# Fractal analysis of the DNA sequence of human chromosomes show non trivial long range correlations over $10^{6\ to\ 7.5}$ base pairs, thus the genome seems to consist of full correlated sequences (FCS)
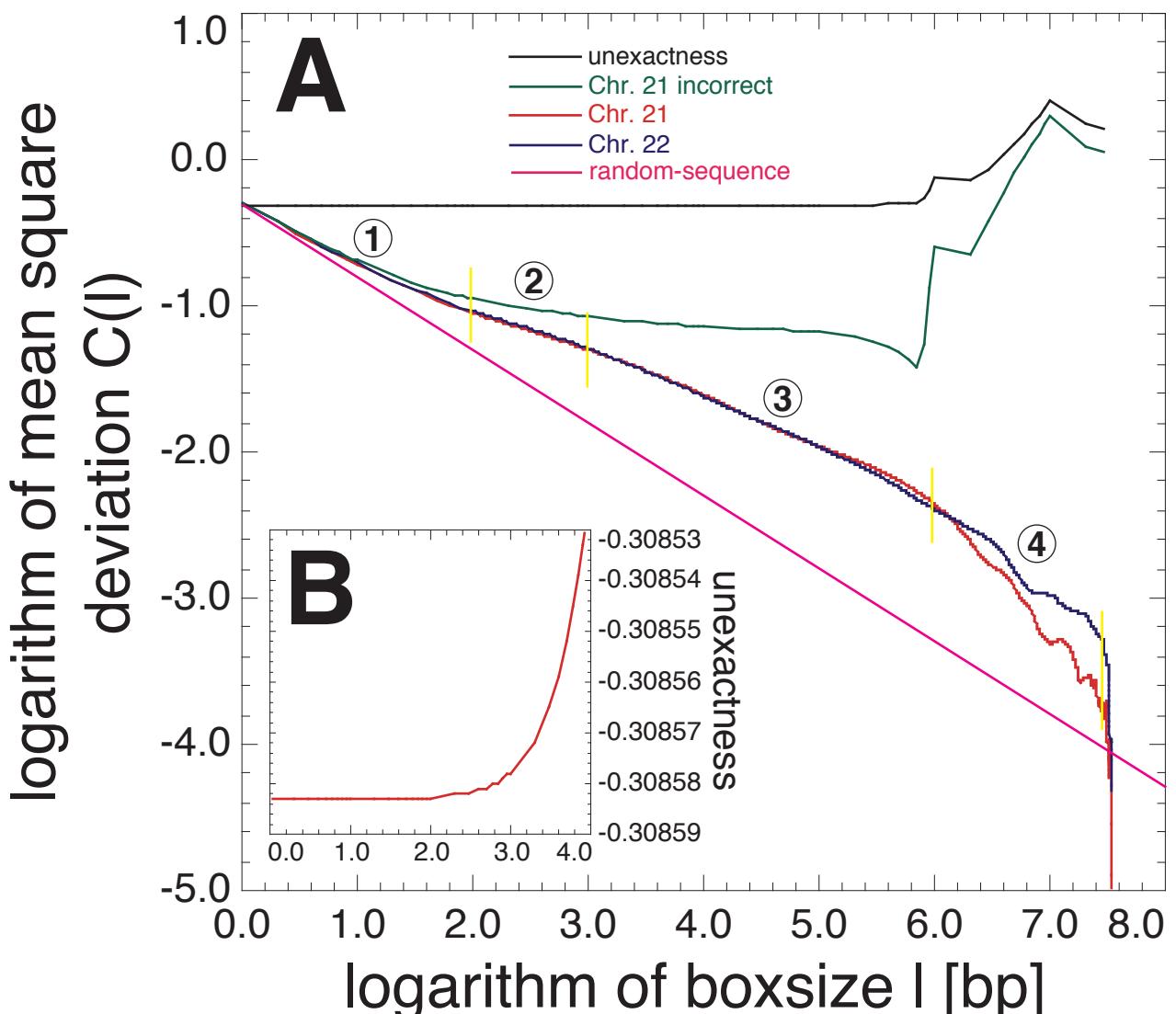
| alpha	①	②	③	④
Chr. 21	-0.37084	-0.24881	-0.34588	-0.93132
Chr. 22	-0.36393	-0.25424	-0.36931	-0.63850

Comparison of sequence correlations between different species Homo sapiens, Saccharomyces cerevisae and Arabidopsis thaliana show differences in their full sequence correlations.
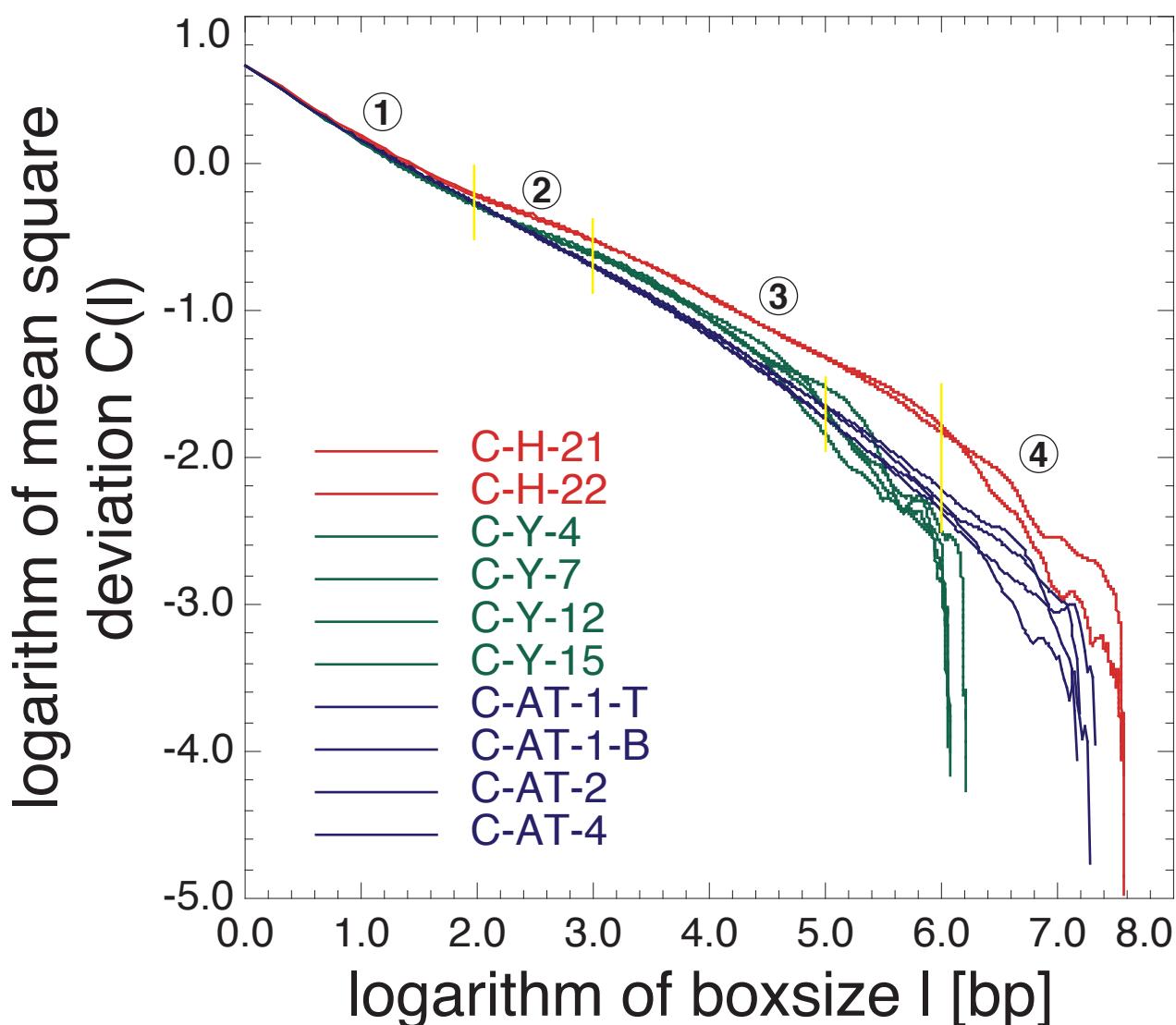
alpha	①	②	③
C-H-21	-0.37084	-0.24881	-0.34757
C-H-22	-0.36393	-0.25424	-0.37079
C-Y-4	-0.38630	-0.25659	-0.48930
C-Y-7	-0.38951	-0.27689	-0.49458
C-Y-12	-0.39239	-0.26320	-0.48487
C-Y-15	-0.39217	-0.27180	-0.53428
C-AT-1-T	-0.38014	-0.35539	-0.43333
C-AT-1-B	-0.38285	-0.35880	-0.44201
C-AT-2	-0.38075	-0.34596	-0.42440
C-AT-4	-0.38195	-0.35161	-0.44370

A more accurate fractal analysis of full correlated sequences is achieved by the local determination of the correlation parameter alpha, through taking the derivative of C(l). Consequently alpha is a measure for the correlation on a scale of the respective boxsize.
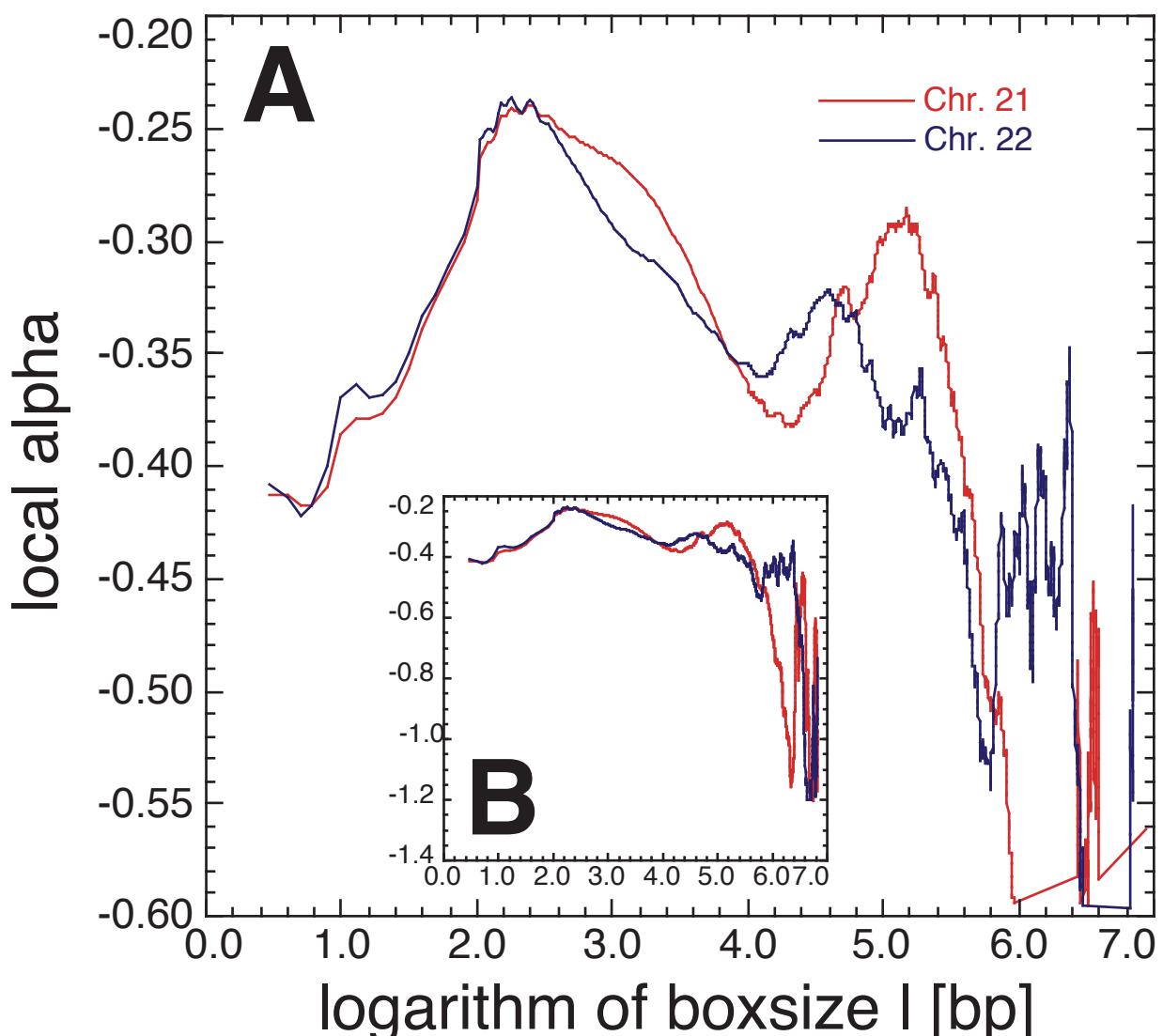

alpha	①	②	③	④
Chr. 21	-0.37084	-0.24881	-0.34588	-0.93132
Chr. 22	-0.36393	-0.25424	-0.36931	-0.63850

Comparison of the local alpha for Homo sapiens, Saccharomyces cerevisae and Arabidopsis thaliana reveals the predicted differences from C(l).
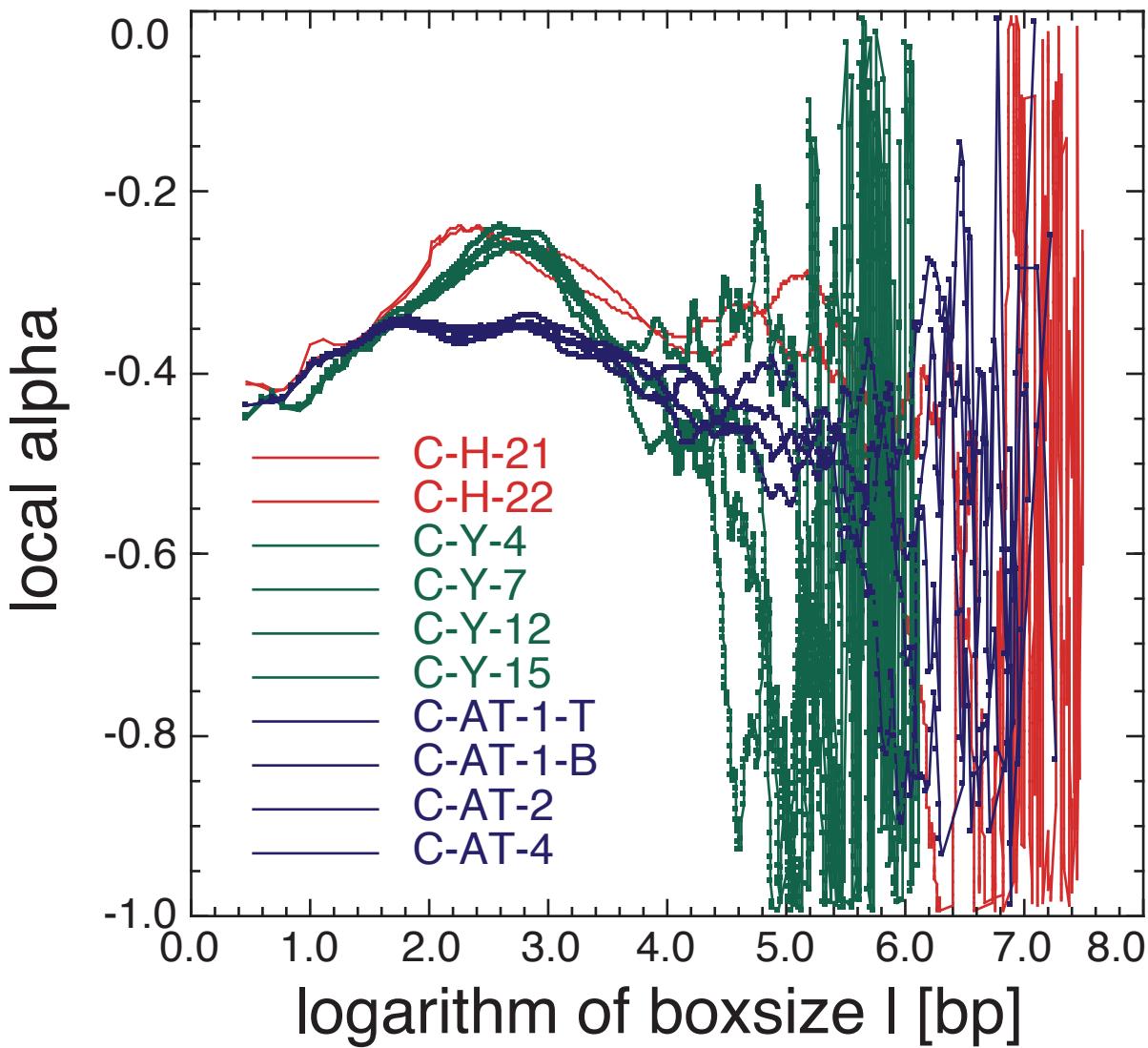

alpha	①	②	③
C-H-21	-0.37084	-0.24881	-0.34757
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C-AT-1-T	-0.38014	-0.35539	-0.43333
C-AT-1-B	-0.38285	-0.35880	-0.44201
C-AT-2	-0.38075	-0.34596	-0.42440
C-AT-4	-0.38195	-0.35161	-0.44370

Local alpha of Saccharomyces cerevisae.

dC-Y4
dC-Y7
dC-Y12
dC-Y15
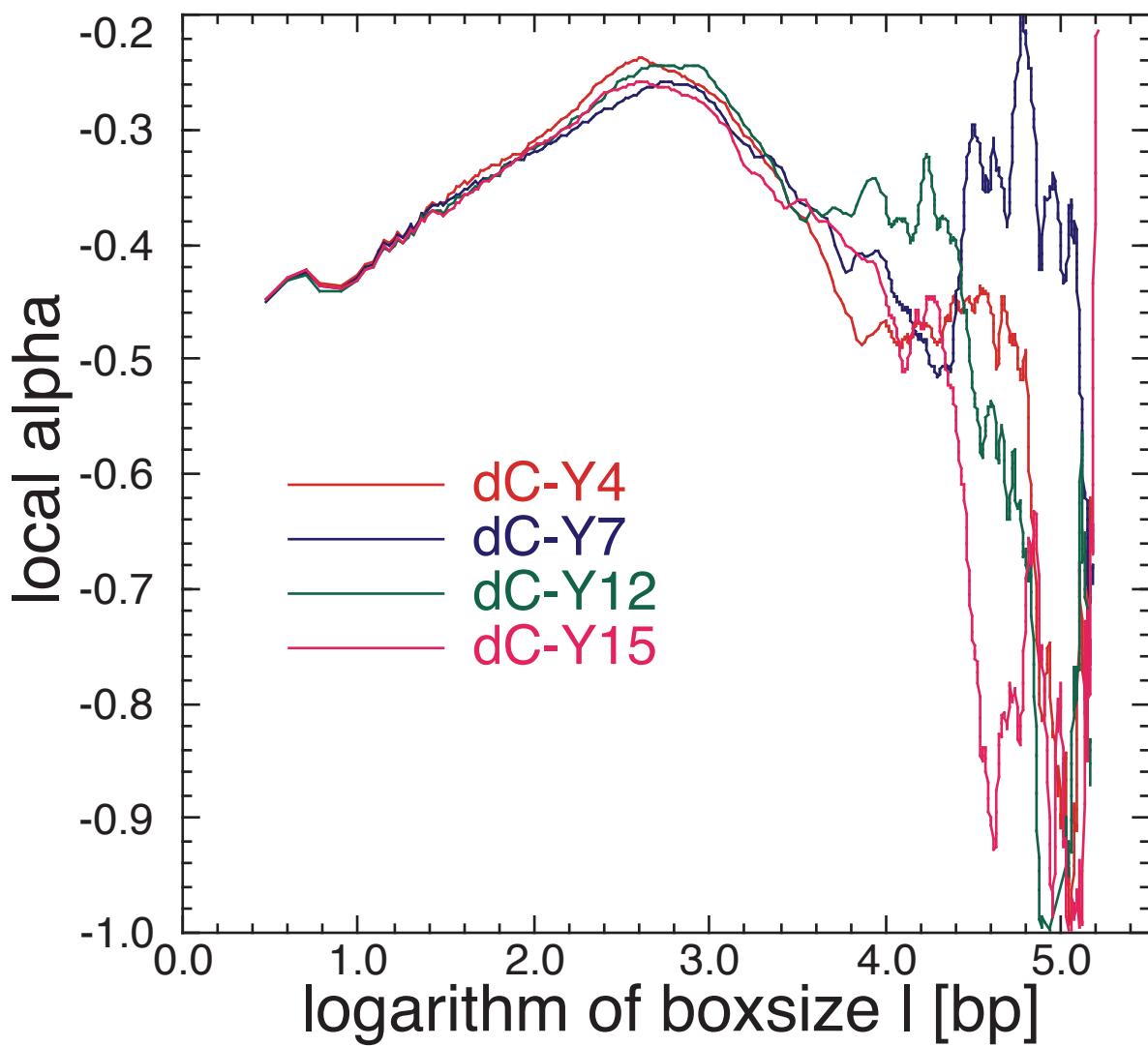
Local alpha of Arabidopsis thaliana.

local alpha

logarithm of boxsize l [bp]

dC-AT-1-T
dC-AT-1-B
dC-AT-2
dC-AT-4
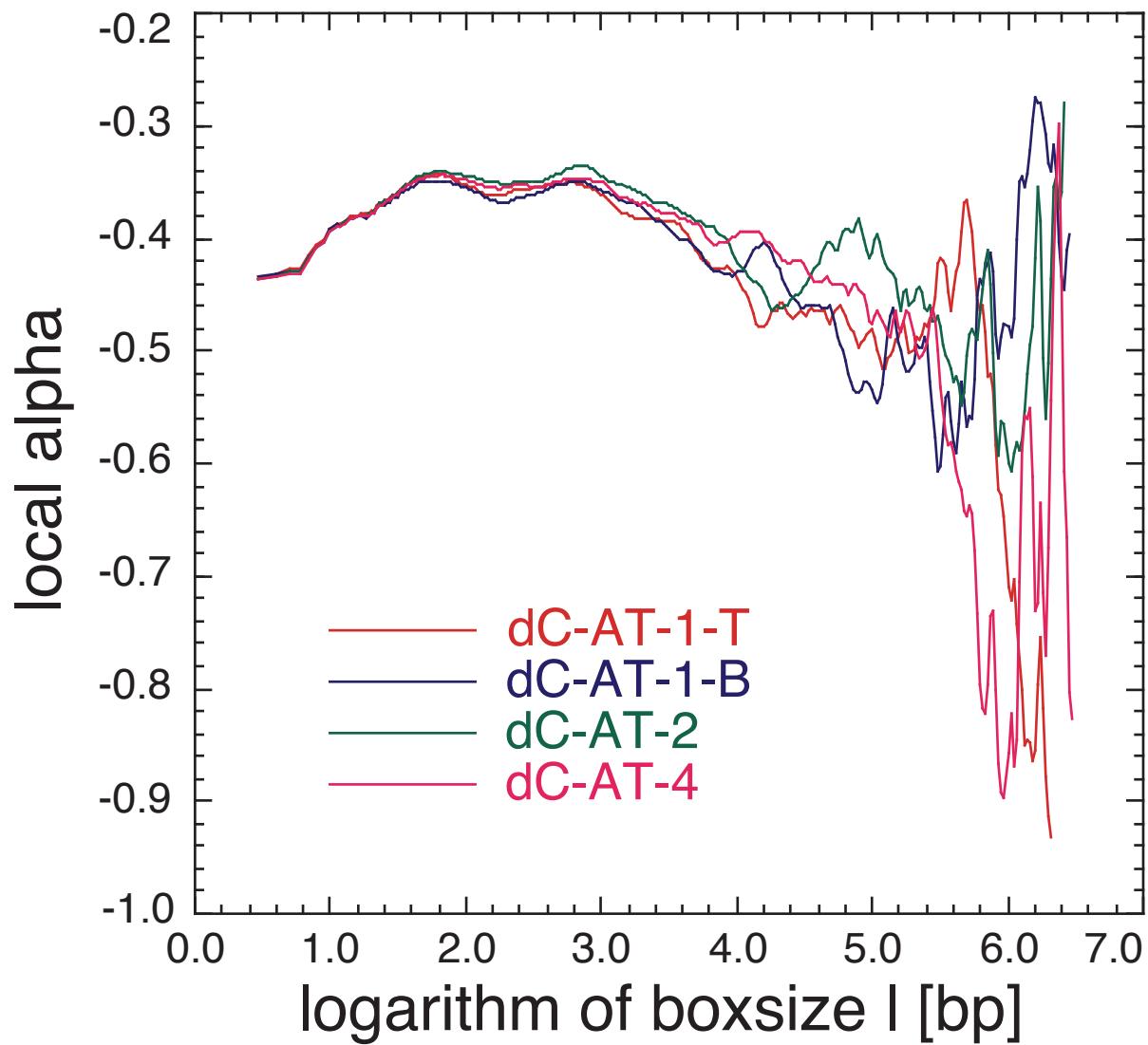
The local alpha reveils distinct structures in the full correlated sequences.
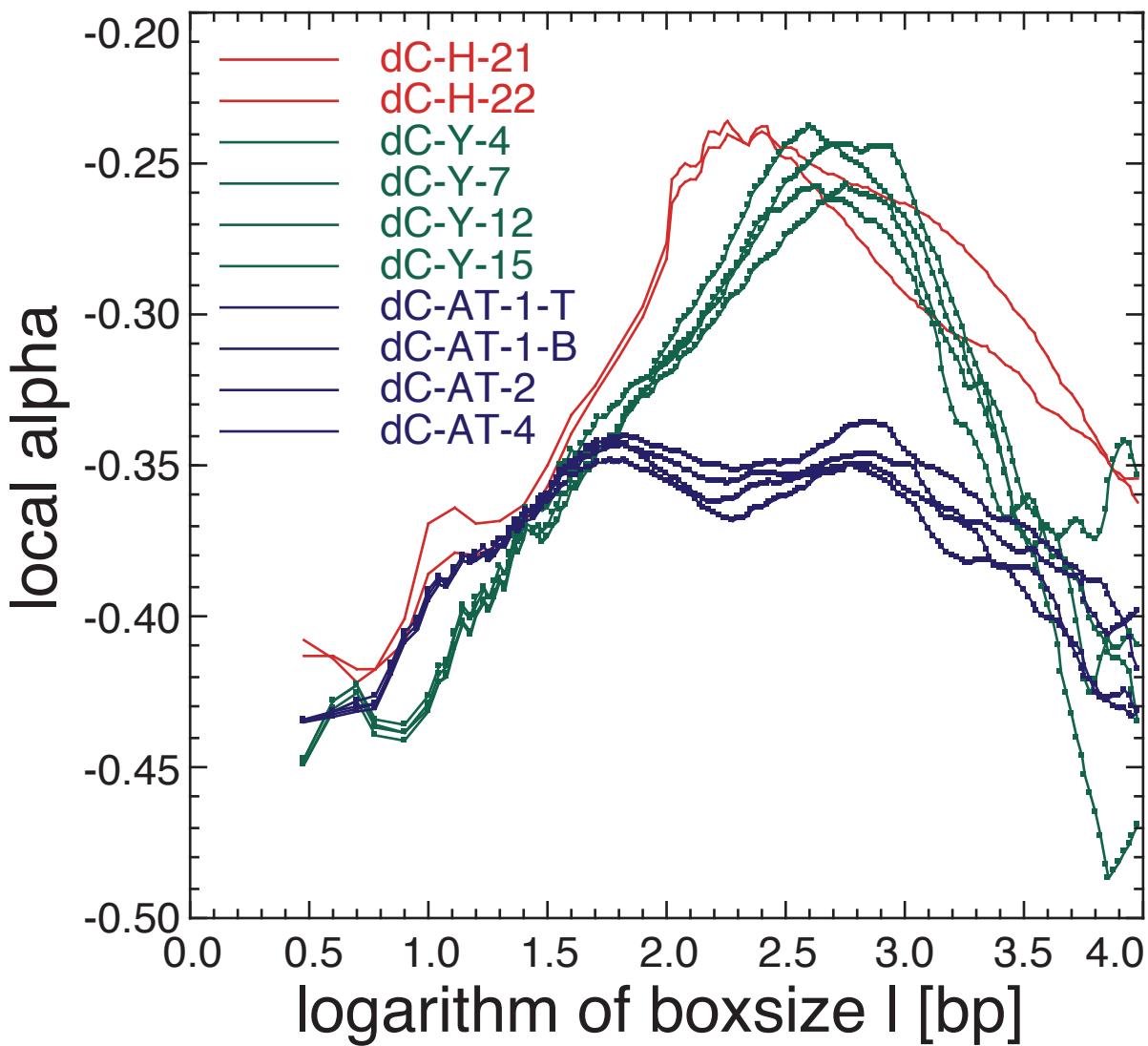
The local alpha reveils distinct structures in the full correlated sequences.
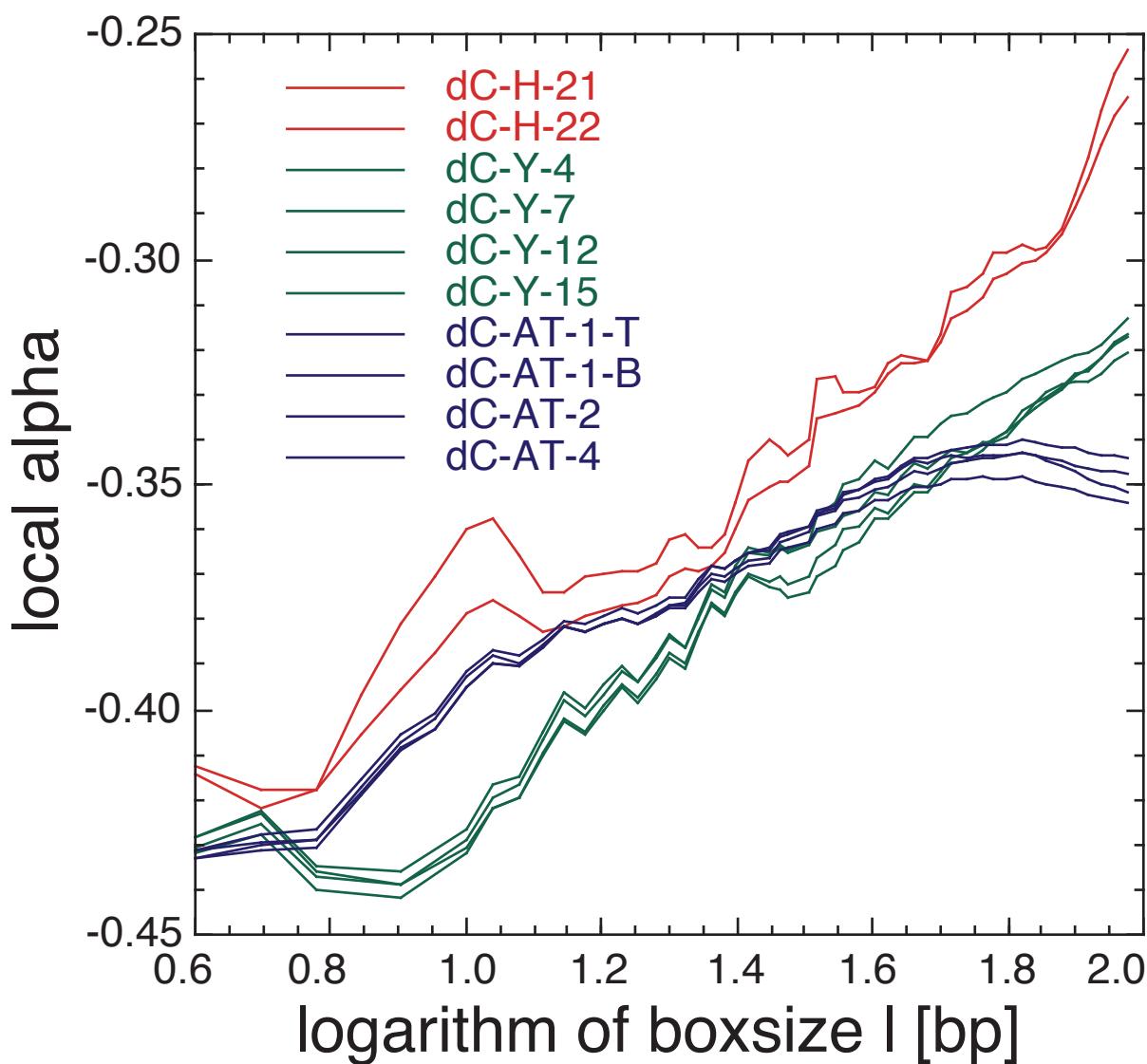
Fractal Analysis of the DNA Sequence of Different Species

Knoch, T. A.

Biophysics of Macromolecules Seminar, German Cancer Research Centre (DKFZ),
Heidelberg, Germany, Oktober, 2001.

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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.

Knoch, T. A. (editor), Backes, M., Baumgärtner, V., Eysel, G., Fehrenbach, H., Göker, M., Hampl, J., Hampl, U., Hartmann, D., Hitzelberger, H., Nambena, J., Rehberg, U., Schmidt, S., Weber, A., & Weidemann, T. Humanökologische Perspectiven Wechsel - Festschrift zu Ehren des 70. Geburtstags von Prof. Dr. Kurt Egger. Human Ecology Working Group, Ruperto-Carola University of Heidelberg, Heidelberg, Germany, 2002.

Knoch, T. A. Approaching the three-dimensional organization of the human genome: structural-, scaling- and dynamic properties in the simulation of interphase chromosomes and cell nuclei, long- range correlations in complete genomes, *in vivo* quantification of the chromatin distribution, construct conversions in simultaneous co-transfections. *Dissertation*, Ruperto-Carola University, Heidelberg, Germany, and TAK†Press, Tobias A. Knoch, Mannheim, Germany, ISBN 3-00-009959-X and ISBN 978-3-00-009959-5 (soft cover, 3rd ed.), ISBN 3-00-009960-3 and ISBN 978-3-00-009960-1 (hard cover, 3rd ed.), ISBN 3-00-035856-9 and ISBN 978-3-00-010685-9 (DVD, 3rd ed.) 2002.

Knoch, T. A. Towards a holistic understanding of the human genome by determination and integration of its sequential and three-dimensional organization. *High Performance Computing in Science and Engineering 2003*, editors Krause, E., Jäger, W. & Resch, M., High-Performance Computing Center (HLRS) Stuttgart, University of Stuttgart, Springer Berlin-Heidelberg-New York, ISBN 3- 540-40850-9, 421-440, 2003.

Wachsmuth, M., Weidemann, T., Müller, G., Urs W. Hoffmann-Rohrer, **Knoch, T. A.**, Waldeck, W. & Langowski, J. Analyzing intracellular binding and diffusion with continuous fluorescence photobleaching. *Biophys. J.* 84(5), 3353-3363, 2003.

Weidemann, T., Wachsmuth, M., **Knoch, T. A.**, Müller, G., Waldeck, W. & Langowski, J. Counting nucleosomes in living cells with a combination of fluorescence correlation spectroscopy and confocal imaging. *J. Mol. Biol.* 334(2), 229-240, 2003.