The GLOBE-Consortium

The Erasmus Computing Grid

&

The Next Generation Genome Viewer

by

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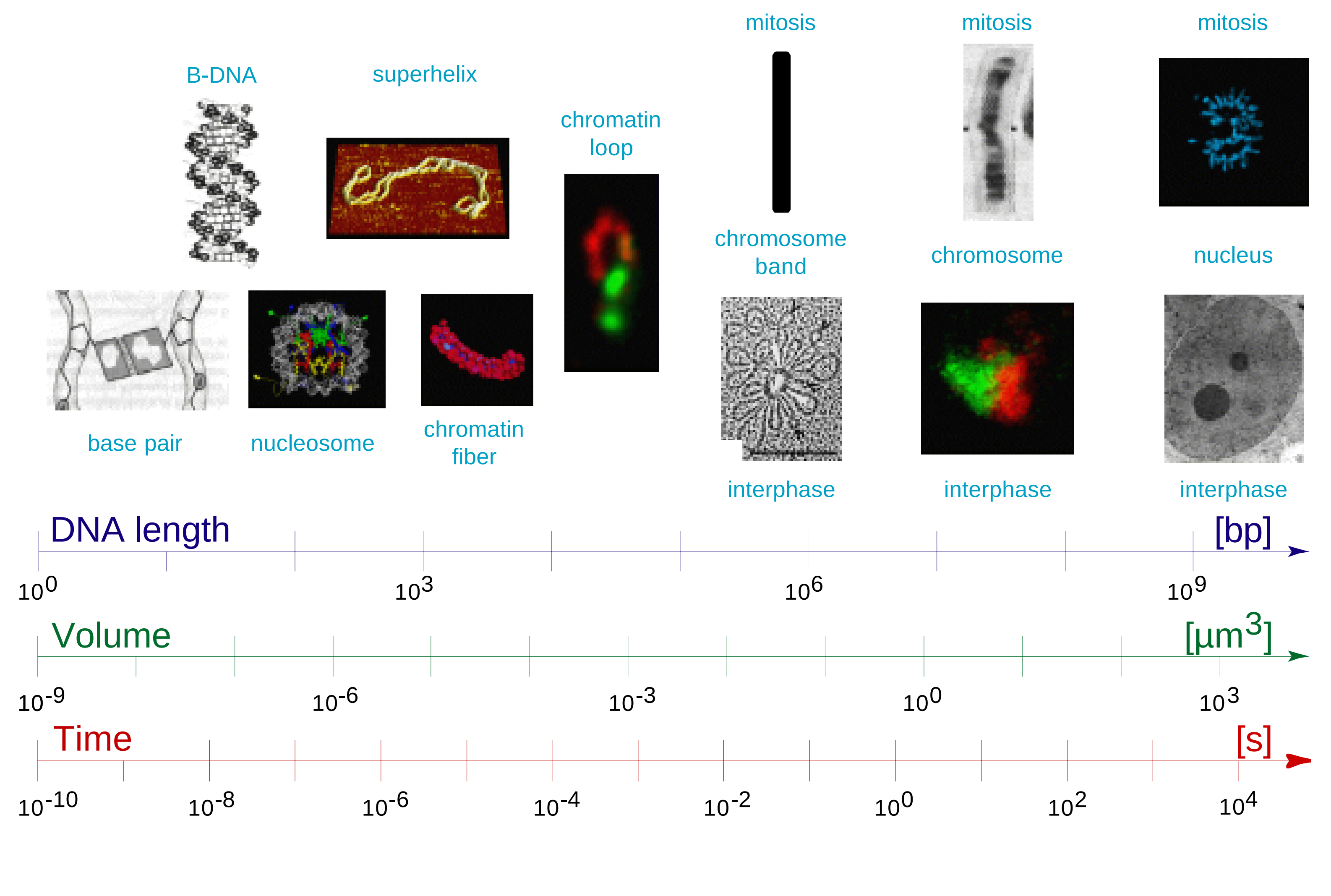
Dynamic and Hierarchical Genome Organization

Erasmus MC
University Medical Center Rotterdam

The different organization levels of genomes bridge several orders of magnitude concerning space and time. How all of these organization levels connect to processes like gene regulation, replication, embryogeneses, or cancer development is still unclear?



The Complexity of Cytogenetic Diagnostics

The process of cytogenetic analysis requires proper patient and sample analysis
as well asa comprehensive evaluation of the results.

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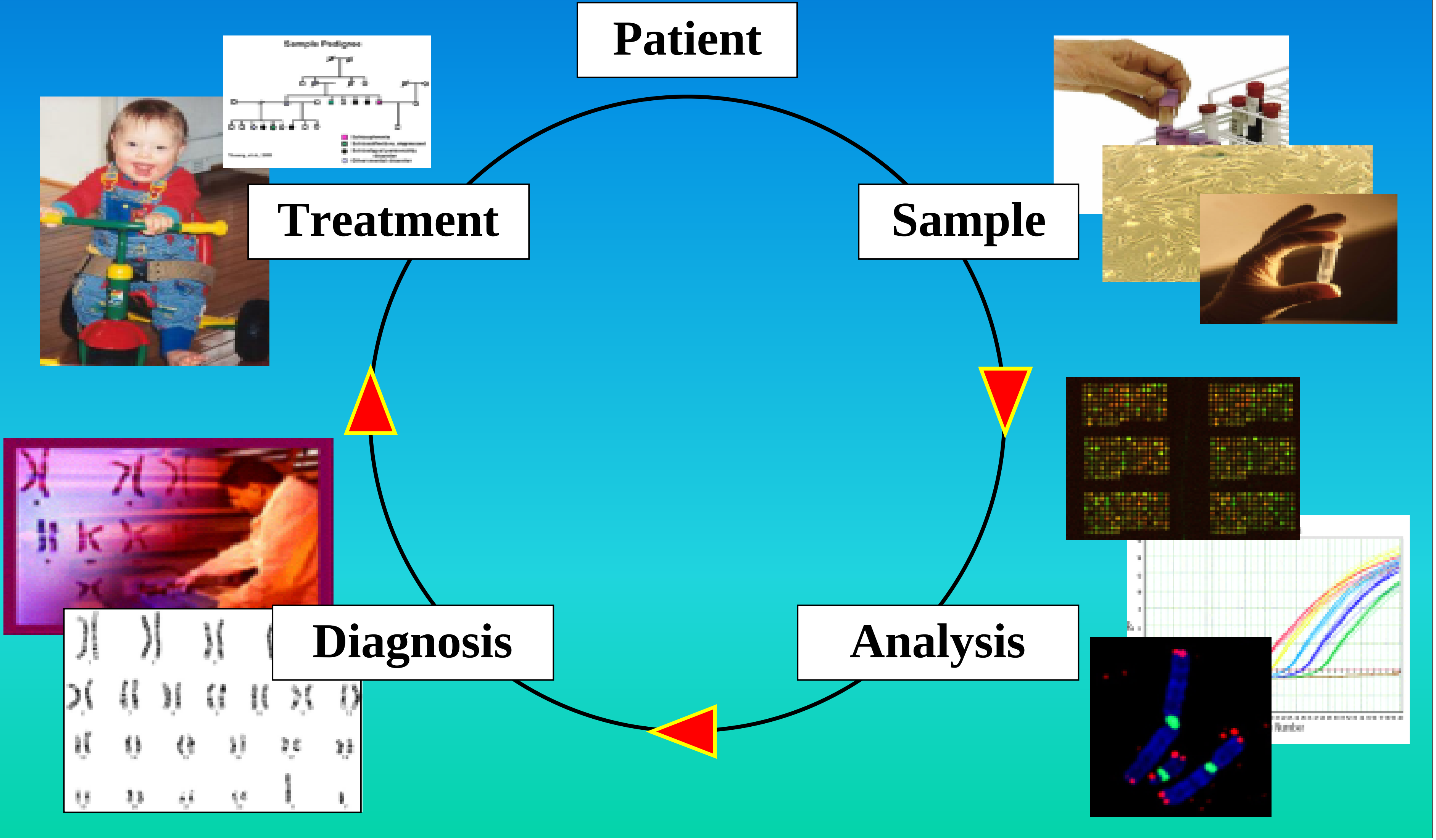
University Medical Center Rotterdam



Patient

Sample

Analysis

Diagnosis

Treatment

The Erasmus Computing Grid

Building a Super-Computer at Erasmus MC for Free!

Applications at Erasmus MC: E.g. genome sequence analysis, protein structure simulations, chip/array analysis, epidemiology of viral infections, patient diagnostic image analysis (AMI).

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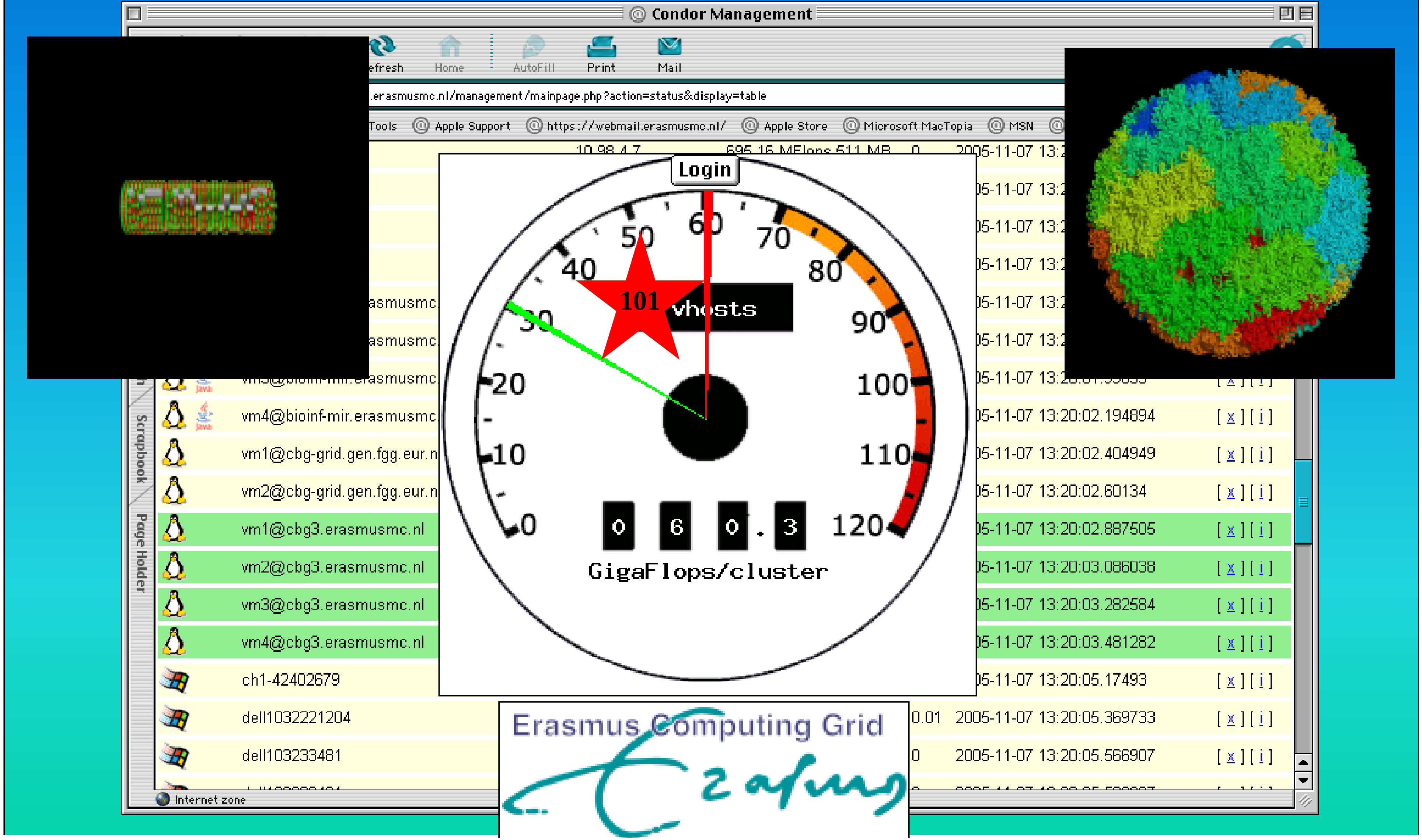

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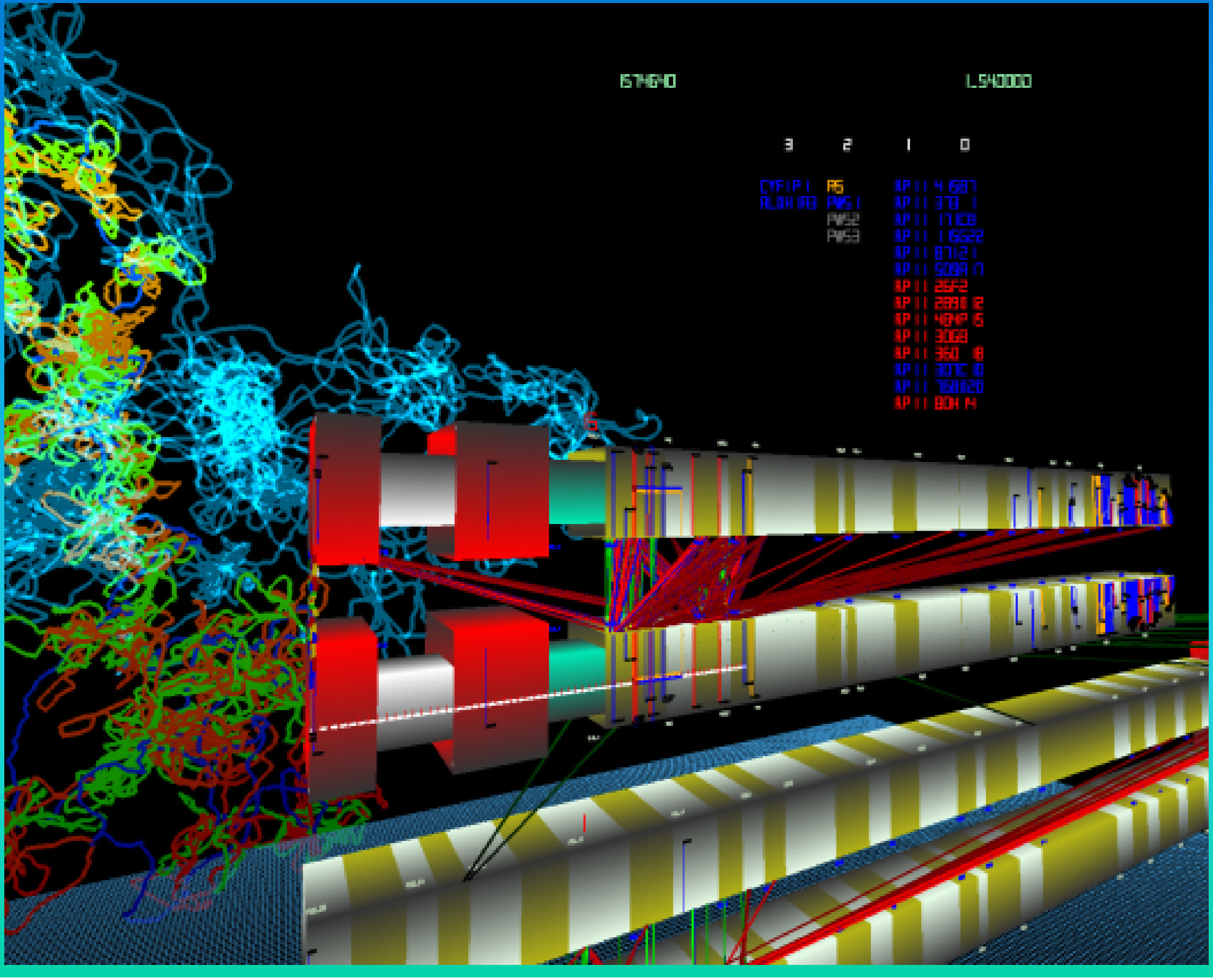
Erasmus Computing Grid

The 3D Genome Viewer

The NEW Standard for Genomic Research and Diagnostics!

Properties: flexible, customizable, and allows intuitive navigation. It provides dynamical resolution and object arrangement as well as real-time analysis of extremely large multi-dimensional data.



Opportunities

The GLOBE-Consortium has started to establish successfully a unique environment for genomic research and diagnostics!

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 3D Genome Viewer:

The 3D Genome Viewer greatly advances the integration of multi-dimensional data, e.g.:

- **sequential genomic data**
- **structural genomic data**
- **clinical diagnosis data**

Both the Erasmus Computing Grid and the 3D Genome Viewer have potential for commercialization!

The GLOBE-Consortium:

The Erasmus Computing Grid and The Next Generation Genome Viewer

Knoch, T. A.

Erasmus Medical Center, Erasmus University of Rotterdam, Rotterdam, The Netherlands, 9th November, 2005.

Abstract

The Set-Up of the 20 Teraflop Erasmus Computing Grid:
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.

The Next Generation Genome Browser GLOBE 3D-Viewer:
The GLOBE 3D Genome Viewer is the novel system-biology oriented genome browser necessary to access, present, annotate, and to simulate the holistic genome complexity in a unique gateway towards a real understanding, educative presentation and curative manipulation planning of this tremendous evolutionary information grail – genomes. This has required completely new approaches to represent the genome architecture realistically in combination with the various types of informational annotation including experimental data or instant analysis capabilities. This creates unrivalled new opportunities for scientific researchers, diagnostic users, educators and publishers as well as PR and commercial applicants. Potential *BETA-TESTERS* of the GLOBE 3D Genome Viewer are asked to sign up now!

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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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