Modell sketches and rendered images of simulated chromosome organizations

A: RW/GL-modell
B: MLS-modell
C: RW/GL, 5 Mbp loops
D: MLS, 126 kbp loops/linkers
E: RWTL, 126 kbp loops
F: Starting configuration

Figure 1:

<table>
<thead>
<tr>
<th></th>
<th>A</th>
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Linker between rosettes consists of DNA (126 kbp)
(in contrast to backbone)
The mean radial mass distribution and radial density of chromosome territories is proportional *only* to the linker size in the MLS model and proportional to the linker *and* loop size in the RW/GL model. In the MLS model the radial density forms a plateau in contrast to the RW/GL model.
The mean extension of MLS subcompartments is proportional to the loop size (A) and the excluded volume interaction (B). The mean distance between succeeding subcompartments is only proportional to the linker size (C). The nearest neighbour subcompartment distance are proportional to the linker size and the embedding volume (D).
The determination of spatial distances between genomic markers as function of their genomic separation depends on different assumptions about the structure, stability and dynamics of chromosome organizations and the experimental error made depends on the microscopic method.
Comparison between simulated and experimental spatial distance measurements as function of their genomic separation.
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Yokota et al., 1995: Fig. 2A 4p16.3
Yokota et al., 1997: Fig. 2B 6p21.3
Fig. 2C 21q22.2
Fig. 2D Xq28
Fig. 2D Xp21.3
Fig. 4B MAA-Xp21.3
Fig. 4B MAA-Xq28
Fig. 4A PFA-Xp21.3
Fig. 4A PFA-Xq28
Comparison between simulated and experimental spatial distance measurements as function of their genomic separation.

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- Tobias A. Knoch

Graph showing the relationship between mean spatial distance [m] and genomic distance between genomic markers [Mbp].

- Our data: J. Rauch, T. A. Knoch
- Monier:
- Fibroblasts 11q13
- Lymphocytes 11q13
- Trask et al., genomics.
Comparison between simulated and experimental spatial distance measurements as function of their genomic separation.

![Graph showing comparison between simulated and experimental spatial distance measurements as function of genomic separation.](image)

- **Legend:**
  - ● our data: J. Rauch, T. A. Knoch
  - Senger *et al.*, 1993:
    - ▲ one colour
    - ○ two colour
  - Warrington *et al.*, 1994:
    - ■ reference
    - ◇ prediction
  - Trask *et al.*, 1991:
    - + Fig. 4A
    - × Fig. 4B.
Position-independent spatial distances are proportional to the loop size for genomic separations below 800 kbp in the MLS model (A). The loop size and the linker size can complement each other (B). With a comparison between the slope below and above 100 kbp and the point of change, it is possible to determine the loop and linker size separately.
Position dependent spatial distance measurements allow the fine mapping of chromosomes (A & B). Position independent spatial distance measurements are the smeared out or the mean of the position dependent spatial distance measurements.
Categorizing the available spatial distance measurements between genomic markers as function of their genomic separation leads to a better evaluation of the comparison between simulations and experiments.

<table>
<thead>
<tr>
<th>Purpose</th>
<th>Preparation Methods</th>
<th>Imaging Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>Order of clones for sequenzing</td>
<td>hypotonic swelling dropping on coverslips</td>
<td>2D fluorescence microscopy</td>
</tr>
<tr>
<td></td>
<td>MAA fixation</td>
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<tr>
<td>Transition phase from sequenzing to</td>
<td>hypotonic swelling dropping on coverslips</td>
<td>2D fluorescence microscopy</td>
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<tr>
<td>packing of chromosomes</td>
<td>MAA fixation</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>digital image analysis</td>
</tr>
<tr>
<td>detailed 3D organization of the genome</td>
<td>PFA fixation</td>
<td>3D/4D CLSM</td>
</tr>
<tr>
<td></td>
<td></td>
<td>image reconstruction methods</td>
</tr>
<tr>
<td></td>
<td></td>
<td>correction for optical errors</td>
</tr>
</tbody>
</table>
Simulation of Single Chromosomes, their Properties and Comparison to Experimental Spatial Distance Measurements

Knoch, T. A.

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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, autofluorescent proteins, CFP, GFP, YFP, DsRed, fusionprotein, in vivo labelling.

Literature References


