

The GLOBE-Consortium

The Next Generation

Genome Viewer

by

Bert Eussen, Michael Moorhouse & Tobias A. Knoch

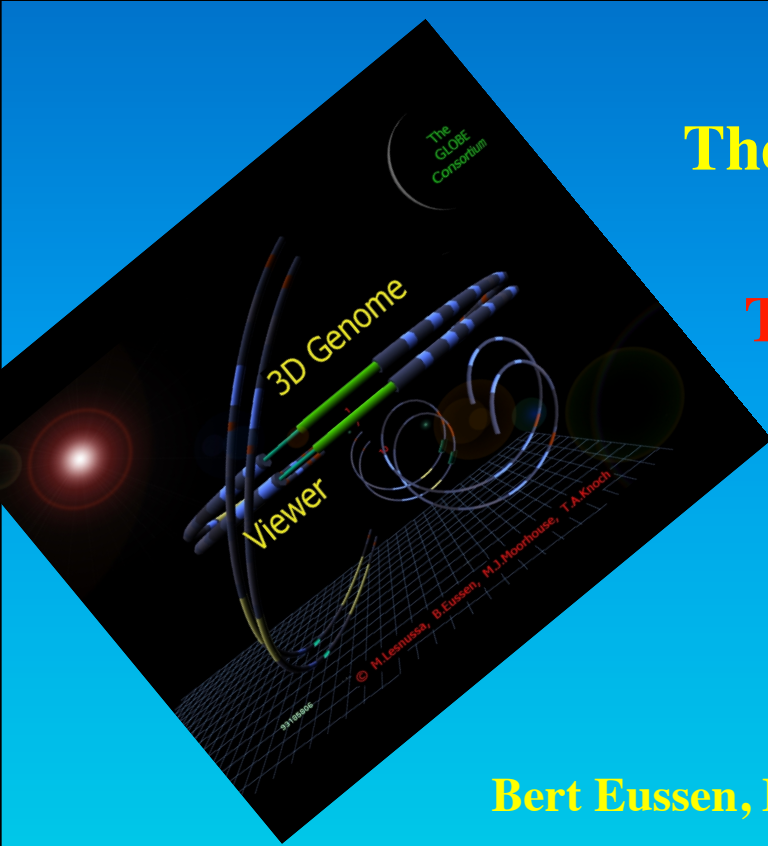
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Annelies de Klein, Albert Osterhaus & Frank Grosveld

Clinical Genetics, Virology, Cell Biology & Genetics

Erasmus MC, Rotterdam, The Netherlands

Contact: globe@erasmusmc.nl and <http://www.erasmusmc.nl/globe-consortium>

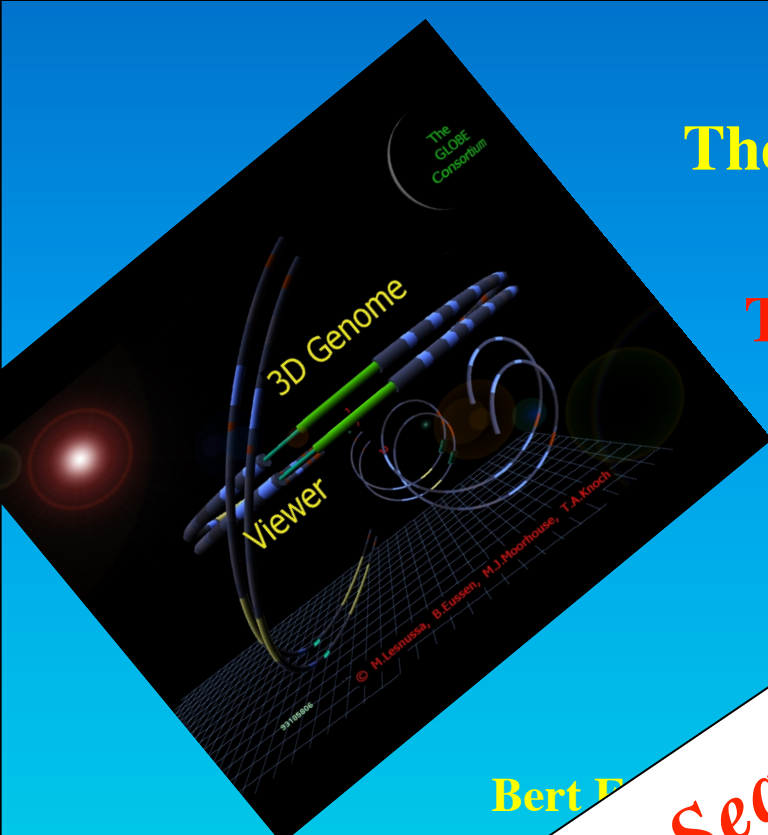




The GLOBE-Consortium

The Next Generation

Genome



Bert Eussen, M.J. Moorhouse & Tobias A. Knoch

**From Sequence to Morphology:
Towards a Holistic Understanding of Genomes!**

supported by

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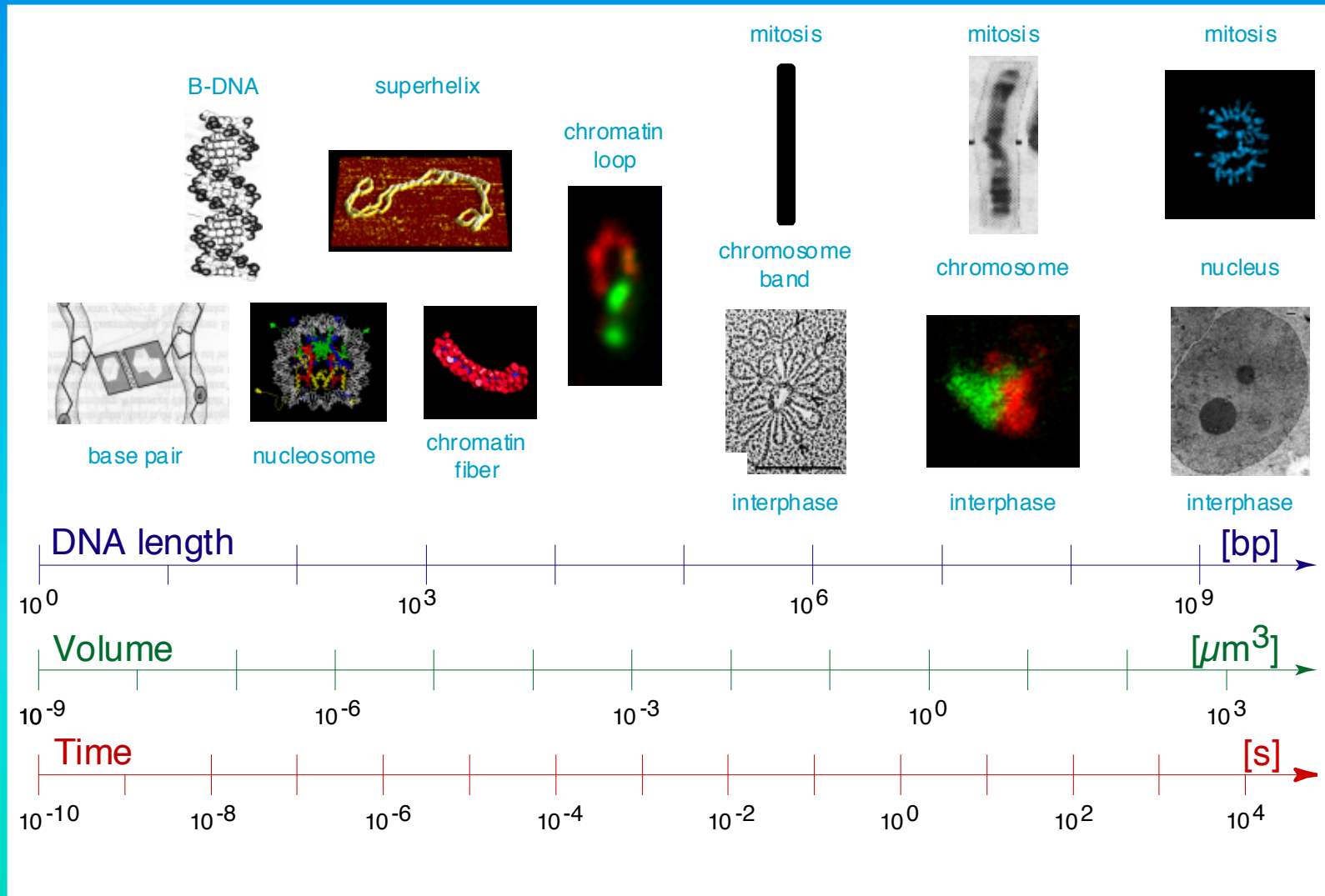
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Dynamic and Hierarchical Genome Organization

Erasmus MC
University Medical Center Rotterdam

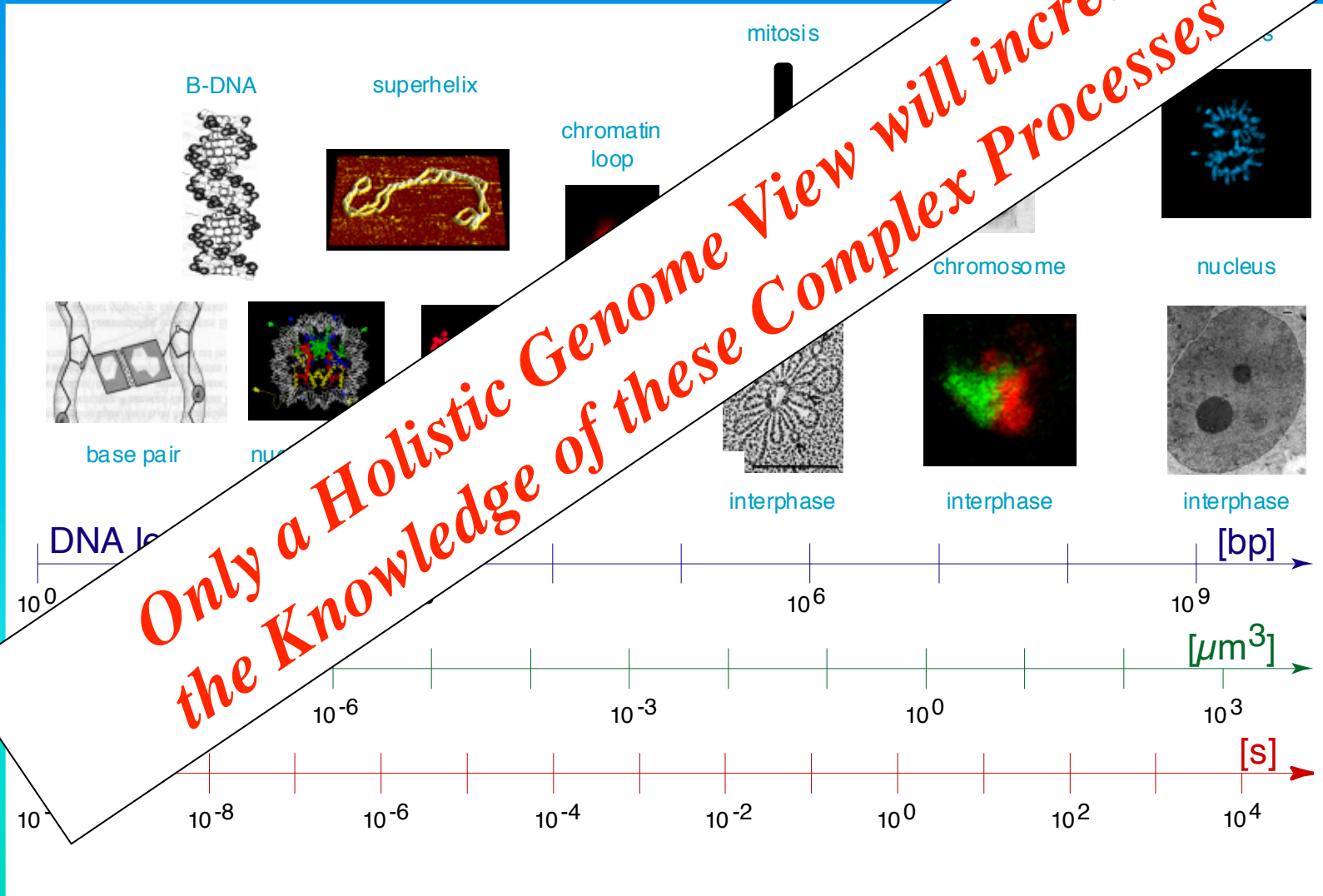
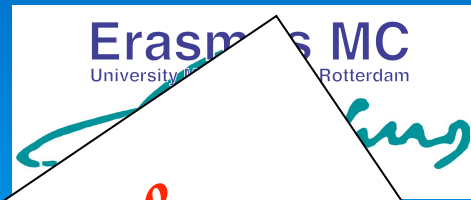


The different organization levels of genomes bridge several orders of magnitude concerning space and time. How all of these organization levels connect to processes like gene regulation, replication, embryogenesis, or cancer development is still unclear?



Dynamic and Hierarchical Genome Organization

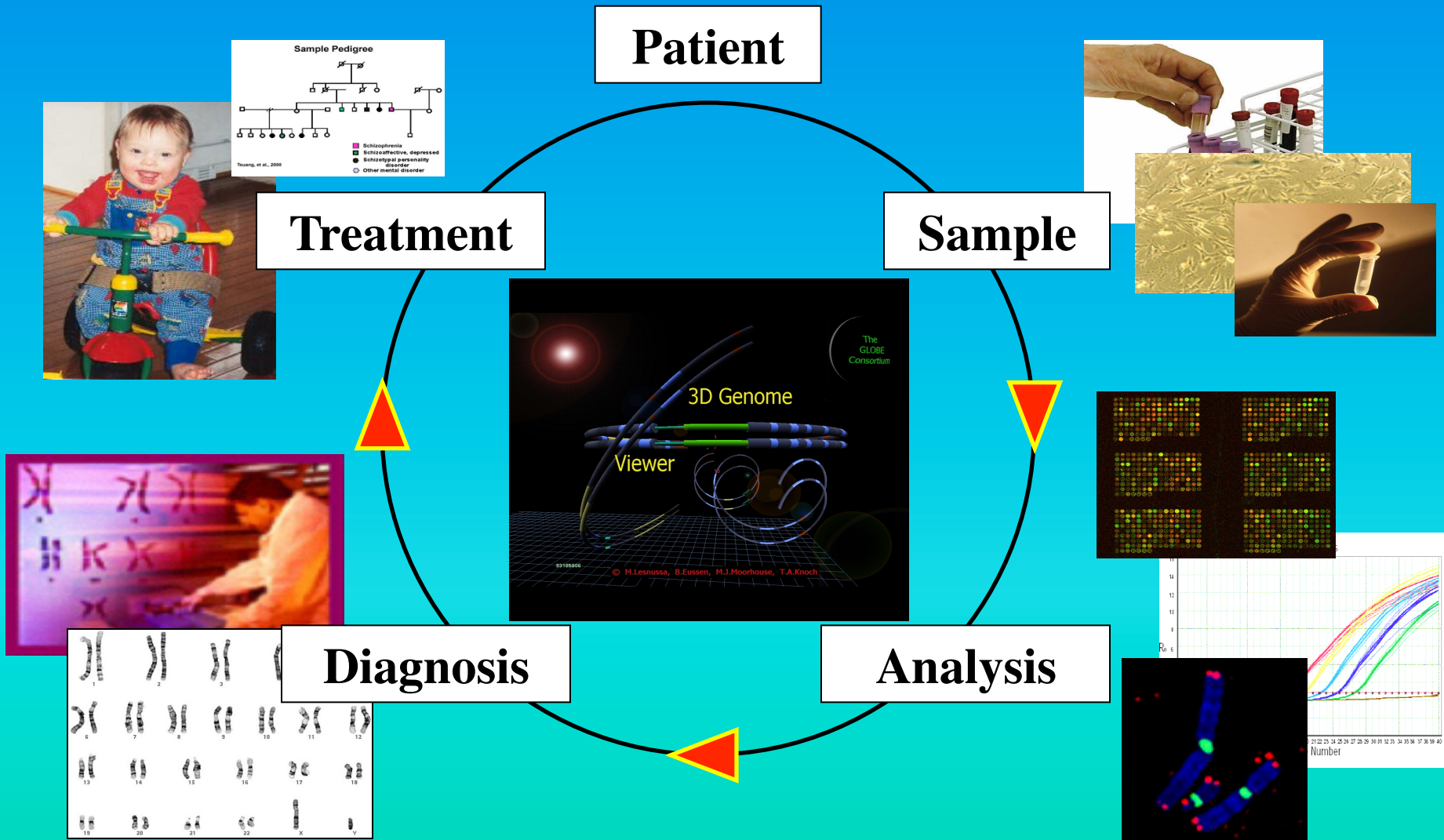
The different organization levels of genomes bridge several orders of magnitude concerning space and time. How all of these organization levels connect to processes like gene regulation, replication, embryogenesis, or cancer development is still unclear?



Only a Holistic Genome View will increase the Knowledge of these Complex Processes

The Complexity of Cytogenetic Diagnostics

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

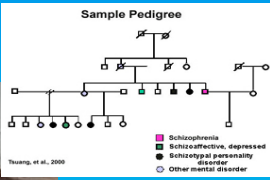


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Patient

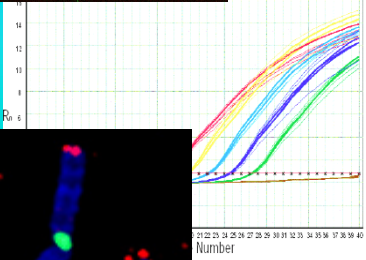
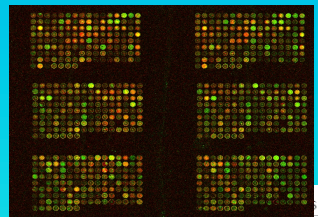


Treatment

Sample

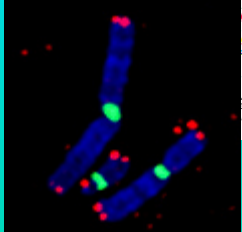
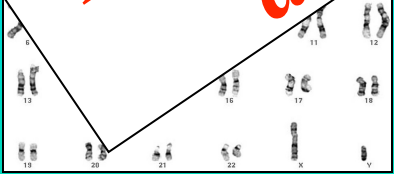


Better Cytogenetic Diagnostics is based on advanced Genome Understanding!



Diagnosis

Analysis



Current 'Best of Breed'

Current solutions are driven by the needs of specific users and data, i.e. they run on a limited paradigm with mostly fixed content, difficult user and data handling possibilities and almost no control options over processes. Thus, they neither represent adequately the complexity of genomes nor the complexity of science and industry processes necessary to work properly.



Ensembl Genome Browser

(Open source; EBI / Sanger Center)

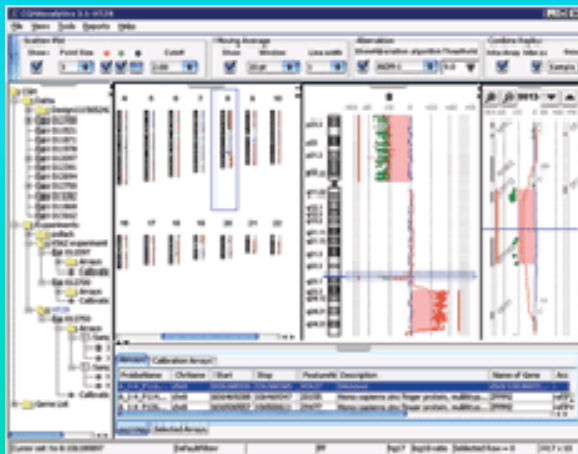
- ❖ fixed paradigm
- ❖ fixed content
- ❖ difficult user and data handling
- ❖ no control options

The screenshot shows the Ensembl Human ContigView interface for Chromosome 15. The top navigation bar includes a search field and a 'Go' button. The main content area is divided into several sections:

- Chromosome 15**: A genomic map showing bands from p13 to q25.2.
- Overview**: A detailed view of the 15q25.2 region, showing DNA contigs, markers (e.g., D15S115), and various gene models including Ensembl Genes, ncRNA Genes, and protein-coding genes.
- Detailed view**: A section for further exploration with dropdown menus for 'Features', 'Comparative', 'DAS Sources', 'Repeats', 'Decorations', 'Export', and 'Image size'. It also includes a 'Jump to region' field with coordinates 15:80599350-80699351 and a 'Refresh' button.

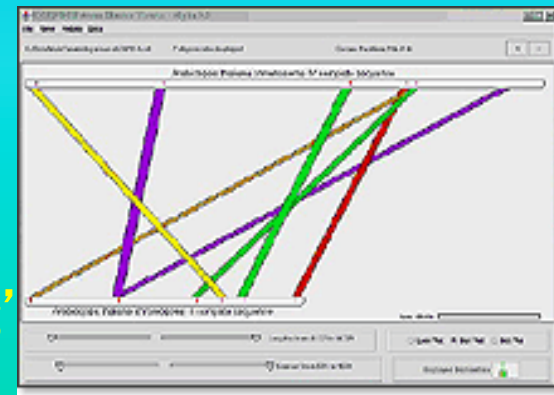
CGH Analytics Software

(Agilent Inc.)



Pattern Hunter 'Swing'

(Solutions Inc. / Sun Inc.)



Current 'Best of Breed'

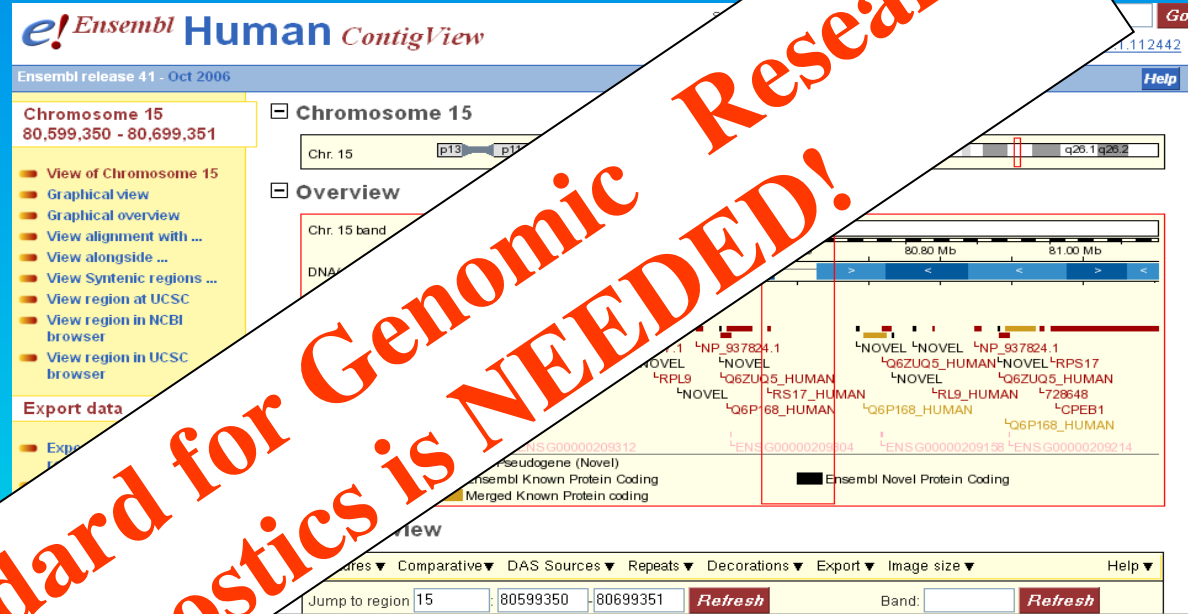
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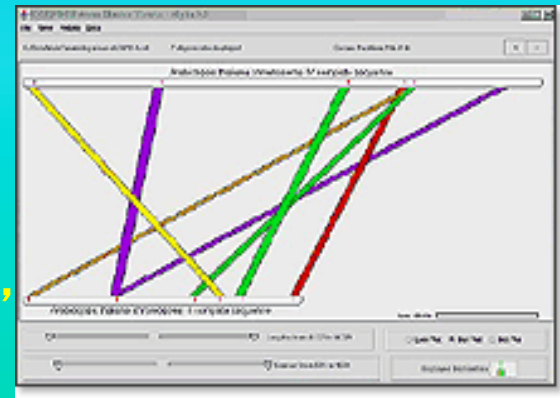


A NEW Standard for Genomic Research and Diagnostics is NEEDED!



Pattern Hunter 'Swing'

(Solutions Inc. / Sun Inc.)



The 3D Genome Viewer

To develop an entire novel system-biology oriented genome browser, i.e. integrating the holistic complexity of genome organization in a single easy comprehensible platform has required completely new approaches to represent the genome architecture realistically in combination with the various types experimental data or instant analysis capabilities and annotation.



Paradigm:

- ❖ simplicity, flexibility, customisability, expandability and open-source sustainability concerning
- ❖ user accessibility and needs, the in-/output of data sources, system modularity, and integration of future developments

Content:

- ❖ all spatial scales from the base-pair to nuclear morphology including all other system composites
- ❖ every type of even large multi-dimensional datasets

User Handling:

- ❖ intuitive navigation with dynamical semantic resolution and relational arrangement

Data Handling:

- ❖ real-time interaction with data manipulation or annotation
- ❖ simple relational or complex correlative multi-dimensional analysis and planning capabilities

Control Options:

- ❖ front-end access and control of virtual system biological genome simulations

The 3D Genome Viewer

Erasmus MC

University Medical Center Rotterdam



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- ❖ simplicity,

- ❖ user access

Content:

- ❖ all spatial

- ❖ every type

User Hand

- ❖ intuitive n

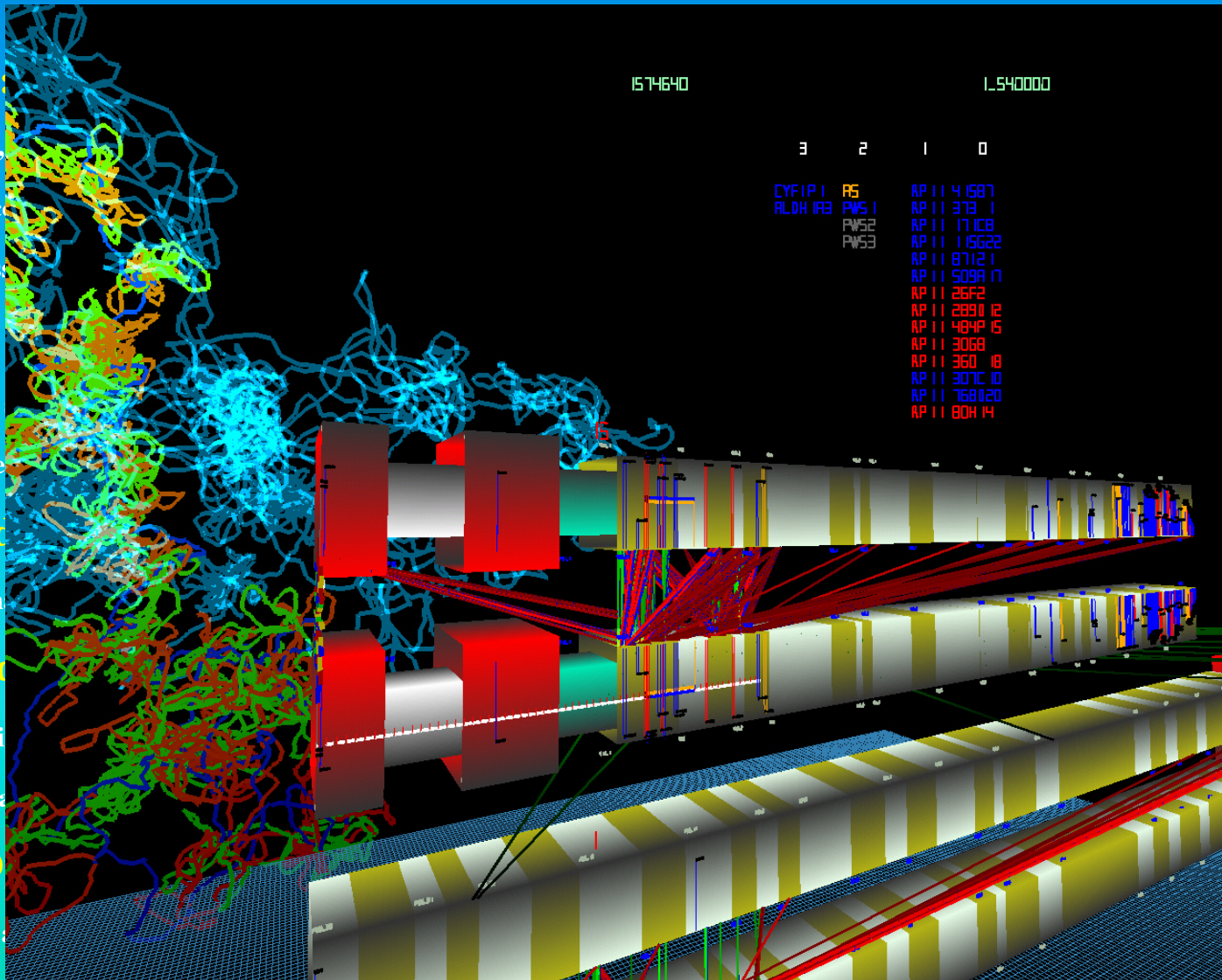
Data Hand

- ❖ real-time i

- ❖ simple rela

Control O

- ❖ front-end



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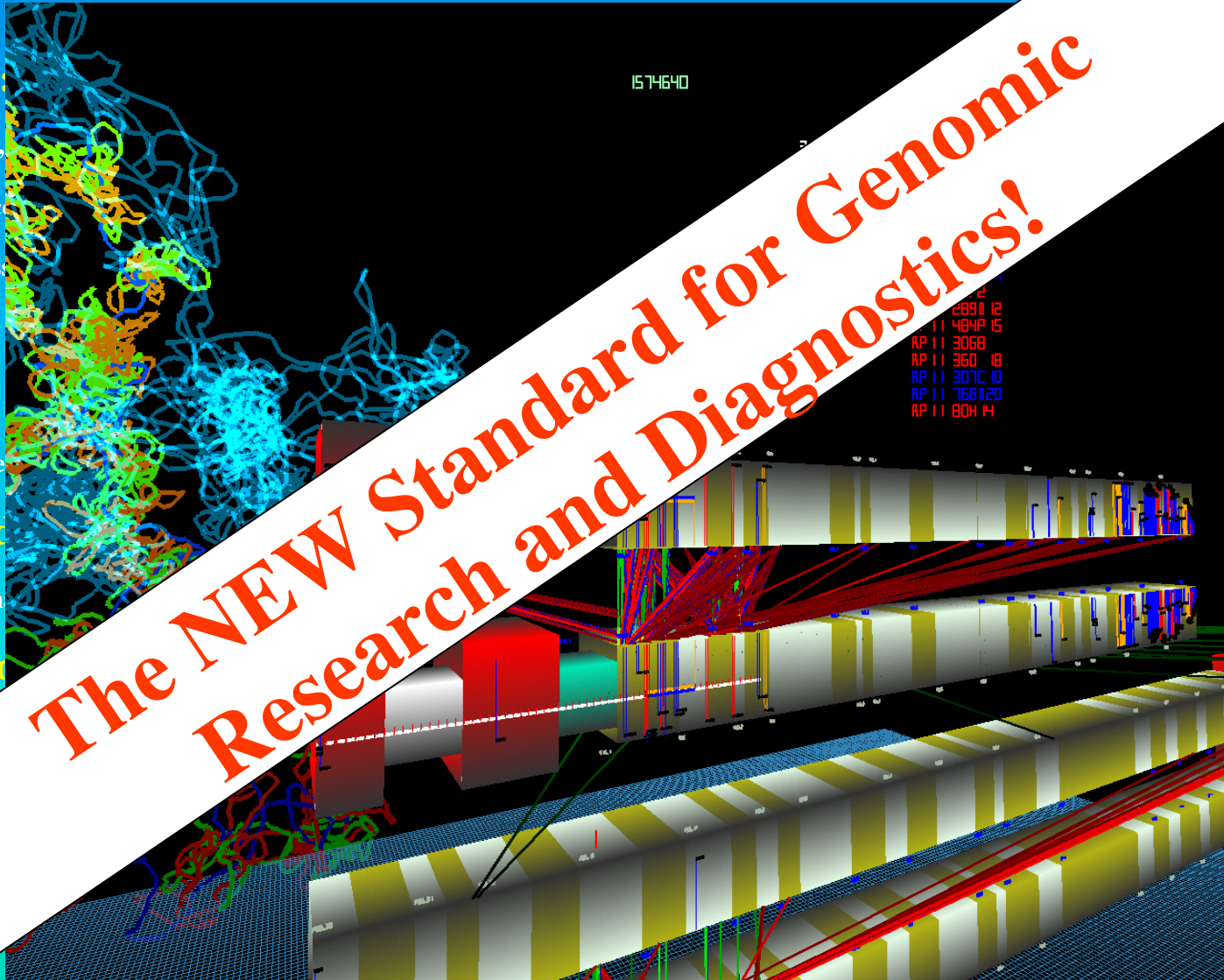
- ❖ intuitive n

Data Hand

- ❖ real

Co

- ❖ from



The 3D Genome Viewer

Erasmus MC
University Medical Center Rotterdam



Due to its broad impact, the GLOBE 3D Genome Viewer addresses different markets and revenue streams in the areas of research, education, diagnostics and industry with different detailed business models and contracting patterns which will guaranty a constant high-profile valorization.

Basic Corporate License:

- ❖ 50% science
- ❖ 50% industry

White Label Products:

- ❖ special customer products

Content Sale

- ❖ specially defined data sets
- ❖ specially connected data sets

Advertising:

- ❖ sponsored free version
- ❖ content and user related

eCommerce:

- ❖ community portal and referral fees

Companies/Organizations:

- ❖ Invitrogen (Karlsbad, CA, USA)
- ❖ Affimetrix (Santa Clara, CA, USA)
- ❖ Soft Genetics (State College, PA, USA)
- ❖ Combimatrix CMDX (San Antonio, CA, USA)
- ❖ Philips (The Netherlands)
- ❖ MediGRID (Goettingen, Germany)

Collaborators:

- ❖ Prof. Dr. Evan E. Eichler (Seattle, WA, USA)
- ❖ Prof. Dr. Stephen W. Scherer (Toronto, Canada)
- ❖ Prof. Dr. Michael Hausmann (Heidelberg, Germany)
- ❖ Dr. Malte Wachsmuth (Seoul, Korea)
- ❖ Dr. Gregory Cox (Karlsbad, CA, USA)
- ❖ Dr. Eberhard Schmitt (Jena, Germany)
- ❖ Dr. Sabine Baars (Leiden, The Netherlands)



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- ❖ (The Netherlands)
- ❖ (Germany)

Potential costumers:
Revenue per customer:
Market:

- ❖ 1.000.000
- ❖ 1000 Euro
- ❖ 1.000.000.000 Euro
- ❖ Prof. Dr. (USA)
- ❖ Prof. Dr. (Germany)
- ❖ Dr. Malte Wac (Germany)
- ❖ Dr. Gregory Cox (Karlsbad, CA, USA)
- ❖ Dr. Eberhard Schmitt (Jena, Germany)
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The 3D Genome Viewer

The NEW Standard for Genomic Research and Diagnostics!

Ready to be Valorized!!!



2007

2008

2009



Basic Corporate Licenses



White Label Products & Advertising



e Commerce



Content Sale



The 3D Genome Viewer

The NEW Standard for Genomic Research and Diagnostics!

Ready to be Valorized!!!

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Erasmus

2007

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The 3D Genome Viewer allows a Holistic Genome View with Clear Benefits for Research, Diagnostics and Treatment!



The GLOBE-Consortium: The Next-Generation Genome Viewer

Knoch, T. A., Eussen, B. & Moorhouse, M.

Incubator Erasmus Medical Center, Erasmus University of Rotterdam, Rotterdam, The Netherlands, October, 2006.

Abstract

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!

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, 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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