

The matrix is available on our server in /pub/mat. The differences may be mirrored to a similarity matrix. The idea presented in the next section enables further improvement.

#### Notation independent Schmidt matrices

To eliminate the dependence of the distance matrix on the formulation of the used properties we systematically negated the formulation of the properties and calculated the mean of the arising matrices. Thus, the improved Schmidt matrix for the Taylor properties (see [1]) reads:

A	0																					
C	19	0																				
D	159	120	0																			
E	25	200	36	0																		
F	99	68	26	168	0																	
G	6	30	179	28	115	0																
H	227	180	166	98	68	25	0															
I	95	63	25	159	47	111	145	0														
K	167	126	117	61	107	187	23	99	0													
L	121	87	29	191	71	138	182	13	126	0												
M	63	36	200	120	23	77	107	20	68	38	0											
N	108	73	26	73	187	125	183	178	129	215	133	0										
P	63	37	74	137	126	77	29	119	216	147	85	40	0									
Q	180	133	73	26	111	202	110	107	70	134	73	36	88	0								
R	26	205	67	23	177	28	60	166	30	198	125	73	138	27	0							
S	73	108	48	104	241	83	229	232	169	27	180	19	66	63	105	0						
T	58	32	65	125	121	72	113	115	73	146	78	30	81	75	129	55	0					
V	43	20	159	25	100	55	230	36	168	54	63	107	62	178	25	146	60	0				
W	161	121	176	103	32	182	27	96	57	128	63	115	198	60	110	154	68	164	0			
Y	193	152	207	127	49	217	43	128	78	96	86	142	235	80	133	184	91	206	13	0		

This distance matrix may be used to calculate multiple alignments and phylogenetic tree reconstruction. We note that maximization of the phylogenetic information content, PIC [2], also leads to a unique notation independent distance matrix.

#### Discussion

The presented changes are implemented in an integrated amino acid sequence analysis tool of Geoff Barton [3]. Our solution always uses the same algebraic distances of amino acid distances. The presented concept improves the analysis of amino acid sequences but also improves Schmidt's general classification method for binary character data.

#### References

- [1] W. Schmidt, *J. Molec. Evol.*, **41** (1995) 522-530.
- [2] W. Schmidt, *Bull. Math. Biol.*, (in the press).
- [3] G. J. Barton, *Methods Enzymol.*, **183** (1990) 403-428.

## SELF-ORGANIZATION OF TRAIL NETWORKS USING ACTIVE BROWNIAN PARTICLES

Frank Schweizer

Humboldt University, Institute of Physics, Invalidenstr. 115, 10115 Berlin, Germany

e-mail: frank@summa.physik.hu-berlin.de

#### Abstract

We propose a simple model for interactive structure formation based on active Brownian particles which have no memory. Just by responding to chemical gradients, these particles first explore the surface to discover food sources unknown to them, and then create trails between the nest and these sources, commonly used for movement.

#### 1. Biological Observation

The formation of complex trail patterns is a widely observed phenomenon in ants colonies commonly foraging for food from a central nest. In addition to visual navigation and internal storage of information, different ant species are capable of external storage of information, e.g. by setting chemical signposts (pheromones), which are used to mark the trails. In this paper, the problem is discussed whether these trail patterns could be also obtained under the restrictions, that (i) no visual navigation and internal storage of information is provided, (ii) in the beginning, no chemical signposts exist which lead the animals to the food sources and afterwards back to the nest.

The phenomenon considered in this paper, is based on two different stages, (i) exploration of the food sources by solitary scours, and (ii) recruitment and exploitation of the food sources. Along this recruitment trail nest mates will move in a single file, one behind the other (and not in a swarm raid) from the nest to the newly discovered food source and transport it to the nest. This foraging behavior is, to a certain extent, different from that of the army ants which has been simulated recently [1].

#### 2. Model

We propose a simple model for interactive structure formation based on microscopic local interactions between active Brownian particles which have no memory. These particles are able to generate a self-consistent field, which in turn influences their further movement and physical and chemical behavior. The analytic description is based on Langevin- and Fokker-Planck equations for the active Brownian particles, coupled by reaction-diffusion equations for the self-consistent field. Active Walker models have been previously used within a physical framework to describe different kinds of pattern formation [3,5,6]. In the considered case, the particles are able to change the conditions of the surface they are moving on by producing two

chemical substances, which can decay again by decomposition. The particles respond to the gradients of these chemicals by changing their moving direction. Further, the particles have an internal degree of freedom which determines the kind of chemical produced and responded to. This internal parameter can be changed by an interaction between the particles and some nodes, which represent the nest and the food sources.

### 3. Results

Using the basic version of the model where the active particles only produce and respond to one kind of chemical substance, we are able to simulate track patterns, which are non-directed trails mainly used by the active particles for their movement (cf. Fig. 1, left part). In the extended version, the active particles produce and respond to two different kinds of chemicals. This model simulates the formation of directed trails, which connect a starting point (nest) with other points of interest (food sources on the top and the bottom of the lattice, cf. Fig. 1, right part) that have to be discovered before. In particular, the typical dendritic foraging patterns of desert ants, reported in [2], are reproduced by the simulations.

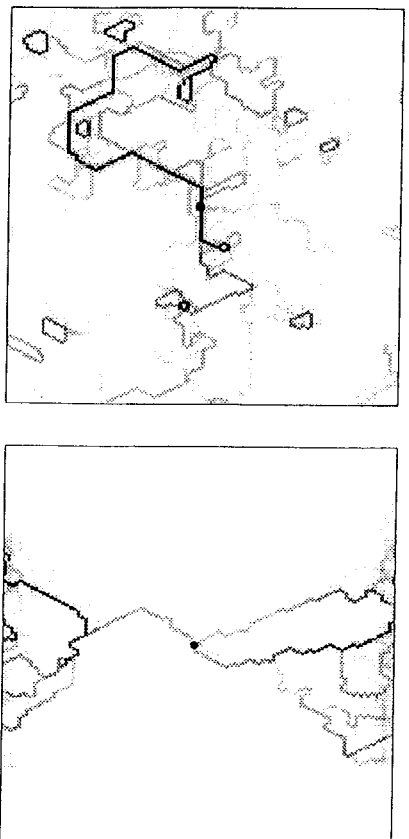


Fig. 1 Examples of non-directed (left) and directed (right) trail networks generated by active Brownian particles (for parameters see [4])

It turns out from the computer simulations (video) that, for different distributions of food sources, the model generates a distinctive trail system commonly used by the particles to exploit the food sources, and performs a high flexibility in order to discover and to link new sources to the trail network. During the evolution of the trail system we can distinguish between two different stages: the first one is a rather random movement of the active particles dropping chemical almost everywhere, and no trail exists. But during the second stage, a

distinct major trail appears, which is re-amplified by the active particles moving for- and backwards on the trail. Thus every trail has to survive a competition process, where trails not amplified enough by the active particles disappears again.

### 4. Discussion

In the model provided, the spontaneous formation of a collective trail system can be described as a self-organizing process, based on the interactions of the active particles on a local or "microscopic" level, which could lead to the emergence of the structure as a whole on the global or "macroscopic" level. The major difference to biology is denoted by the fact, that the active Brownian particles used in the simulations, have far less complex capabilities than the biological creatures. They rather behave like physical particles which respond to local forces in a quite simple manner, "Knowing" nothing else than the local concentration of a chemical. With respect to the formation of trunk trails, this could indicate, that visual navigation and information storage does not necessarily have to be indispensable presumptions to obtain those advanced and efficient foraging patterns. Our model therefore may serve as a toy model to test what kind of interaction between individuals may lead to a trail system and what are the minimal conditions for its existence.

### References

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