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

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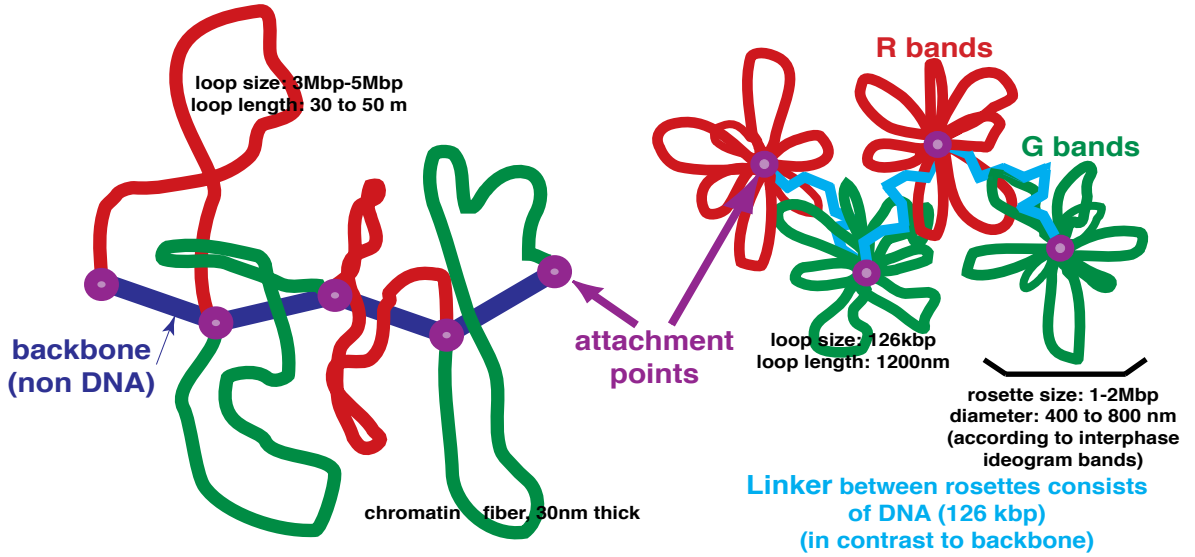

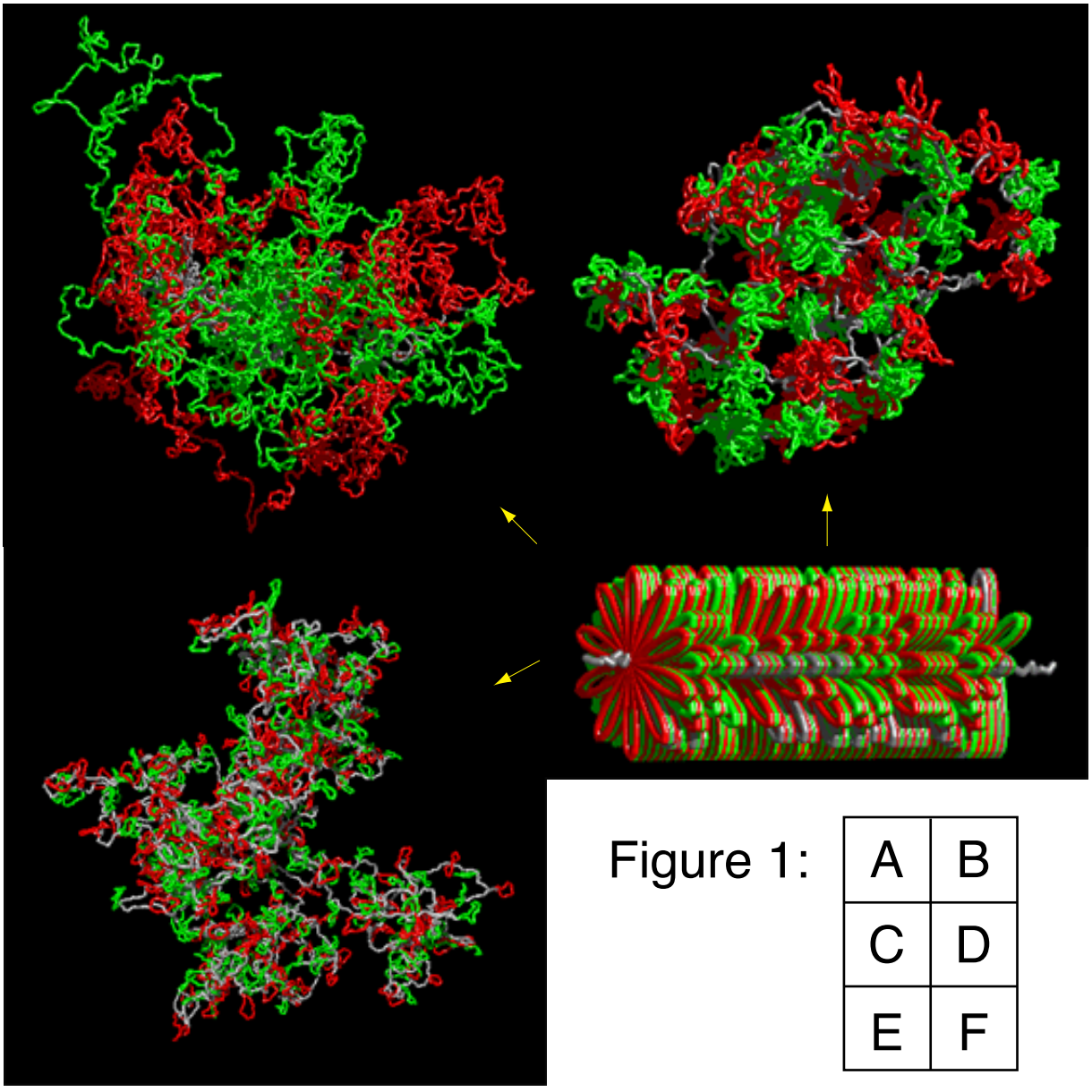

Figure 1:

A	B
C	D
E	F

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.

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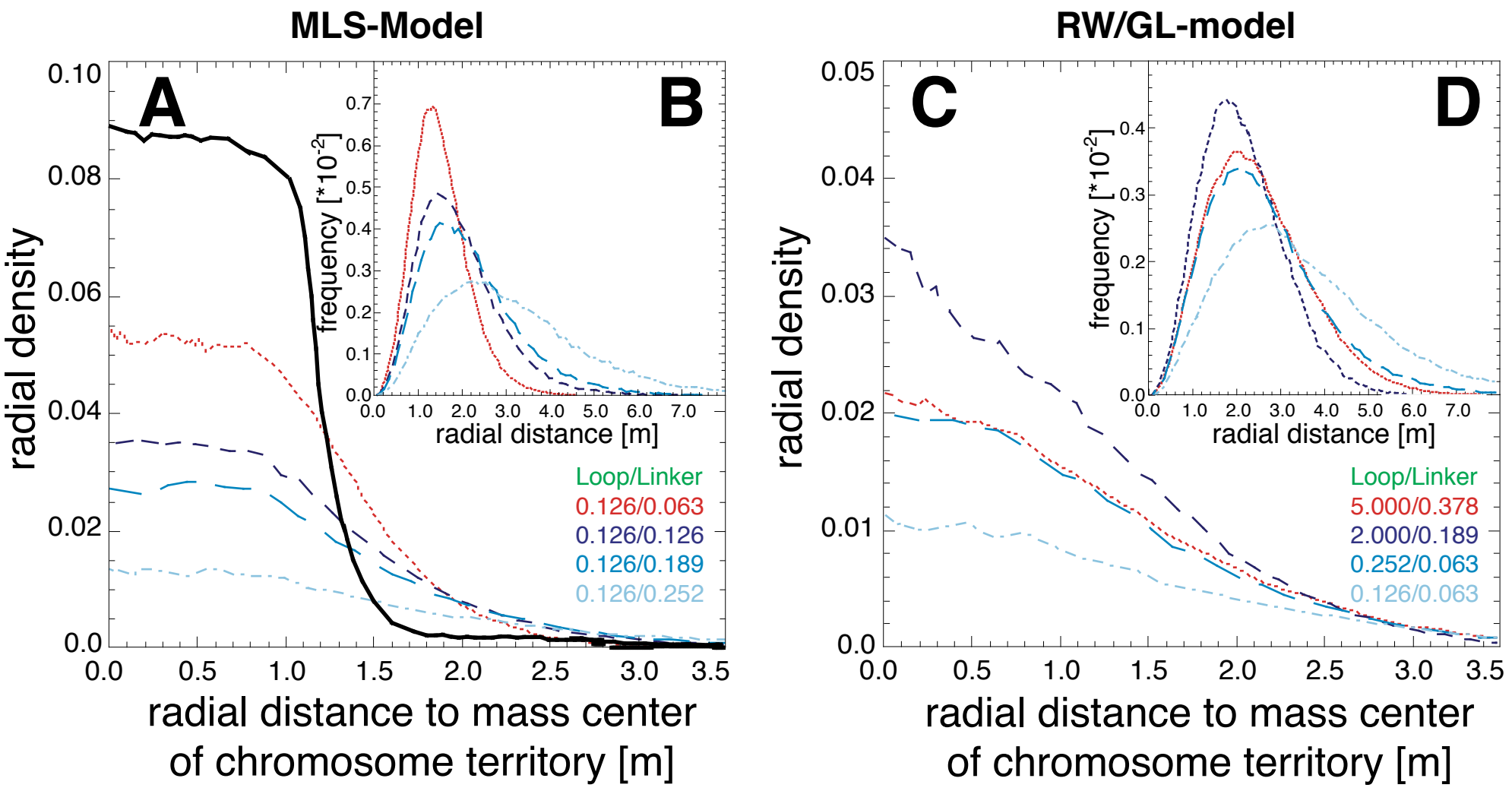

The mean extension of MLS subcompartments is proportional to the loop size (A) and the excluded volume interaction (B). The mean distance between succeeding subcompartments is only proportional to the linker size (C). The nearest neighbour subcompartment distance are proportional to the linker size and the embeding volume (D).

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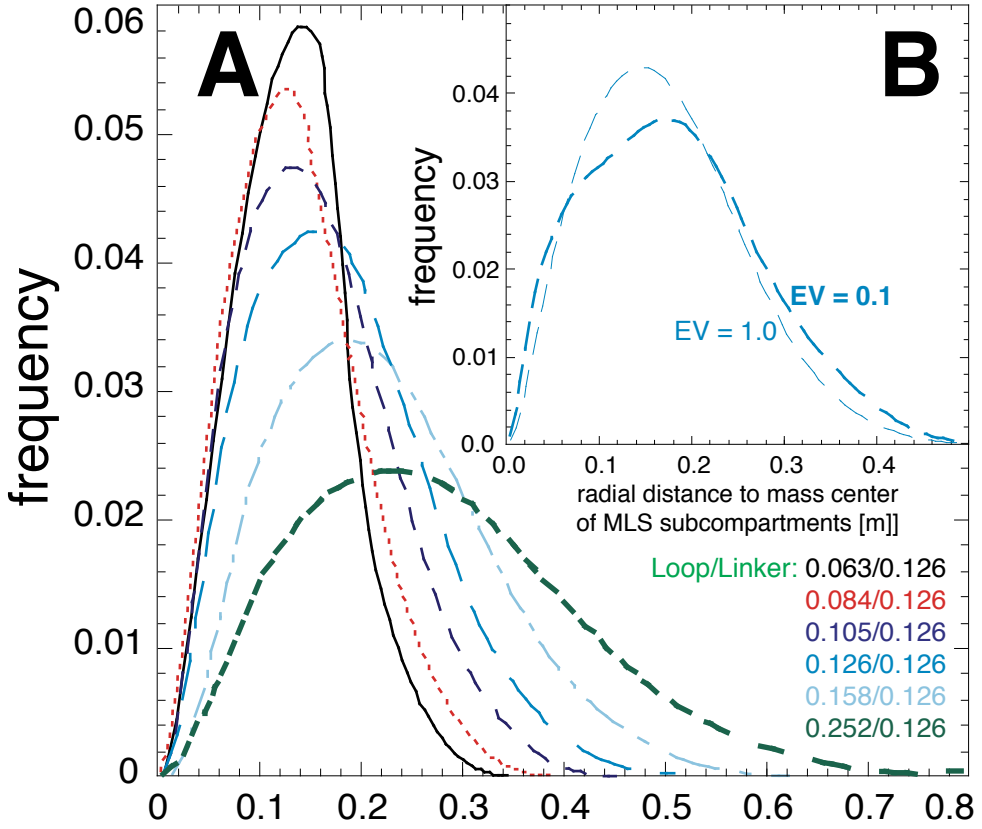
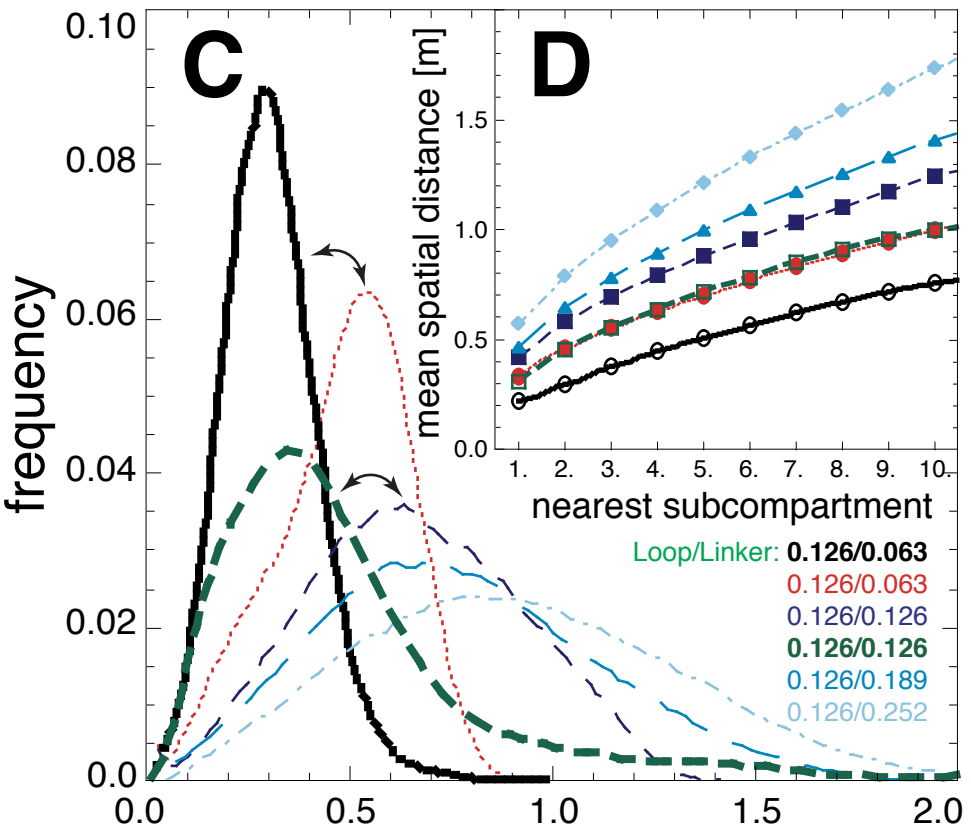
MLS-Model



MLS-model



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.

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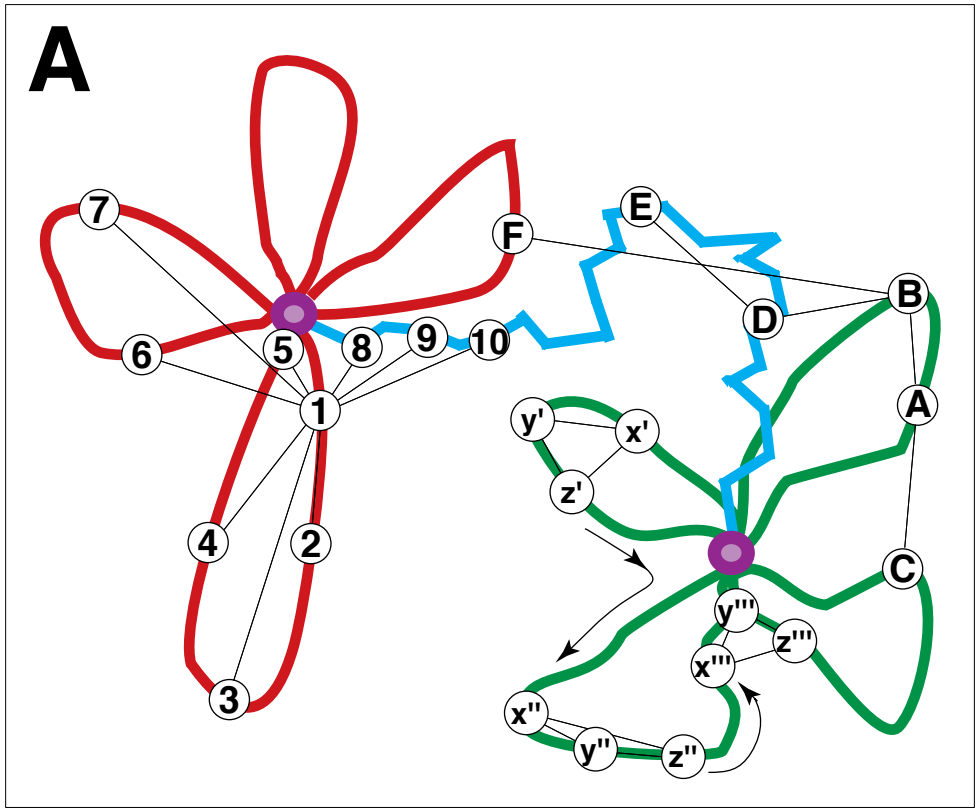

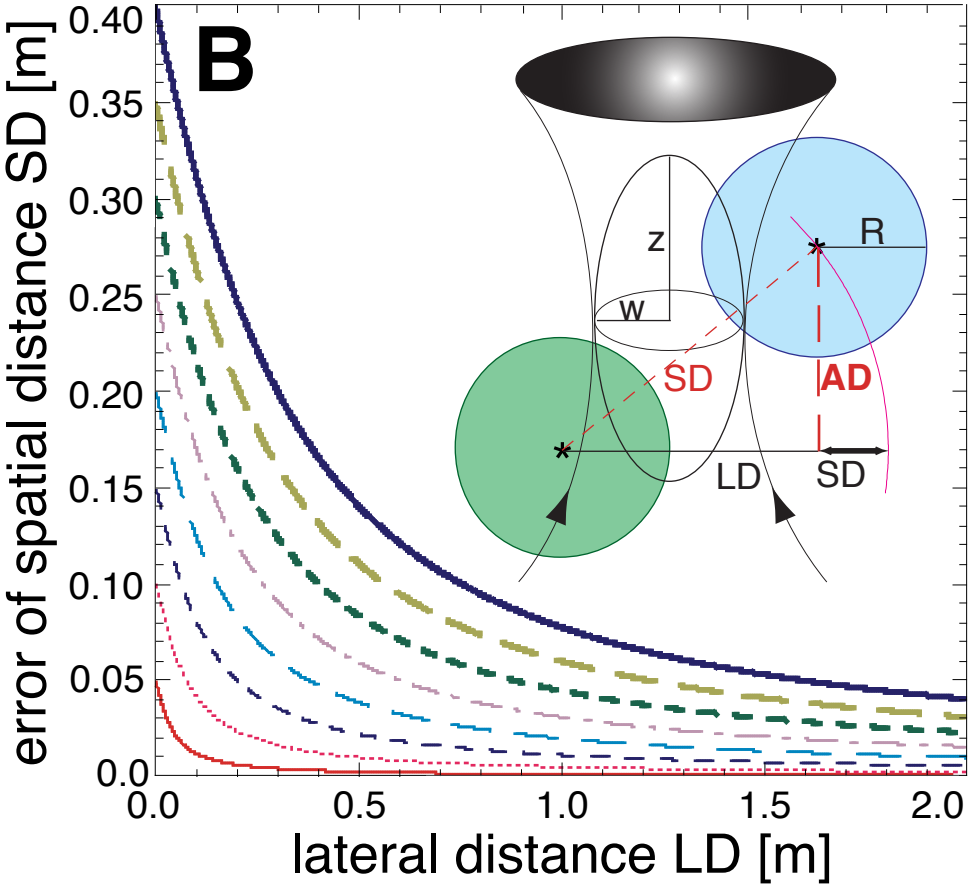

Comparison between simulated and experimental spatial distance measurements as function of their genomic separation.

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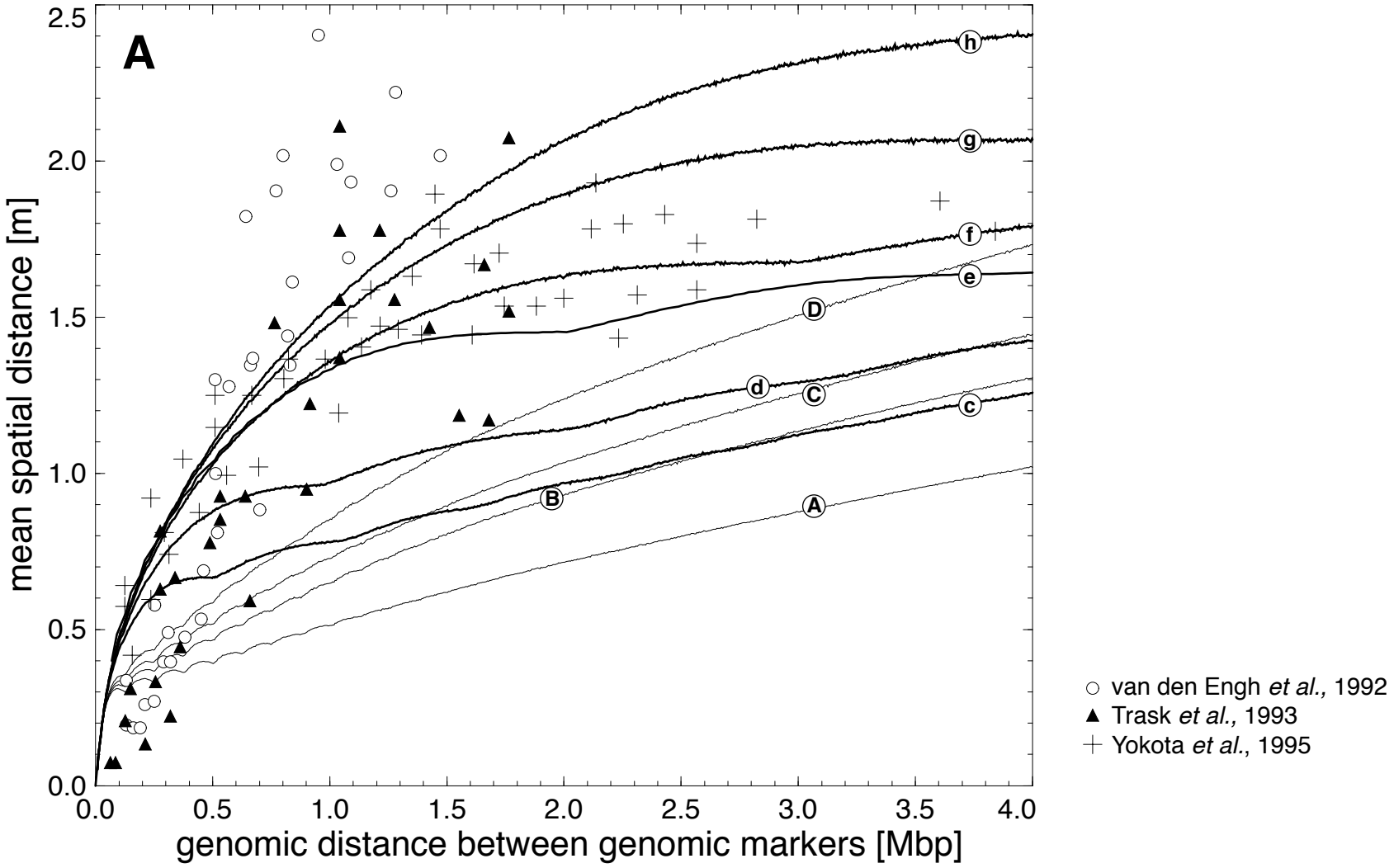
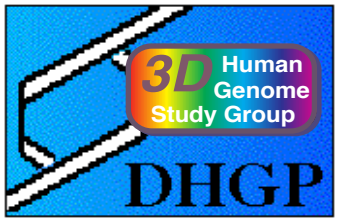


Comparison between simulated and experimental spatial distance measurements as function of their genomic separation.



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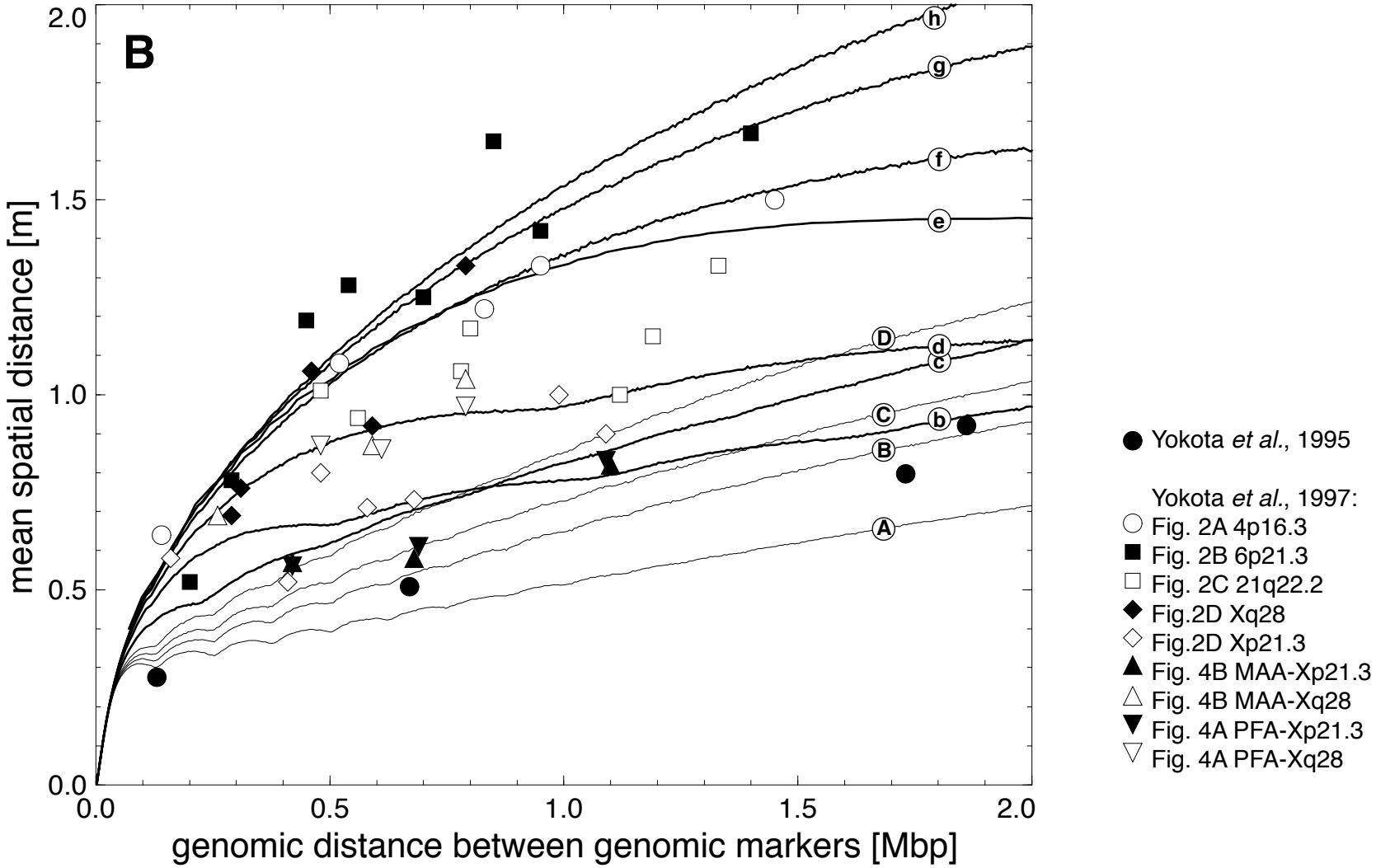

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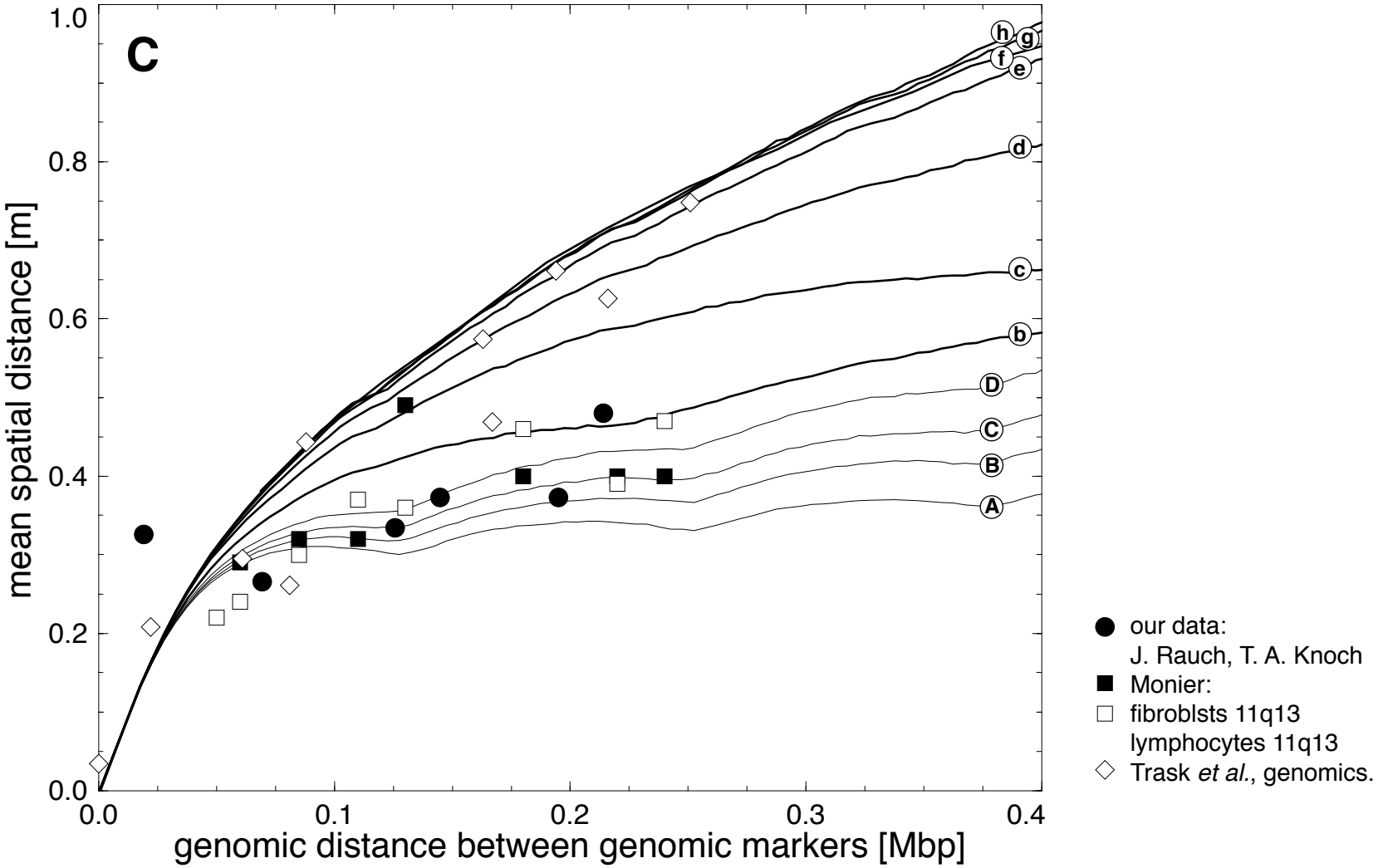

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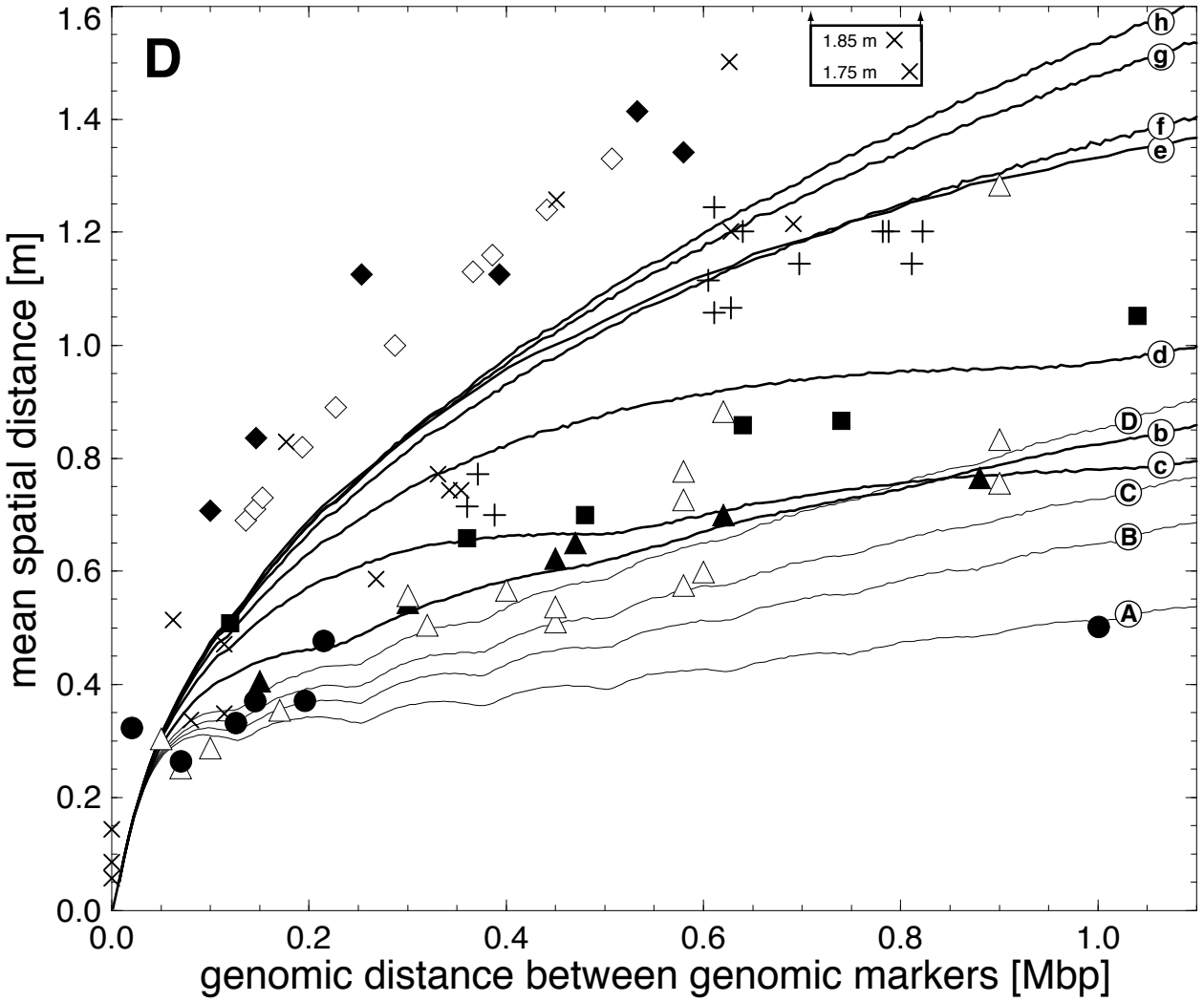

- our data: J. Rauch, T. A. Knoch
- Lawrence *et al, 1990.*
- Senger *et al.,1993*:
  - one colour
  - two colour
- Warrington *et al., 1994*:
  - reference
  - prediction
- Trask *et al.,* 1991:
  - Fig. 4A
  - Fig. 4B.

Position indipendent 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.

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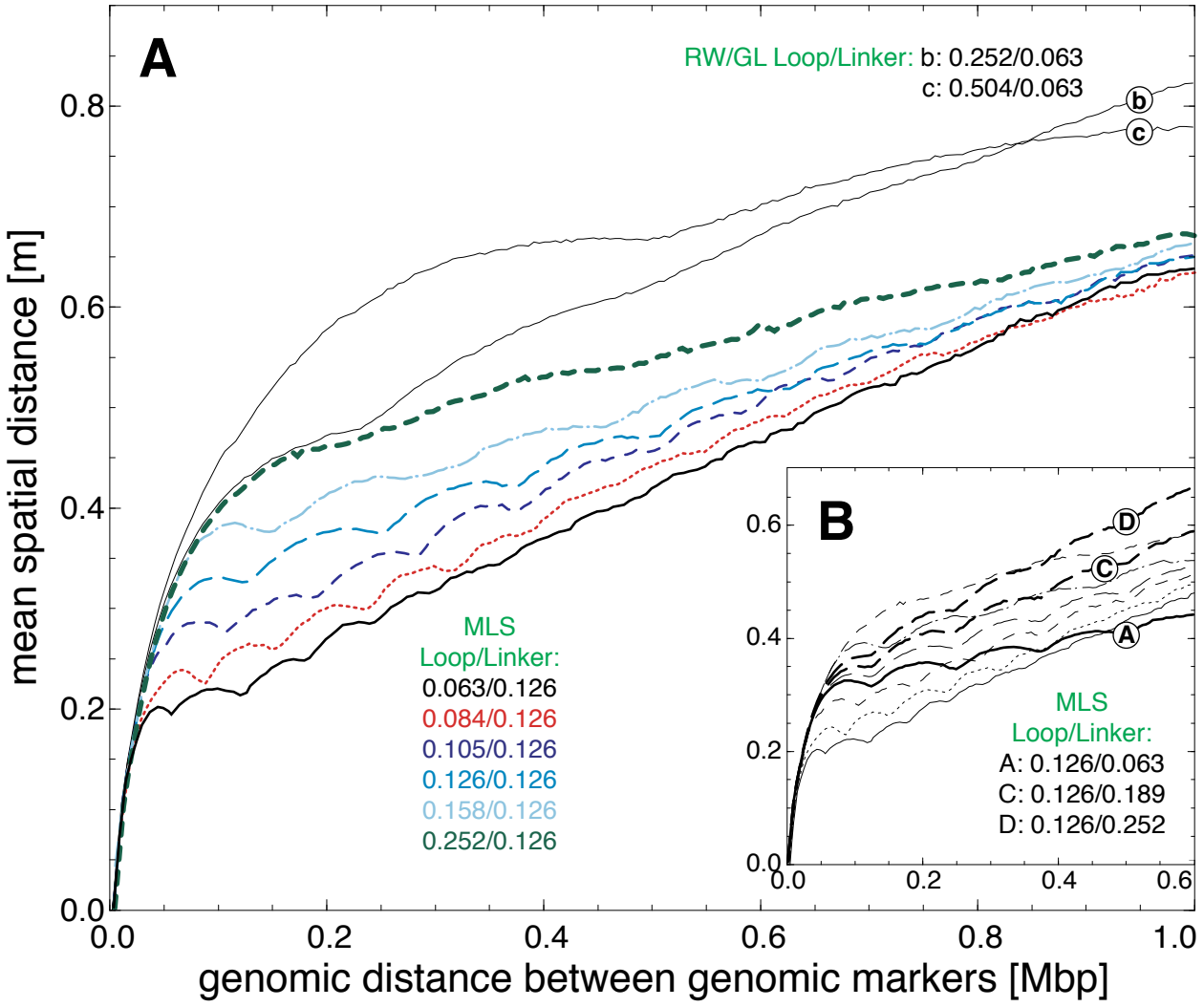

Position dependent spatial distance measurements allow the fine mapping of chromosomes (A & B). Position indedpendent spatial distance measurements are the smeared out or the mea of the position dependent spatial distance measurements.

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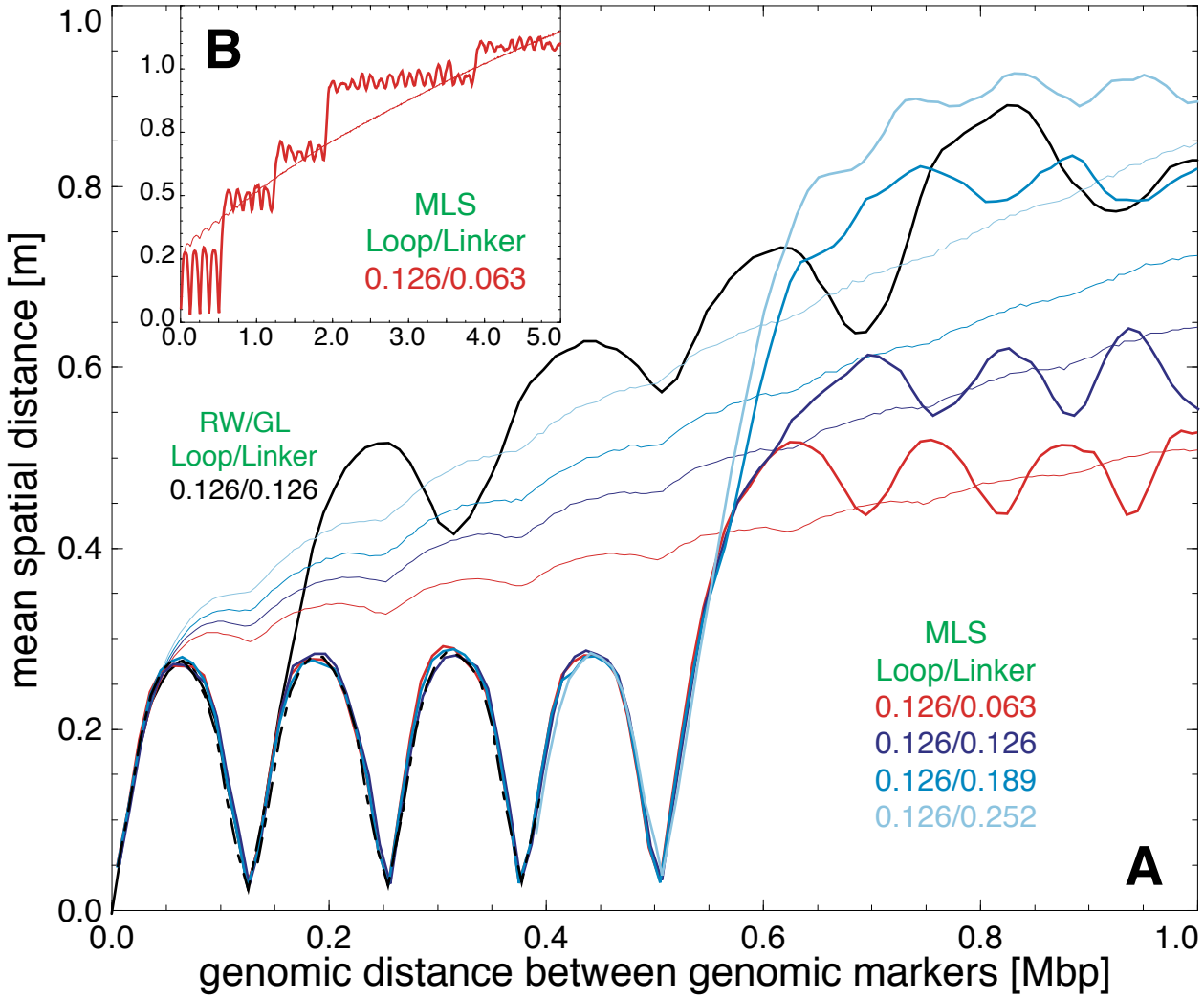
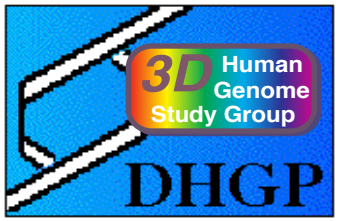


Categorizing the available spatial distance measurements between genomic markers as function of their genomic separation leads to a better evaluation of the comparison between simulations and experiments.



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Purpose	Preparation Methods	Imaging Methods
Order of clones for sequenzing	hypotonic swelling dropping on coverslips MAA fixation	2D fluorescence microscopy
Transition phase from sequenzing to packing of chromosomes	hypotonic swelling dropping on coverslips MAA fixation	2D fluorescence microscopy digital image analysis
detailed 3D organization of the genome	PFA fixation	3D/4D CLSM image reconstruction methods correction for optical errors

Simulation of Single Chromosomes, their Properties and Comparison to Experimental Spatial Distance Measurements

Knoch, T. A.

Biophysics of Macromolecules Seminar, German Cancer Research Centre (DKFZ), Heidelberg, Germany, April, 2000.

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.

Literature References

Knoch, T. A. Dreidimensionale Organisation von Chromosomen-Domänen in Simulation und Experiment. (Three-dimensional organization of chromosome domains in simulation and experiment.) *Diploma Thesis*, Faculty for Physics and Astronomy, Ruperto-Carola University, Heidelberg, Germany, 1998, and TAK Press, Tobias A. Knoch, Mannheim, Germany, ISBN 3-00-010685-5 and ISBN 978-3-00-010685-9 (soft cover, 2rd ed.), ISBN 3-00-035857-9 and ISBN 978-3-00-0358857-0 (hard cover, 2rd ed.), ISBN 3-00-035858-7, and ISBN 978-3-00-035858-6 (DVD, 2rd ed.), 1998.

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.

Knoch, T. A., Münkel, C. & Langowski, J. Three-dimensional organization of chromosome territories in the human interphase nucleus. *High Performance Computing in Science and Engineering 1999*, editors Krause, E. & Jäger, W., High-Performance Computing Center (HLRS) Stuttgart, University of Stuttgart, Springer Berlin-Heidelberg-New York, ISBN 3-540-66504-8, 229-238, 2000.

Bestvater, F., **Knoch, T. A.**, Langowski, J. & Spiess, E. GFP-Walking: Artificial construct conversions caused by simultaneous cotransfection. *BioTechniques* 32(4), 844-854, 2002.