The GLOBE-Consortium

The Erasmus Computing Grid

Building a Super-Computer at Erasmus MC

for *Free*

by

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ECG Basic Grid Structure

The ECG consists of the computer pools the Erasmus MC and the Hogeschool Rotterdam. The client computers are controlled by the general ECG Emperor of the grid at EMC and a local master at HR. "Condor" is used as middleware since it is very well established and open-source.

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University Medical Center Rotterdam

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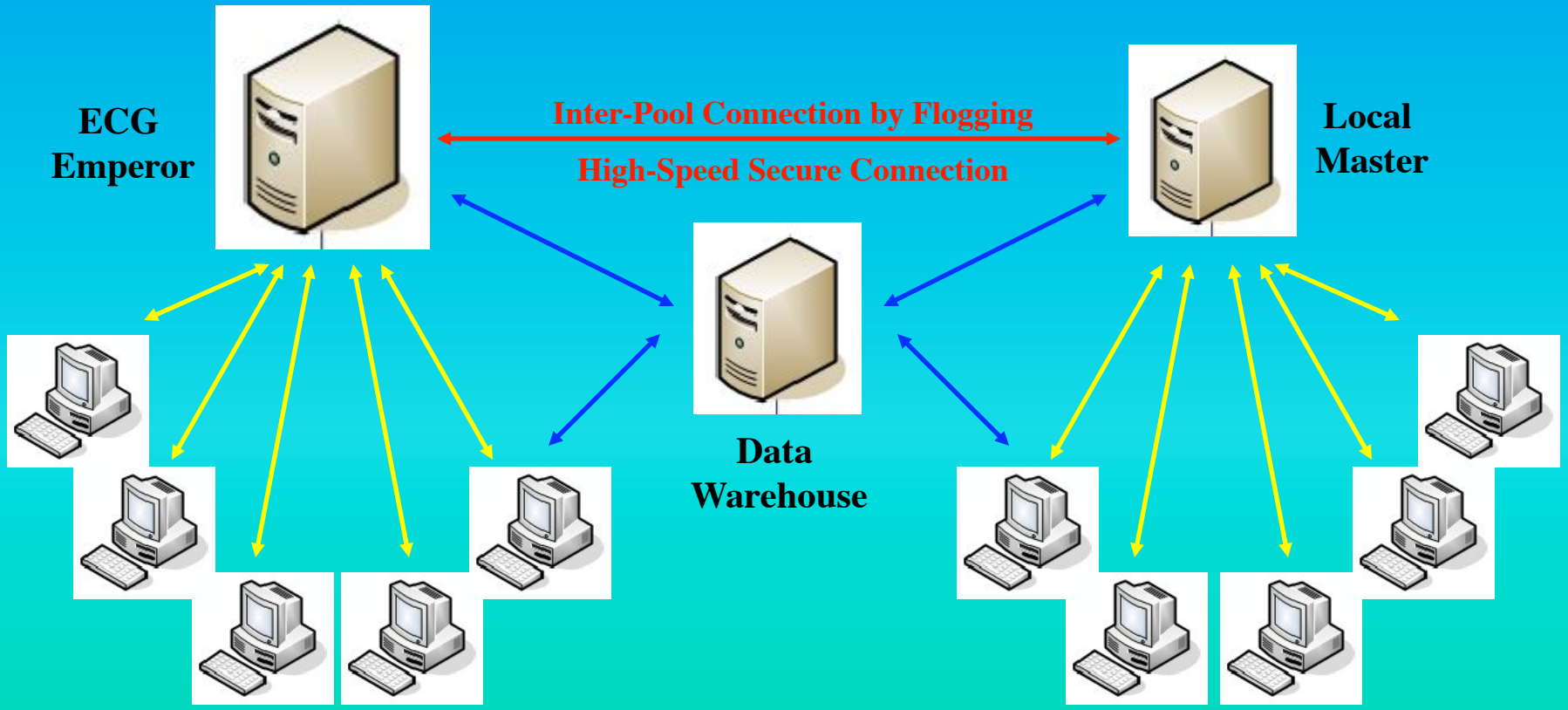
HOGESCHOOL ROTTERDAM

~9000 CPUs or ~18000 vHosts

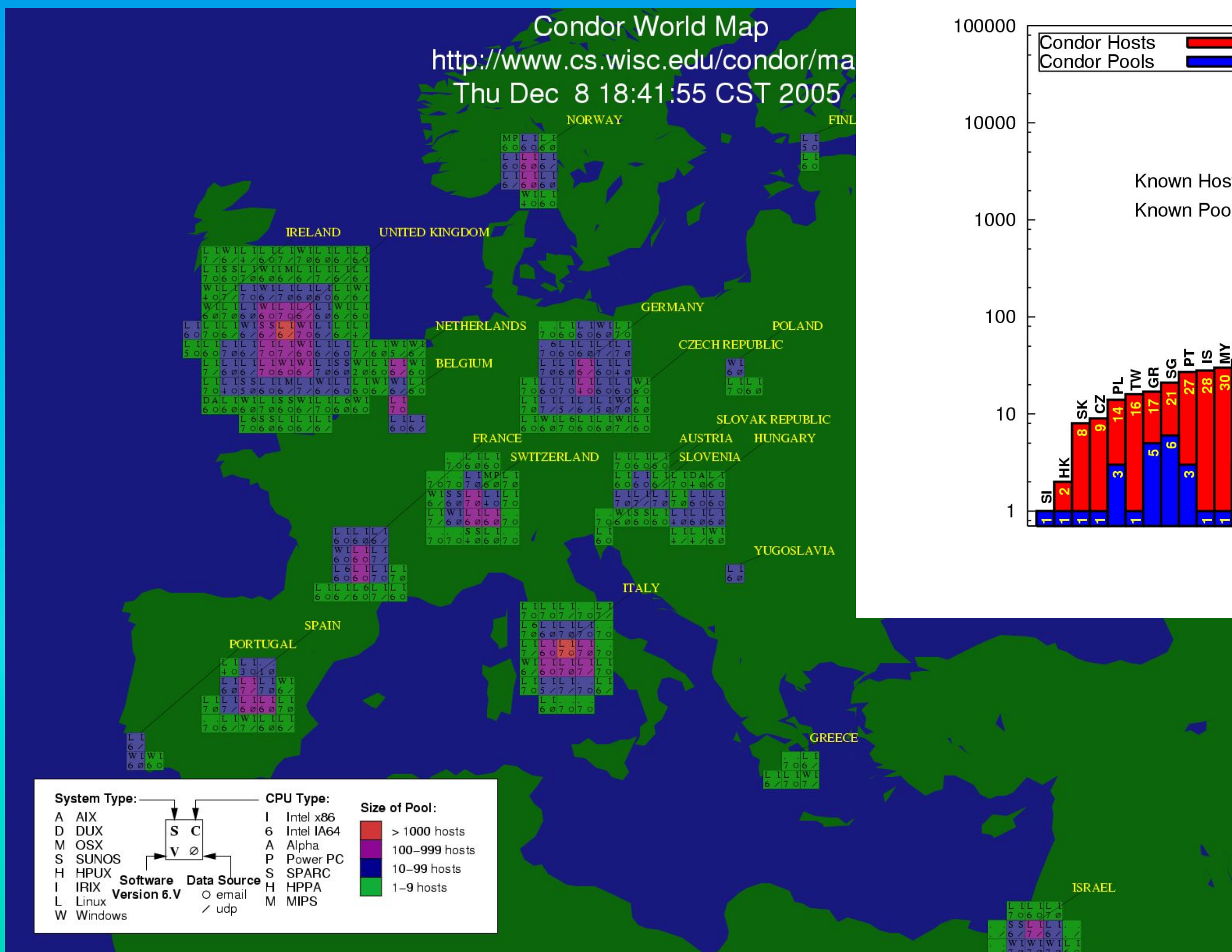
~3500 CPUs or ~7000 vHosts

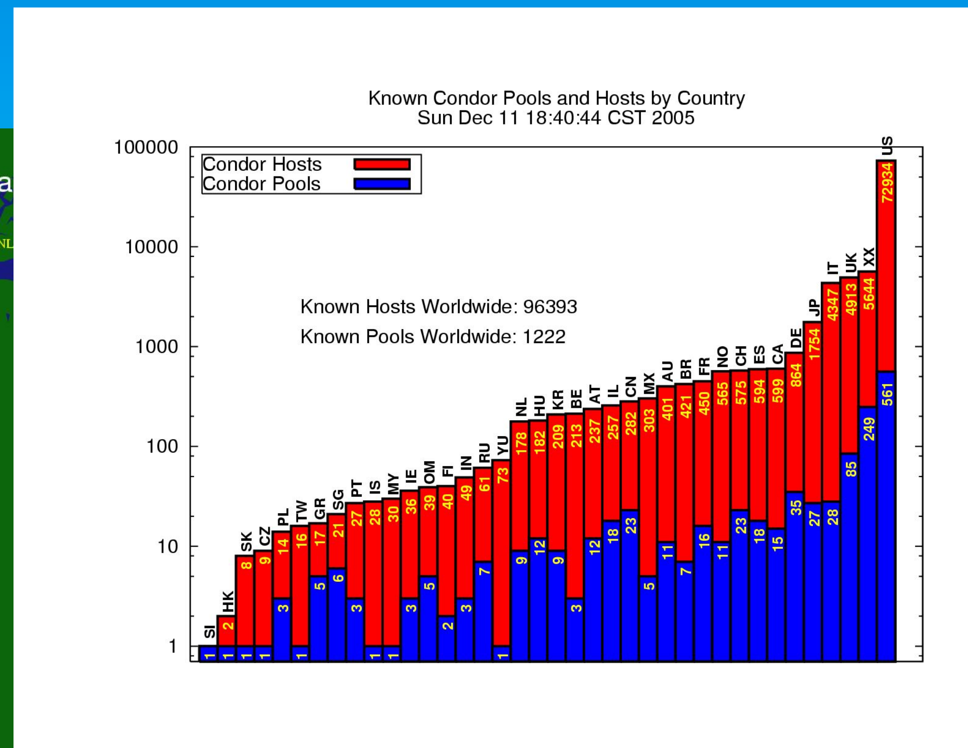


World-Map of Condor Grids

Condor is used as the standard for batch systems on many real parallel super-computers as well as in many distributed trivial parallel computing grids. It is running in very diverse environments of the highest security levels as e.g. governmental or industry R&D.

With a potential capacity of ~20.000 Gflops the ECG could become one the 20 biggest grids!





Based on pool operator reports only!

Installation and Security

For installation, Condor is installed administratively via a secure login from the ECG management site using the corresponding installers.

Condor is an established middleware with no known risks: Condor is running as a guest, no data can be accessed in any form, and nothing can be changed on the local client computer!

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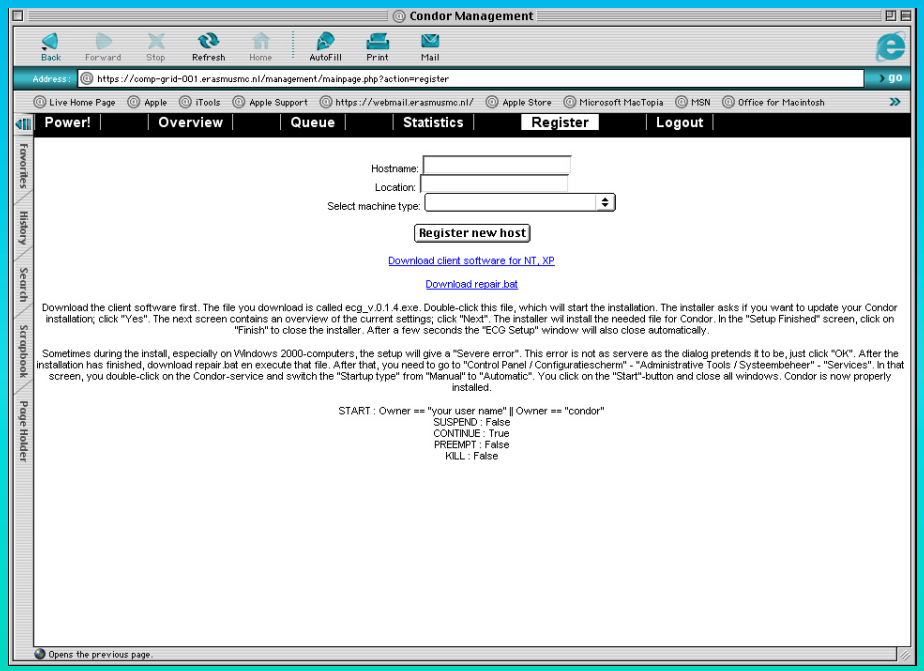
Installation

2 Minutes per computer using the ECG management system

- software install
- registration
- general maintainence



Security

The ECG is *NO* Risk to the client computer or EMC/HR

- runs as a *guest*
- data connection to master is *secure*
- *no* local data are visible to condor
- the local system *cannot* be changed
- application executables are *certified*
- input data is *certfied* by ECG
- local user *always* has usage priority
- runs *only* if vhosts are available
- jobs can be stopped *always* automatically
- ECG can be used as a security monitoring system (e.g. power outage or flooding)
- PRIVACY RULES ARE APPLIED AND GUARANTIED!!!

ECG - Management

To maintain the ECG a data base with installed and registered hosts was created. It allows to track the status of the local clients and gives global statistical data about performance. A job-submission and accounting system is currently implemented.

Usage of the grid is through the GLOBE-Consortium in a secure manner only!

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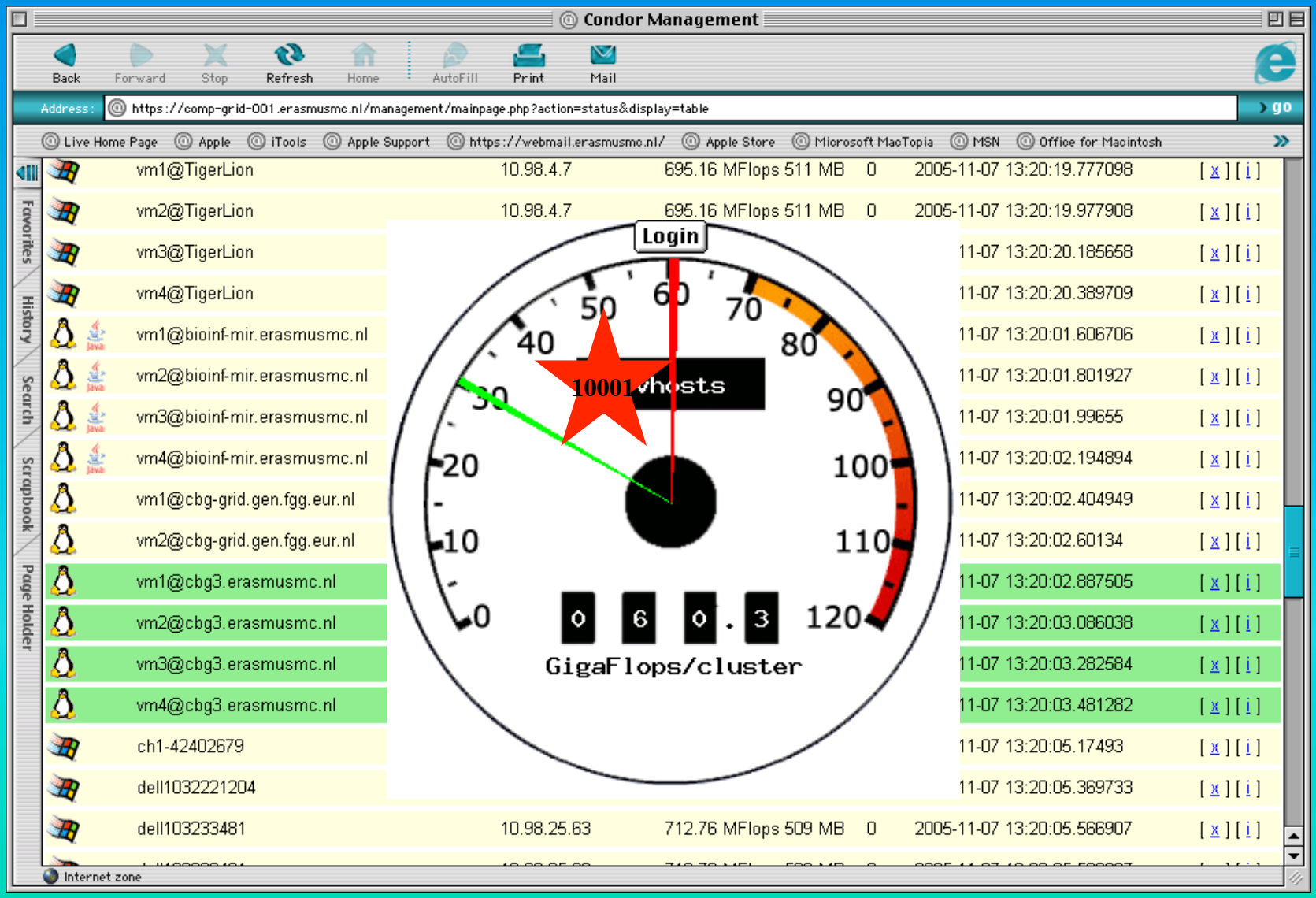

Opportunities

The GLOBE-Consortium has started to establish successfully a Super-Computer at Erasmus MC!

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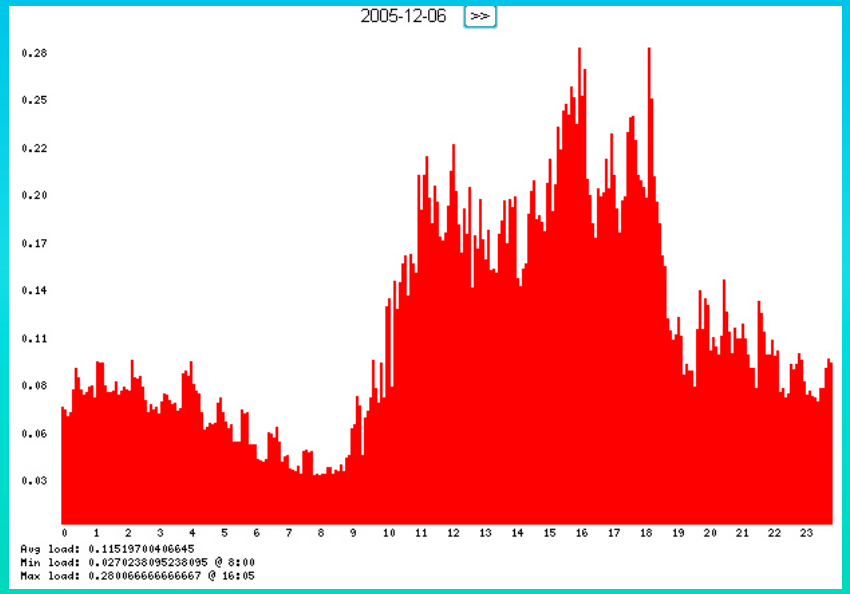
The Erasmus Computing Grid:

The Erasmus Computing Grid greatly advances the computing capabilities of the Erasmus Mc, e.g. for:

- **genomic and proteomic analysis**
- **epidemiology**
- **clinical image analysis, e.g. Applied Molecular Imaging (AMI)**

The Erasmus Computing Grid has also great potential for commercialization!



The GLOBE-Consortium: The Erasmus Computing Grid

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Building a Super-Computer at Erasmus MC for FREE

Knoch, T. A.

Bridge Meeting, Erasmus Medical Center, Erasmus University of Rotterdam, Rotterdam, The Netherlands, September, 2005.

Abstract

To meet the enormous computational needs of live-science research as well as clinical diagnostics and treatment the Hogeschool Rotterdam and the Erasmus Medical Center are currently setting up one of the largest desktop computing grids in the world – The Erasmus Computing Grid. Currently 3 Tera flops are operational and in early production, installation up to the today available maximum capacity of 20 Tera flops in both institutions is planned and partly underway. Thus the Erasmus Computing Grid transforms the existing and sustained huge computer capacity available into usable form via a reliable and secure installing and management system, so that the academic and industrial opportunities depending on such huge computing capacities can be realized for the benefit of society.

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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, auto-fluorescent proteins, CFP, GFP, YFP, DsRed, fusion protein, in vivo labelling, information browser, visual data base access, holistic viewing system, integrative data management, extreme visualization, three-dimensional virtual environment, virtual paper tool.

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