Structure of Cell Nuclei and Fractal Analysis

1) Histone-GFP fusion proteins -> mass distribution in cell nuclei:

- mass distribution with H1-GFP and H2B-GFP
- carrier plasmid used and overview of constructed plasmids
- histone derivatives: MacroH2A1.1 and MacroH2A1.2
- synergetic effects for Thomas and Malte

2) Fractal Geometry as method of Analysis - some aspects:

- general introduction
- methods for determening the fractal dimension
- construction of objects with a certain fractal dimension
- overview of fractal dimensions of various objects
- surface fractal dimensionof lysozyme and implications
- fractal dimension determined by scattering experiments
- fractalalaty as one basis of scaling laws in mamals

3) Current results and future aspects:

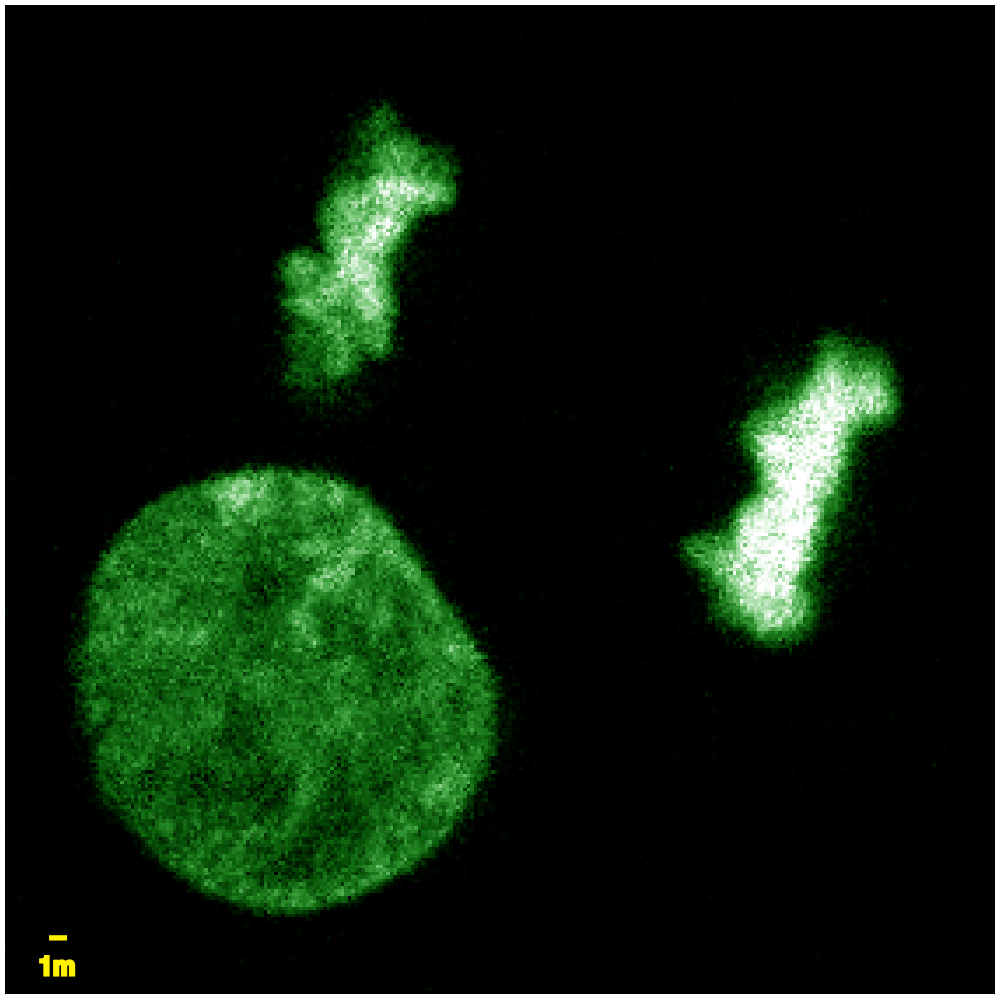
- analysis of H1 cell nuclei with a fractal analysis
- leave cutting ants: foraging strategy
- multifractal behaviour of chromatinfolding of chromosomes and future aspects

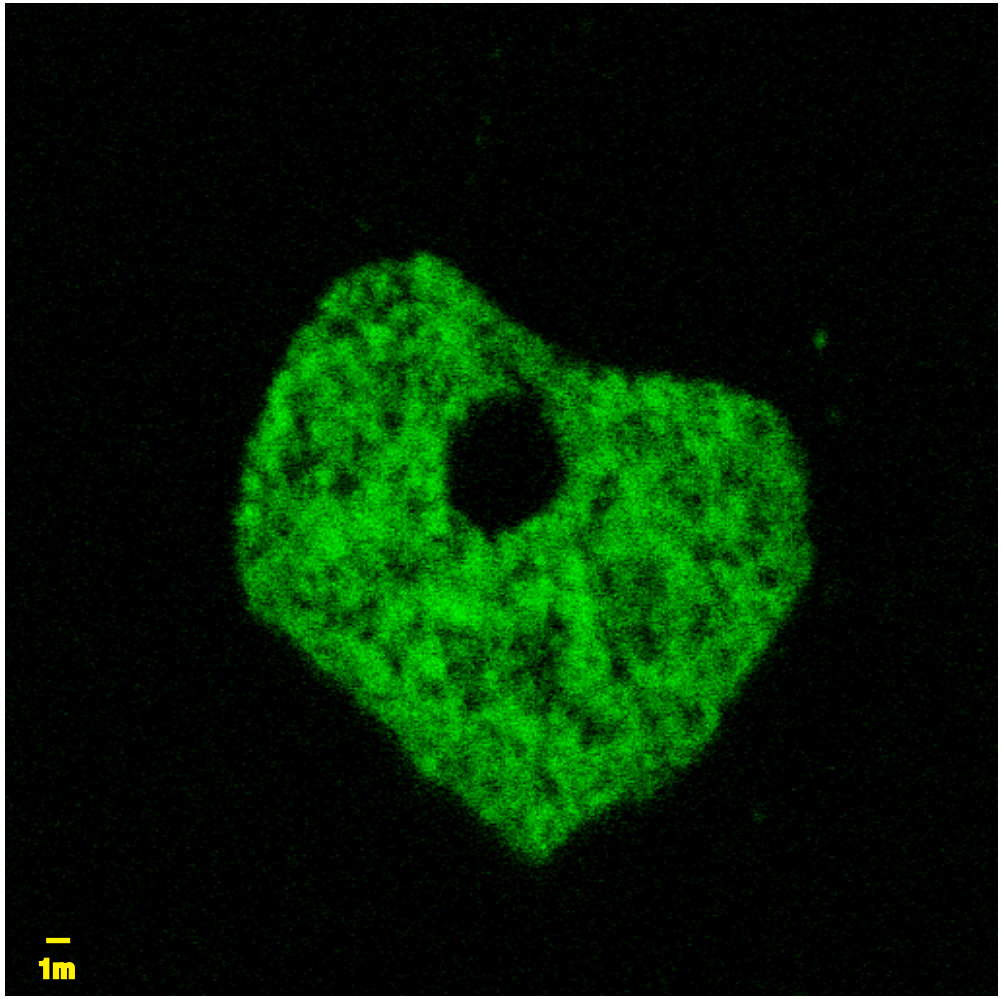
Mapping of Histone H2B-GFP and H1-GFP distribution in vivo.

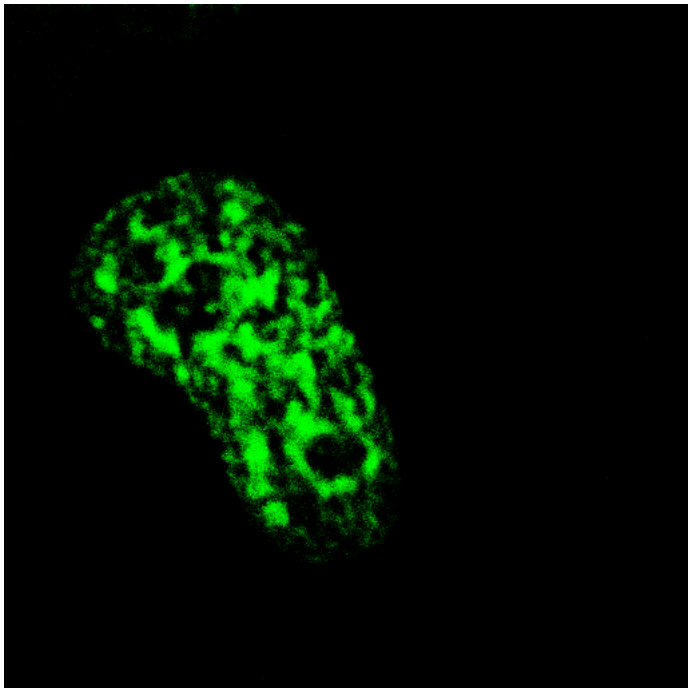
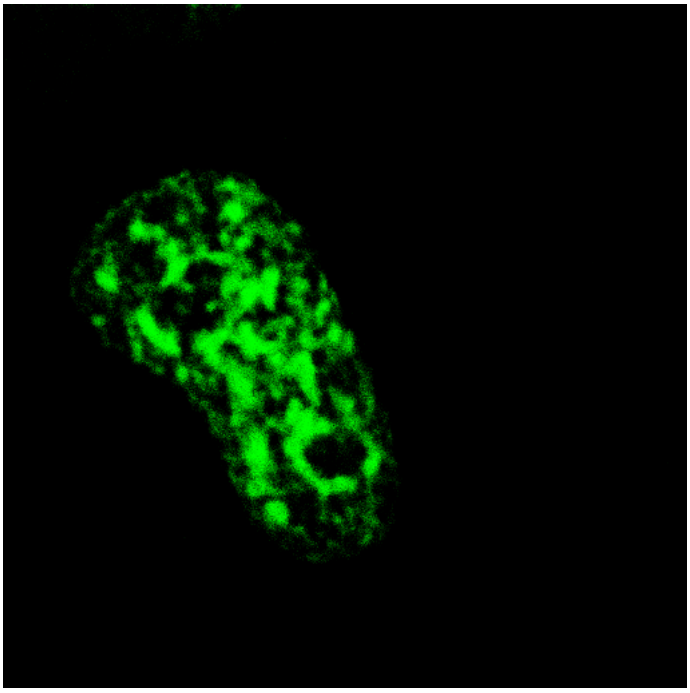
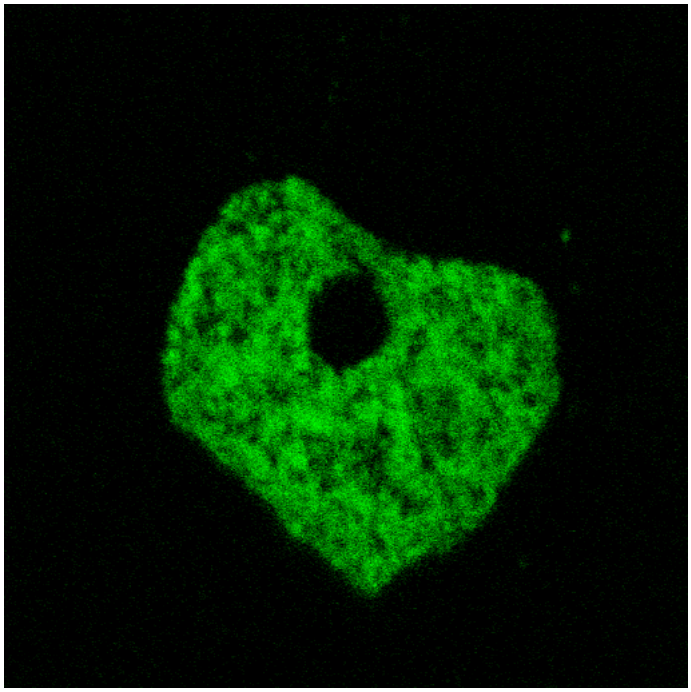
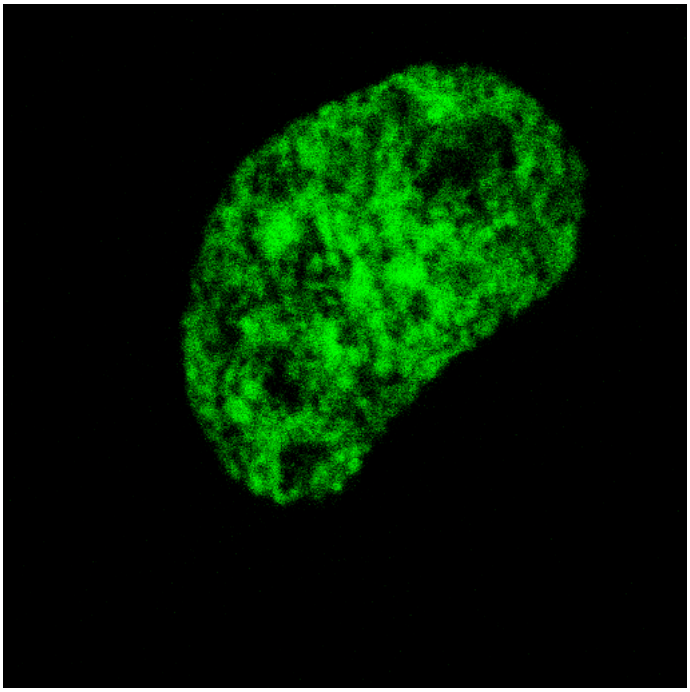
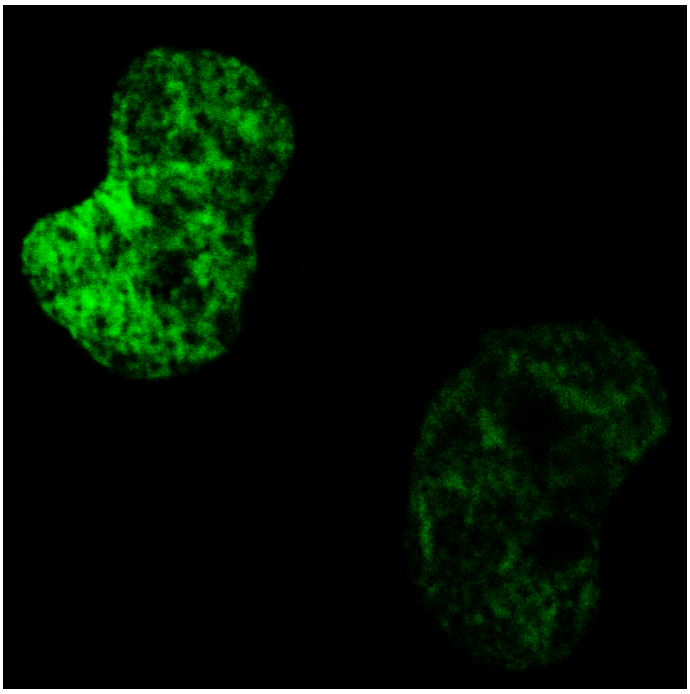
The Histone-GFP reflects the distribution of chromatin in interphase.
The structure visible in the images is similar to those found in simulations.

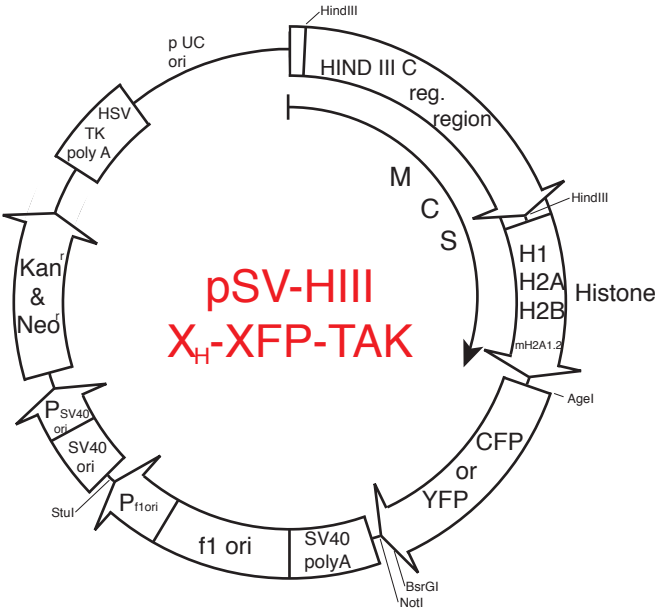
Left: HeLa cells stabaly transfected with H2B-GFP (K. Sullivan, Scripps Institute).
Confocal in vivo section of a cell nucleus and a mitosis.
Right: Cos7 cell stabaly transfected with H1-GFP (A. Alonso, DKFZ). Confocal in vivo section.

Tobias A. Knoch





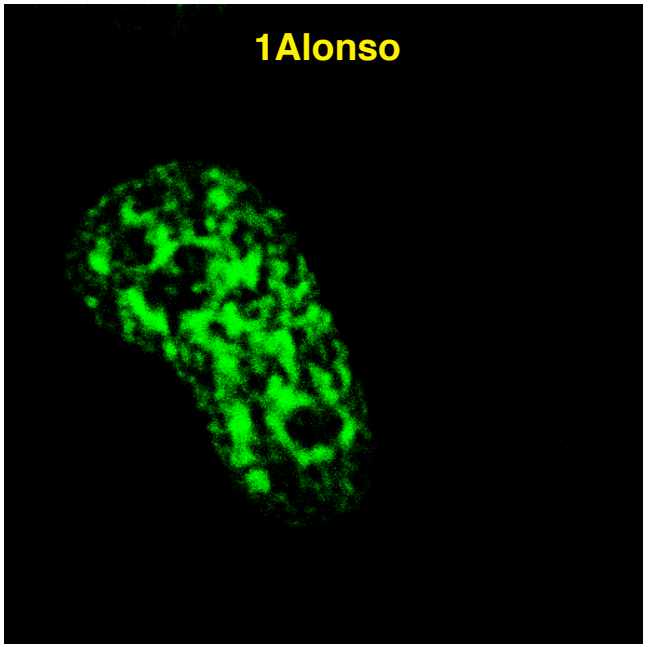


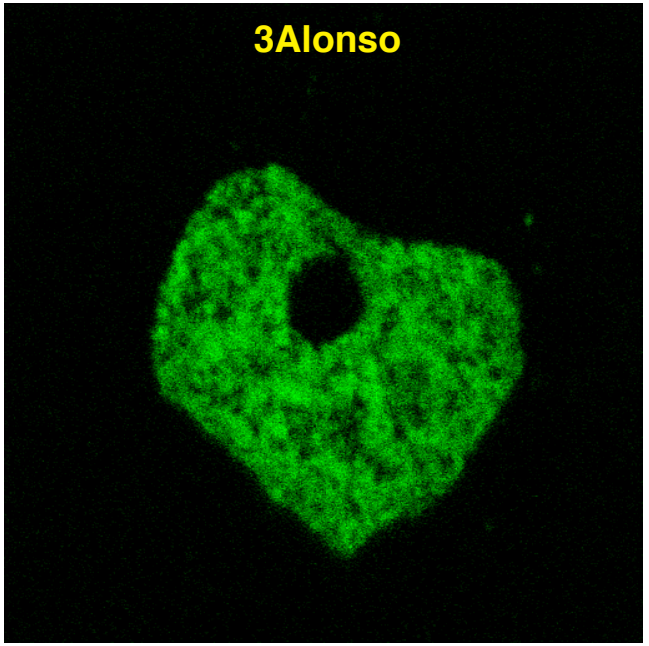
pSV-HIII-H1-CFP-TAK
pSV-HIII-H2A-CFP-TAK
pSV-HIII-H2B-CFP-TAK
pSV-HIII-macroH2A-CFP-TAK

pSV-HIII-YFP-TAK

pSV-HIII-H1-YFP-TAK
pSV-HIII-H2A-YFP-TAK
pSV-HIII-H2B-YFP-TAK
pSV-HIII-macroH2A-YFP-TAK

Mass-Fractal-Analysis

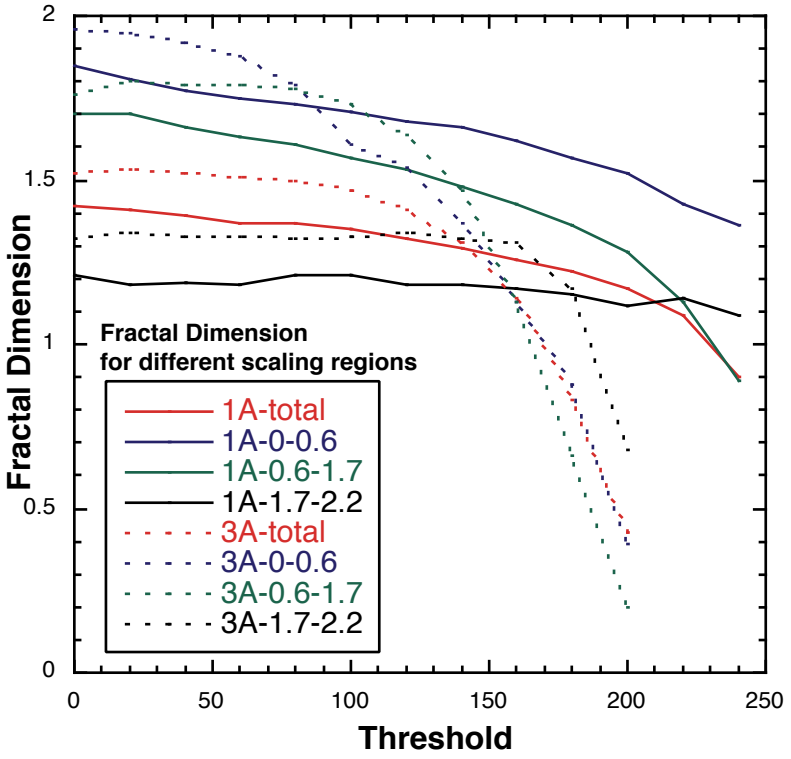




FracTAK

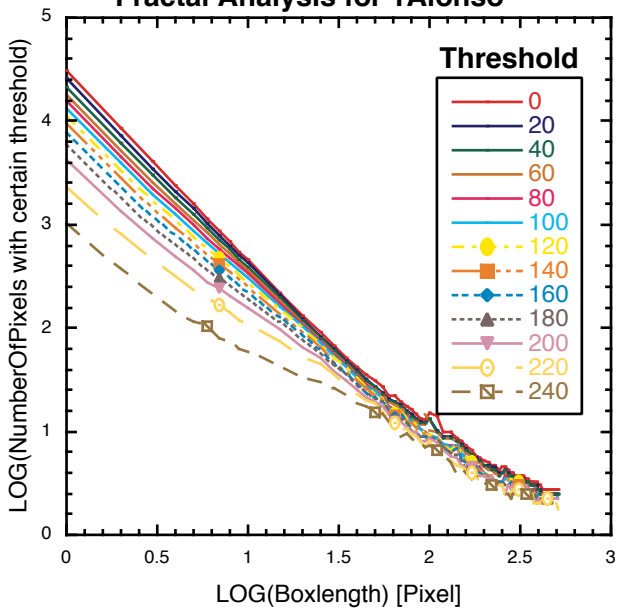
FracTAK

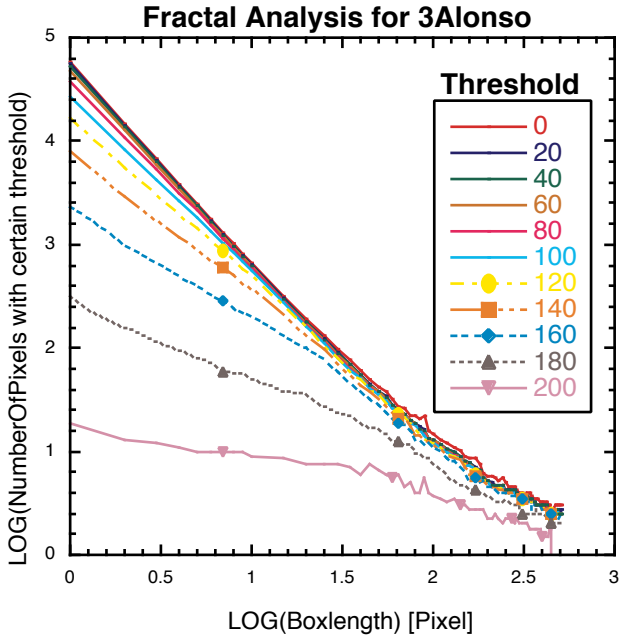
Fractal Dimension as Function of Threshold differs significantly between 1Alonso compared to 3Alonso

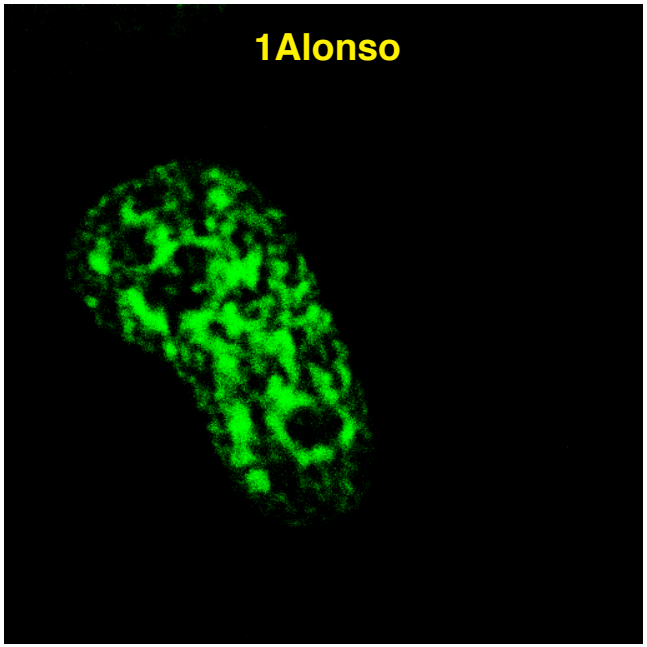


Linear Fit

Linear Fit

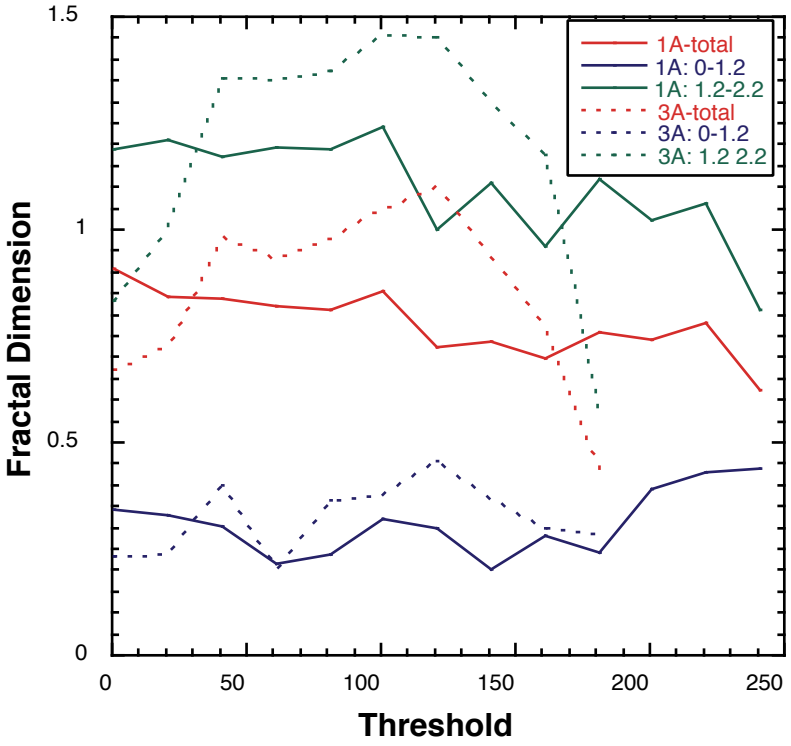


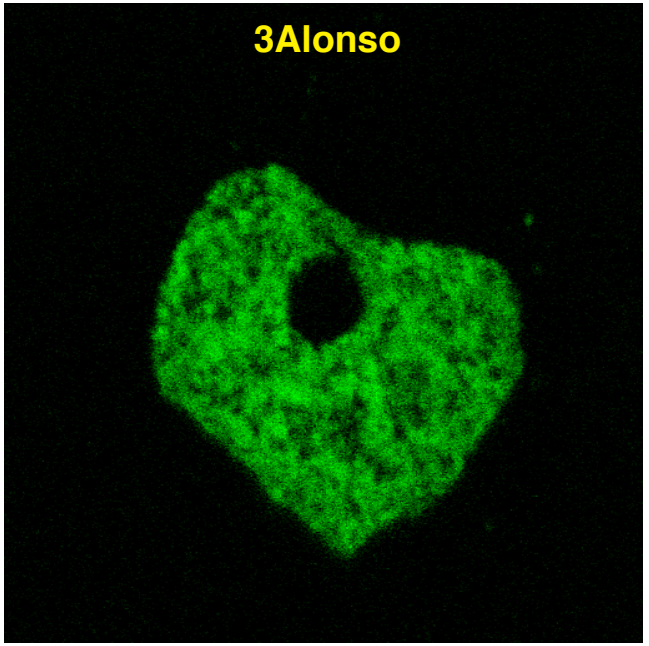




EquiSurf-Fractal-Analysis

Fractal Dimension as Function of Threshold differ significantly between 1Alonso compared to 3Alonso





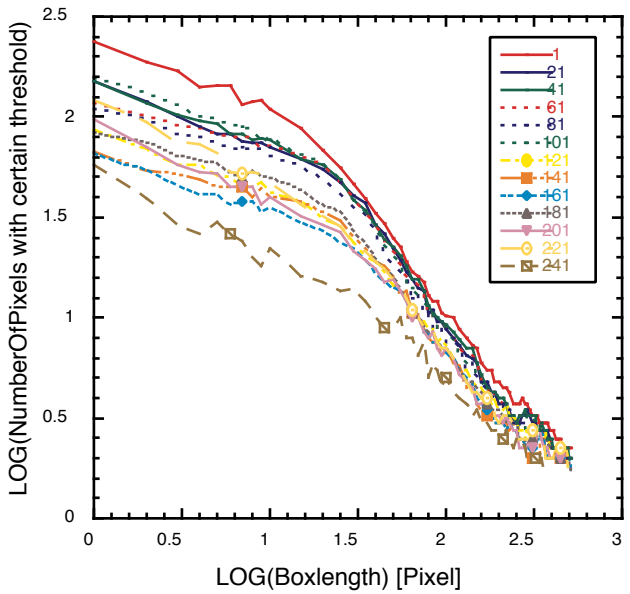
FracTAK

FracTAK

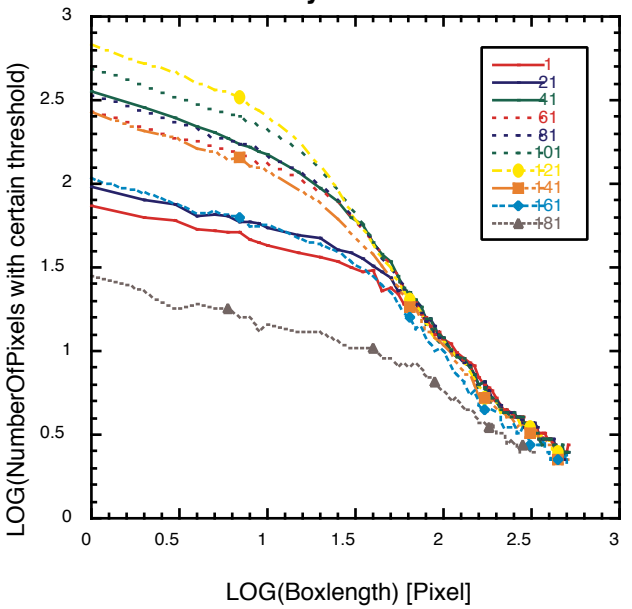
Linear Fit

Linear Fit

Fractal Analysis for 1Alonso



Fractal Analysis for 3Alonso



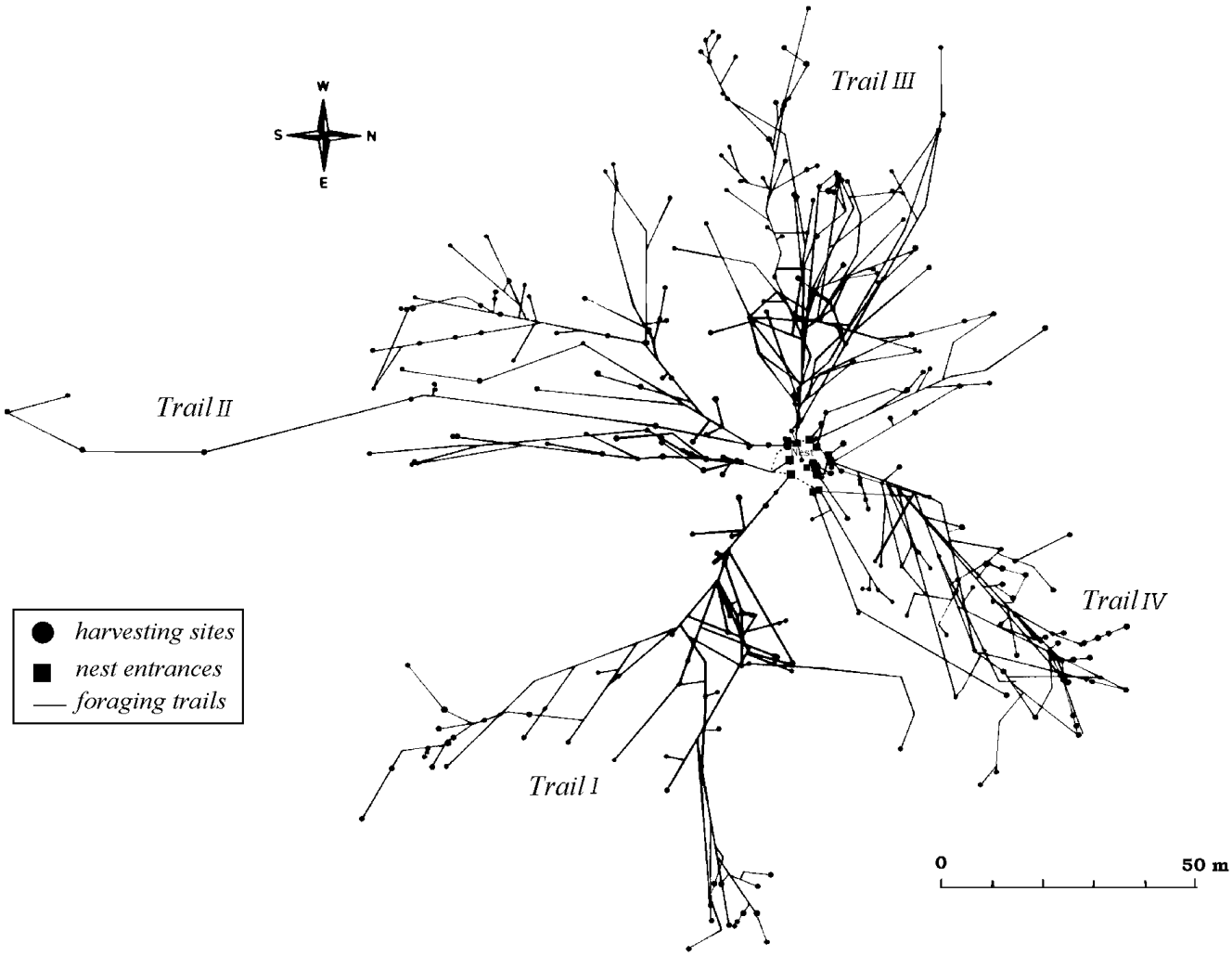
Atta colombica
Foraging analyzed with Fractal Geometry

Overview of foraging strategy:

1) Each trail is cleaned regularly from leaves -> minimized transport on trail (?).
2) Each new trail originates in an old trail -> minimize effort to build new trails (?).

3) Rain season (May - December): Leave cutting from trees.
4) Dry season (December - May): Leave and flower collecting from ground.
5) Amount of harvest stays nearly the same over the year.
6) Leaves (trees etc.) "homogeniously" distributed.
7) Trails are independent from ground structures.

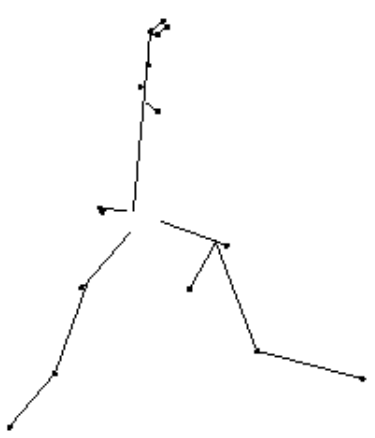
== >> Is there a deeper strategy behind trail structure ?



Foraging data from Rainer Wirth, University of Kaiserslautern

Evolution Foraging

06-1993



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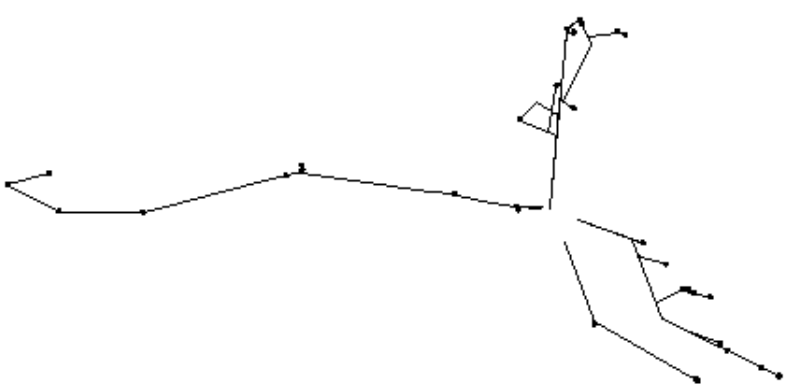

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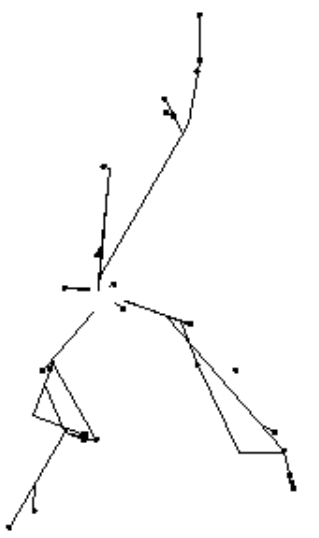

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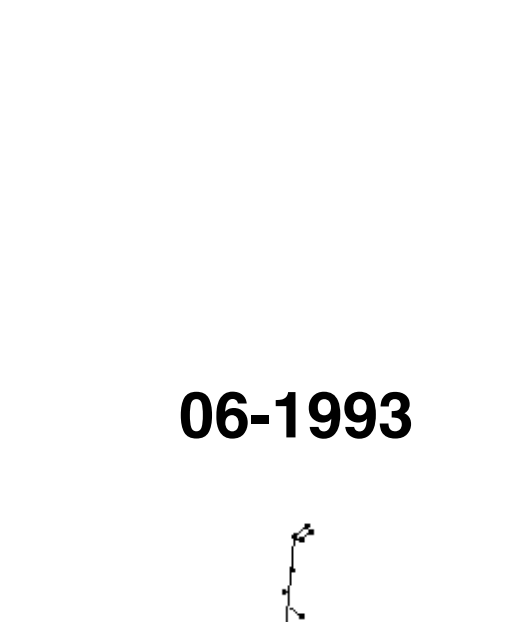

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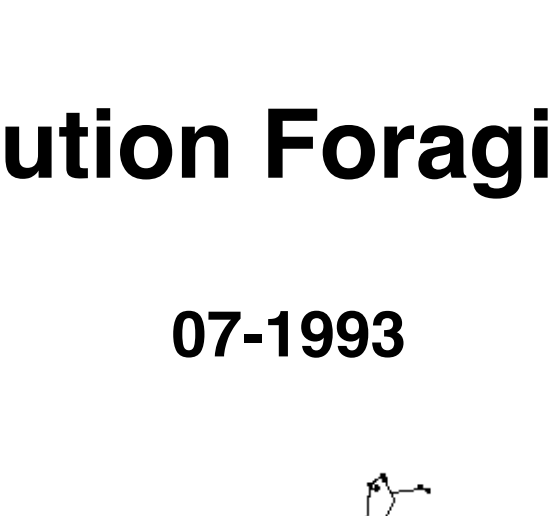

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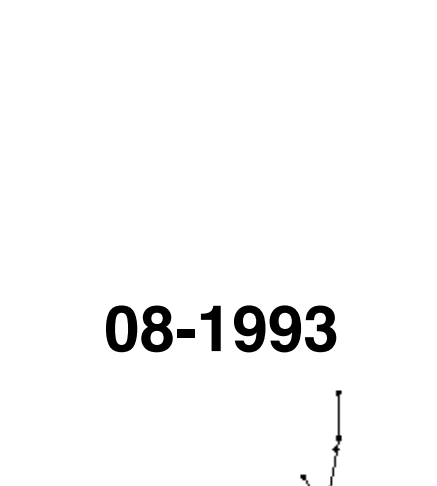

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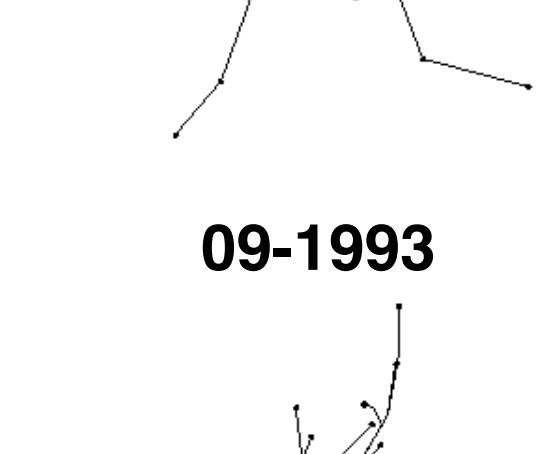

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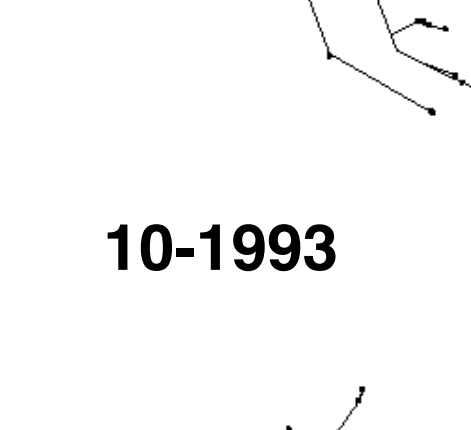

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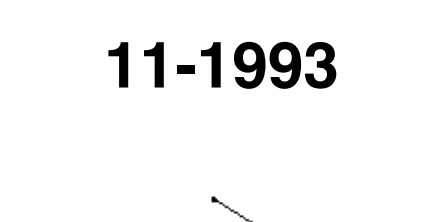

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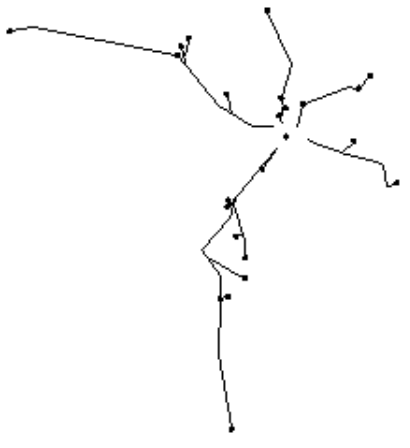

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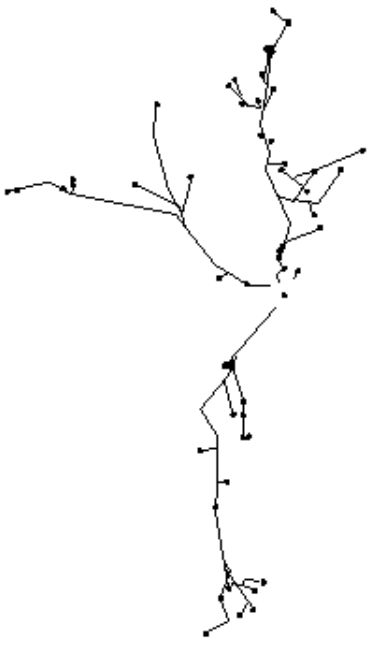

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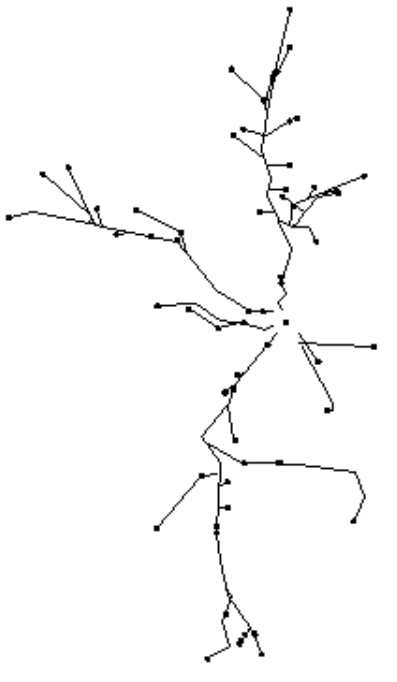
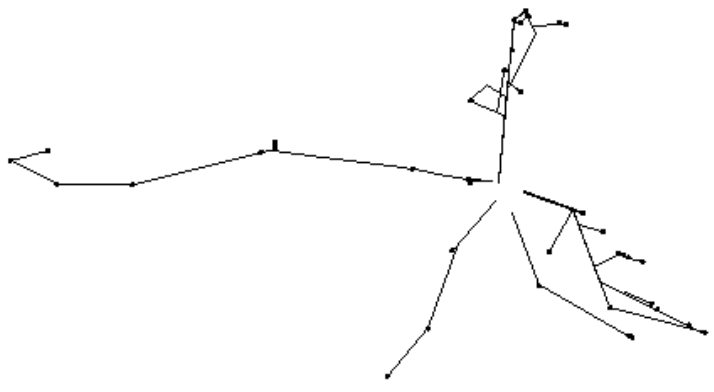


Cumulative Foraging

07-1993



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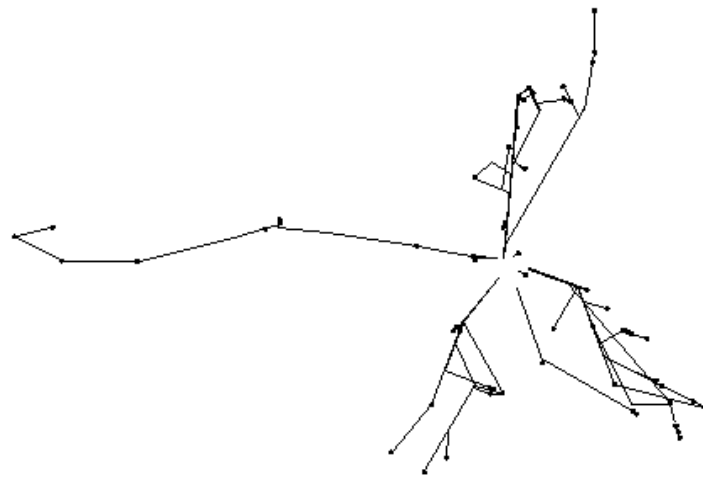

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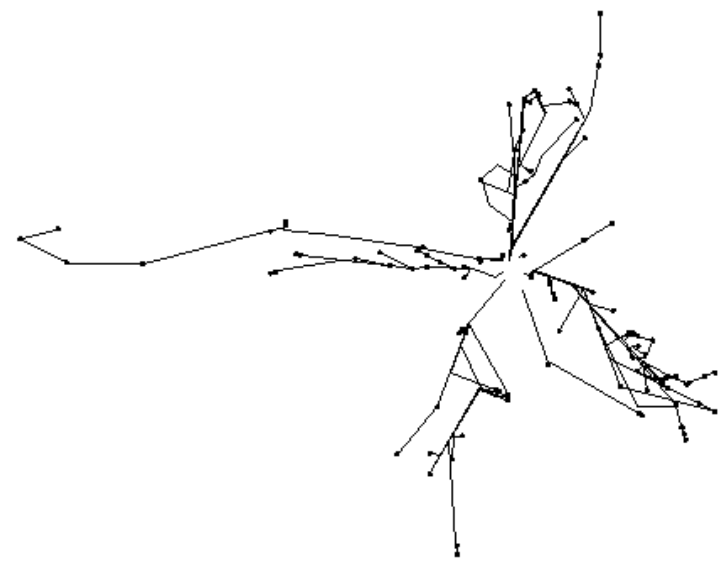

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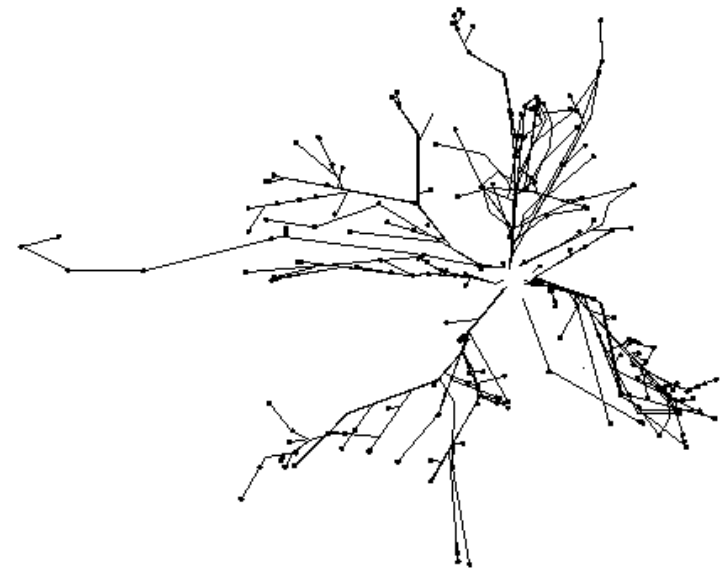

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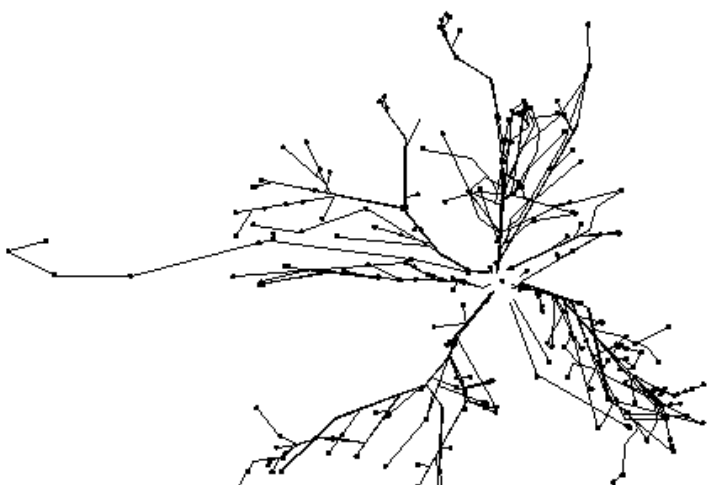

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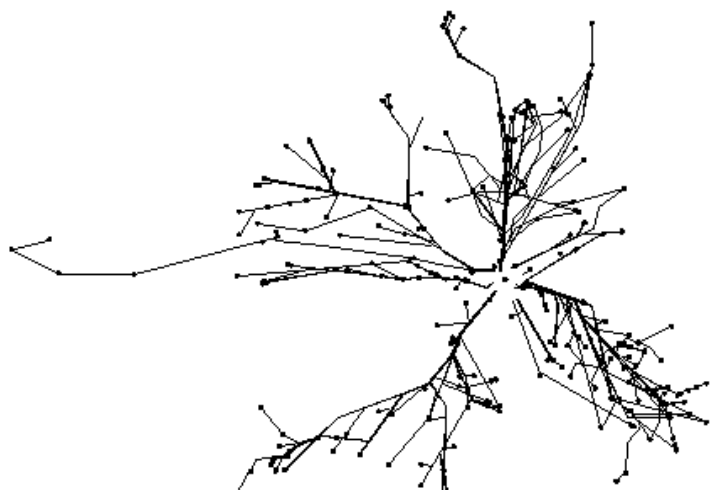

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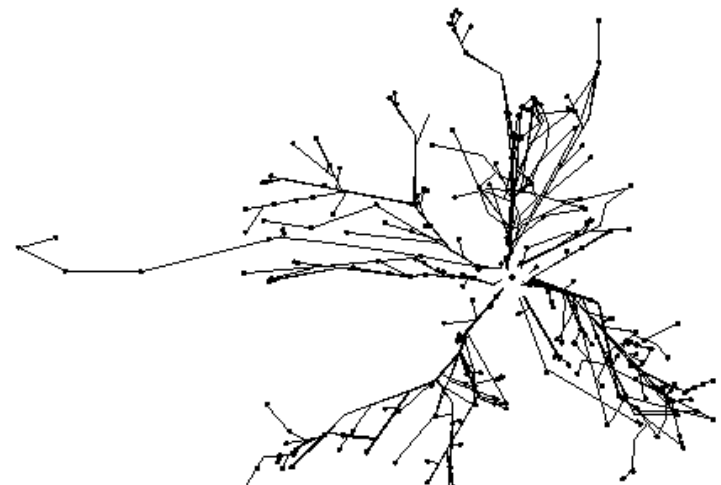

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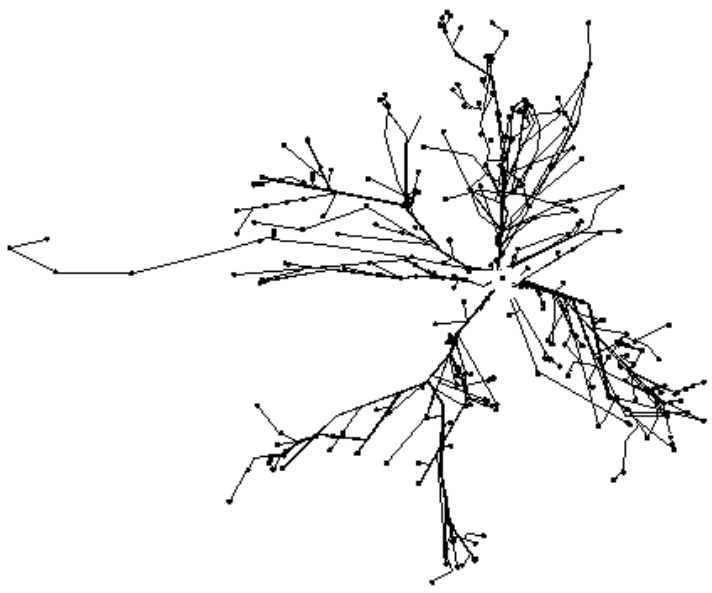

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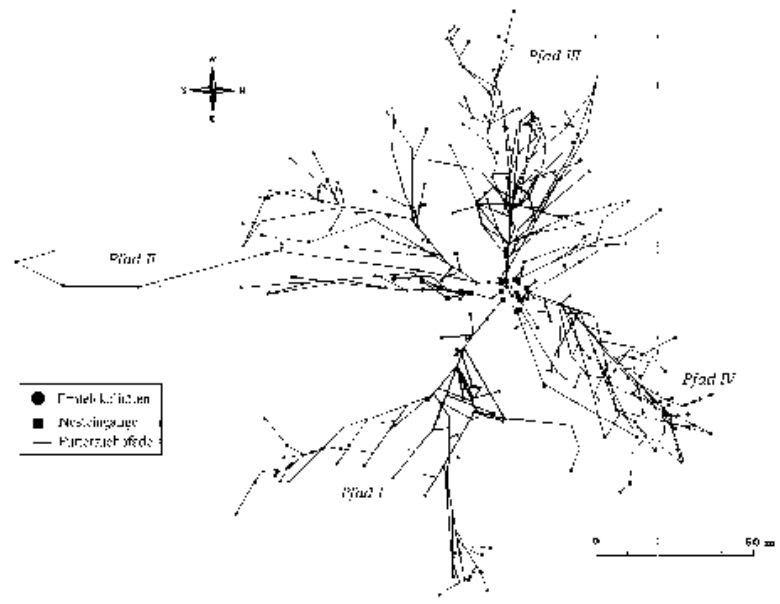
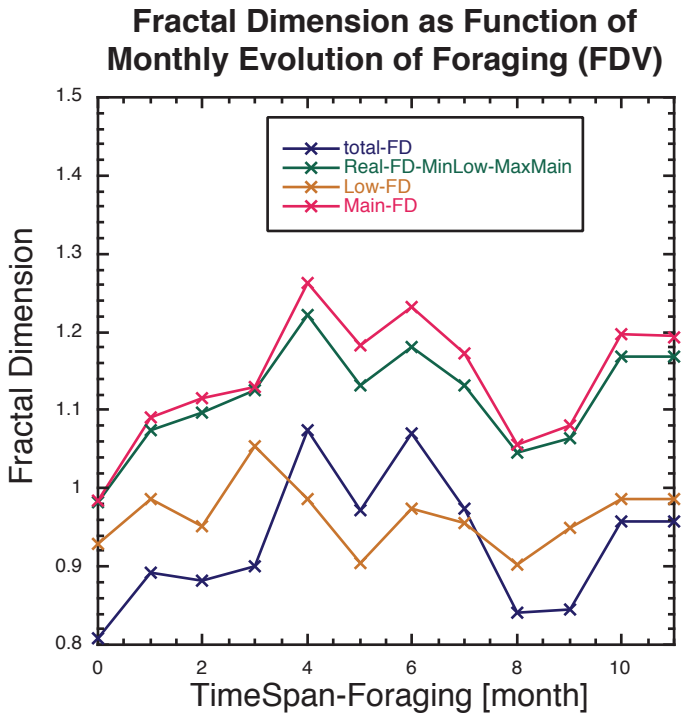
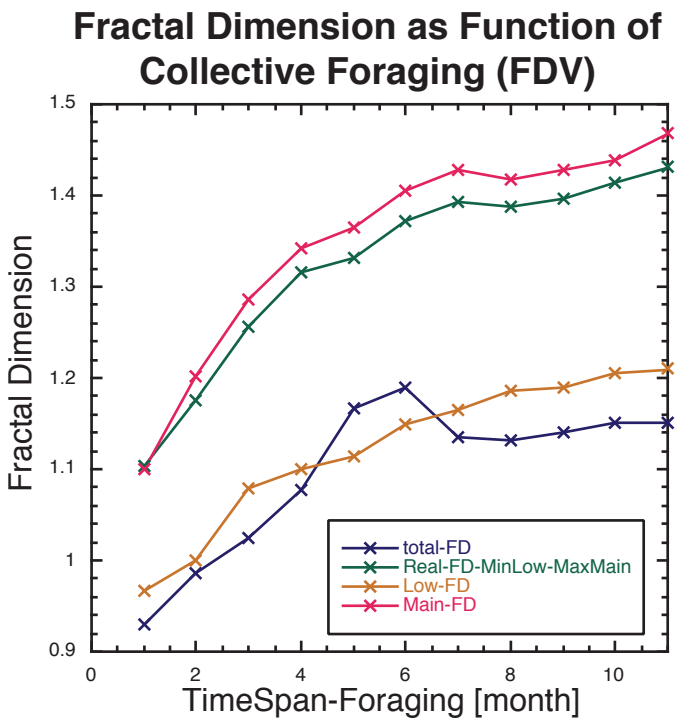
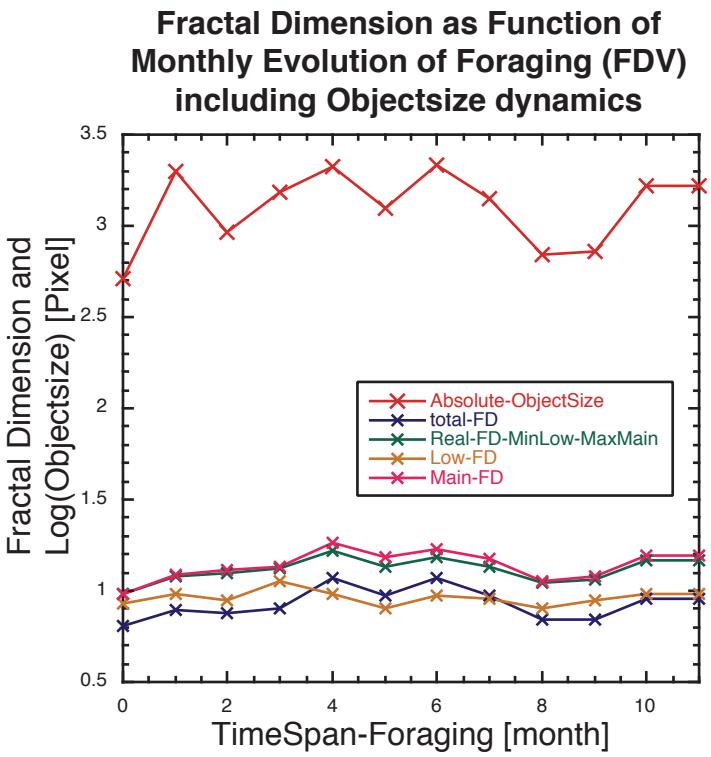
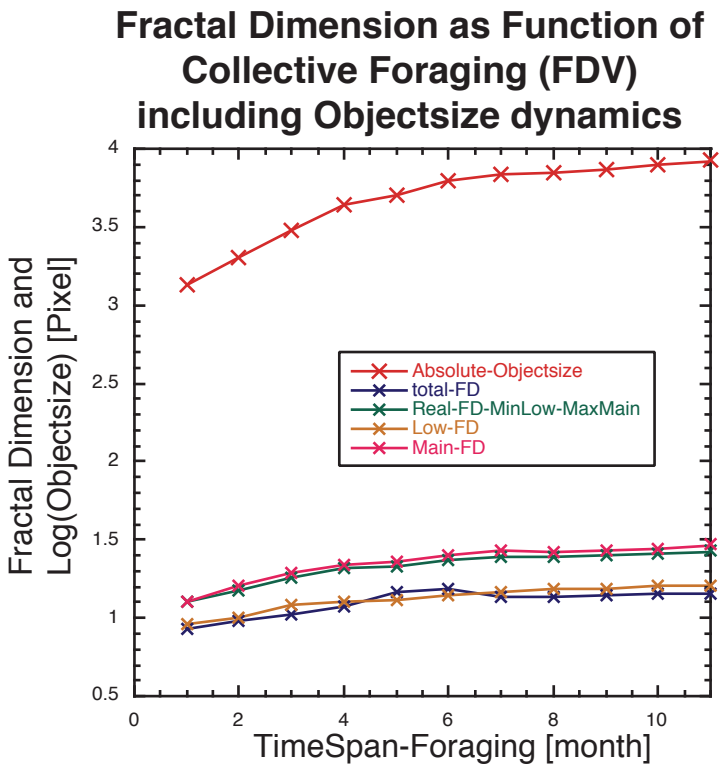


Results of Ata-Foraging analyzed with Fractal Geometry









Results:

1) Evolution of foraging shows no clear causal dependency but fractal dimension stays roughly the same (mean D = 1.15).

2) Cummulative foraging reaches plateau in fractal dimension (mean D = 1.4).

3) Clear dependency between changes in fractal dimension and total trail length.

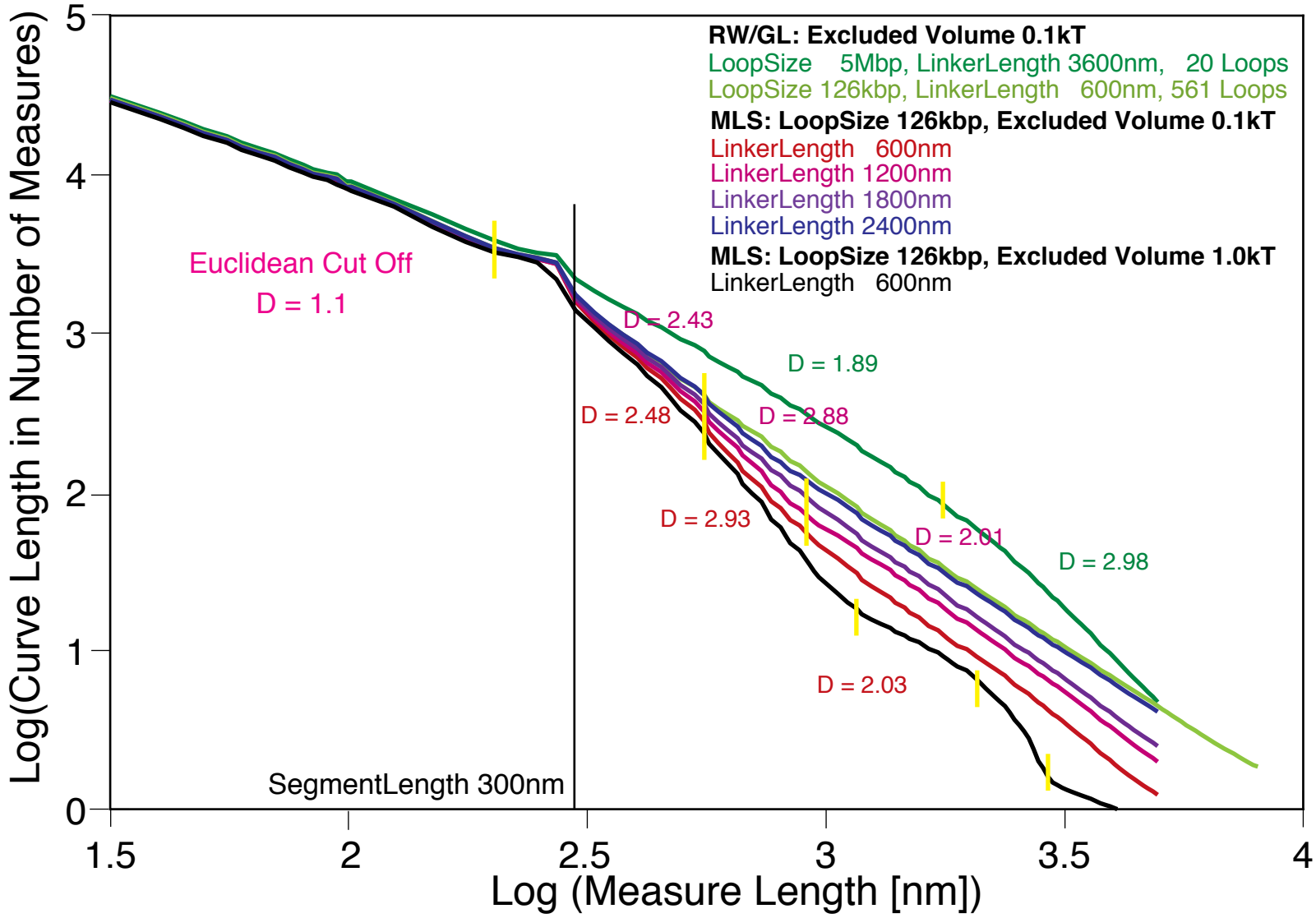
== >> - Atta does "Wanderfeldbau" in a defined manner.

- Atta minimizes the trail system because trail structure and total trail length strongly depend.

=== >>> What search/build strategy is causial for this system ?

In agreement with porous network research fractal analysis show multifractal behaviour in simulations of chromosome 15. Different fractal dimensions mean different process-dynamics in these spaces. Therefore chromosomal territories show a higher degree of determinism than previously assumed.

Tobias A. Knoch



Fractal Geometry and Analysis of the Structure of Cell Nuclei

and the

Foraging of *Atta colombica*

Knoch, T. A.

Biophysics of Macromolecules Seminar, German Cancer Research Centre (DKFZ),
Heidelberg, Germany, May, 1999.

Corresponding author email contact: TA.Knoch@taknoch.org

Keywords:

Genome, genomics, genome organization, genome architecture, structural sequencing, architectural sequencing, systems genomics, coevolution, holistic genetics, genome mechanics, genome function, genetics, gene regulation, replication, transcription, repair, homologous recombination, simultaneous co-transfection, cell division, mitosis, metaphase, interphase, cell nucleus, nuclear structure, nuclear organization, chromatin density distribution, nuclear morphology, chromosome territories, subchromosomal domains, chromatin loop aggregates, chromatin rosettes, chromatin loops, chromatin fibre, chromatin density, persistence length, spatial distance measurement, histones, H1.0, H2A, H2B, H3, H4, mH2A1.2, DNA sequence, complete sequenced genomes, molecular transport, obstructed diffusion, anomalous diffusion, percolation, long-range correlations, fractal analysis, scaling analysis, exact yard-stick dimension, box-counting dimension, lacunarity dimension, local nuclear dimension, nuclear diffuseness, parallel super computing, grid computing, volunteer computing, Brownian Dynamics, Monte Carlo, fluorescence in situ hybridization, confocal laser scanning microscopy, fluorescence correlation spectroscopy, super resolution microscopy, spatial precision distance microscopy, autofluorescent proteins, CFP, GFP, YFP, DsRed, fusionprotein, in vivo labelling.

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Knoch, T. A., Münkel, C. & Langowski, J. Three-dimensional organization of chromosome territories and the human cell nucleus - about the structure of a self replicating nano fabrication site. *Foresight Institute - Article Archive*, Foresight Institute, Palo Alto, *CA, USA,* http://www. foresight.org, 1- 6, 1998.

Knoch, T. A., Münkel, C. & Langowski, J. Three-Dimensional Organization of Chromosome Territories and the Human Interphase Nucleus. *High Performance Scientific Supercomputing*, editor Wilfried Juling, Scientific Supercomputing Center (SSC) Karlsruhe, University of Karlsruhe (TH), 27- 29, 1999.