 0.04 respectively.

The first graph corresponds to the greatest possible standard deviation in the sense that at each time step all the ants move from part 1 to part 2 or vice versa; in this case the average cross-correlation is almost equal to 1. In the second case the same move occurs in two time steps, while in the third it occurs in 4 time steps. In the actual experiment one time step was 5 mn which means that in this last case all ants would change side within 20 minutes. Finally, the last graph corresponds to a case in which the variance of the simulated curve is similar to the variance of the observed curve.

Conclusion: the route ahead

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[42] The only exception to this rule may occur when the number n of pairs is very large (say several thousands) so that the confidence interval becomes smaller than 0.04.

The experiments carried out over the past months were tentative and provisional in many ways. The research involved the following steps.

- New measurement methods had to be designed
- Appropriate devices had to be bought and pieced together
- The consistency of the results obtained by different methods must be checked.

Whereas the first two steps have been largely completed, for the last one more work is still needed.

Once the methodology will be found to work two important questions will have to be addressed.

- How does the strength of interaction change with the average distance between the elements?
- How can one estimate the level of noise?

Why are these questions important?
In our discussion of phase transitions in physics, we have found that they are mainly determined by two facteurs: (i) the average inter-molecular distance (ii) the velocity of the molecules which is directly related to the temperature of the suystem. A change of state can be achieved through either (or both) of these parameters.

So far we did not consider the question of the temperature in non-physical systems because we were not really in a position to do so.
Indeed, a given level of fluctuations can be due

- To a strong interaction combined with a low level of noise, or
- To a weak interaction combined with a substantial amount of noise.

These two possibilities are well illustrated by the formula for a sum of coupled random variables that we have written earlier.

$$\sigma^2(S_n) = n\sigma^2\left[(n-1)\overline{r} + 1\right]$$

In this formula $S(n)$ is the number of molecules contained in a subset of the system. For a given n the same $\sigma^2(S_n)$ can be obtained with a high $\overline{r}$ combined with a small σ or with a $\overline{r}$ close to zero and a large σ. The first case would correspond to a solid at a low temperature T_1 whereas the second would correspond to a gas at a high temperature T_2 $(T_1 \ll T_2)$.

We leave this question open for further discussion.

Appendix A: Practical hints for doing experiments

In recent decades experiments in molecular biology, biochemistry or biogenetics have become more and more sophisticated. It seems that costly technical devices had become a must. Yet, the history of physics tells a fairly diferrent story. For instance, the experiments done par Galileo (1564-1642), Torricelli (1608-1647) or Pascal (1623-1662) which opened the road of modern experimental physics relied on fairly simple devices. Similiarly, the experiments done by Gregor Mendel required great care and patience but fairly little in terms of equipment. It is likely that for developing the statistical mechanics of living organisms that is envisioned in this report it is more essential to find appropriate experimental ideas than to rely on high-technology measurement devices. Once the bases have been laid and the need emerges for more accuracy in the measurements then, but only then, will be the right time for resorting to high-tech equipment.

Fig A1: Ants and drosophiles On the left: collecting ants. The white Bristol board was left a few centimeters from the exit hole of a colony for about half an hour. The brown product is chesnut cream with a few drops of water.
On the right: a tube containing drosophila as prepared by a research laboratory in population genetics.

To do experiments on populations of ants, fruit flies or small fishes is somewhat similar to running simulations on a computer in the sense that the experimenter asked questions and the experiment provides the answer. As will be seen, the techniques which are necessary for such experiments are fairly simple to implement.
We will successively describe how to get the populations, how to keep and control them and how to do the experiments

How to get the fishes or insects?

Small fishes The organisms which are probably the simplest to buy and handle are

Fig. xx: Carbon dioxide gas cylinder. As compressed carbon dioxide is necessary in many activities, small cylinders similar to the one shown on the picture can be bought fairly easily and at low cost. The one represented here is used for the production of sparkling water, it weighs only one kilogramme and costs about 20 euros (10 euros for the empty bottle and 8 euros for a refill).

small fishes. Why *small* fishes. The answer is obvious for in order to reduce statistical fluctuations it is often necessary to use populations of one or several hundred fishes. Thus, to minimize cost and size of containers one must focus on fishes of less than 2 or 3 cm in length. Fresh-water fishes of such a small size are usually sold to serve as preys for bigger fishes and for that reason are fairly inexpensive.
Such small fishes are not only easy to buy, they are also easy to handle in the sense that, unlike ants or fruit flies, they remain in their container.

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