CITED REFERENCES

Afreixo V, Rodrigues JM, Bastos CAC, Silva RM. 2016. The exceptional genomic word symmetry along DNA sequences. BMC bioinformatics. 17(1):1–10.

Arhondakis S, Milanesi M, Castrignanò T, Gioiosa S, Valentini A, Chillemi G. 2020. Evidence of distinct gene functional patterns in GC-poor and GC-rich isochores in Bos taurus. Animal genetics. 51(3):358–368.

Ayad LAK, Dourou A-M, Arhondakis S, Pissis SP. 2020. IsoXpressor: a tool to assess transcriptional activity within isochores. Genome biology and evolution. 12(9):1573–1578.

Belle EMS, Smith N, Eyre-Walker A. 2002. Analysis of the phylogenetic distribution of isochores in vertebrates and a test of the thermal stability hypothesis. J Mol Evol. 55(3):356–363. eng. doi:10.1007/s00239-002-2333-1.

Benjamini Y, Hochberg Y. 1995. Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. Journal of the Royal Statistical Society: Series B (Methodological). 57(1):289–300. doi:10.1111/j.2517-6161.1995.tb02031.x.

Bernardi G. 1993. The vertebrate genome: isochores and evolution. Mol Biol Evol. 10(1):186–204. eng. doi:10.1093/oxfordjournals.molbev.a039994.

Bernardi G. 2000. Isochores and the evolutionary genomics of vertebrates. Gene. 241(1):3–17. eng. doi:10.1016/s0378-1119(99)00485-0.

Bernardi G. 2001. Misunderstandings about isochores. Part 1. Gene. 276(1-2):3–13. eng. doi:10.1016/s0378-1119(01)00644-8.

Bernardi G, Olofsson B, Filipski J, Zerial M, Salinas J, Cuny G, Meunier-Rotival M, Rodier F. 1985. The mosaic genome of warm-blooded vertebrates. Science. 228(4702):953–958. eng. doi:10.1126/science.4001930.

Bernardi G. 2015. Chromosome architecture and genome organization. PLoS One. 10(11):e0143739.

Bovine Genome Sequencing and Analysis Consortium. 2009. The genome sequence of taurine cattle: a window to ruminant biology and evolution. Science. 324(5926):522–528. eng. doi:10.1126/science.1169588.

Clauset A, Shalizi CR, Newman MEJ. 2009. Power-Law Distributions in Empirical Data. SIAM Rev. 51(4):661–703. doi:10.1137/070710111.

Clay O, Bernardi G. 2005. How not to search for isochores: a reply to Cohen et Al. Mol Biol Evol. 22(12):2315–2317. eng. doi:10.1093/molbev/msi231.

Clay OK, Bernardi G. 2011. GC3 of genes can be used as a proxy for isochore base composition: a reply to Elhaik et al. Mol Biol Evol. 28(1):21–23. eng. doi:10.1093/molbev/msq222.

Cock PJA, Antao T, Chang JT, Chapman BA, Cox CJ, Dalke A, Friedberg I, Hamelryck T, Kauff F, Wilczynski B, et al. 2009. Biopython: freely available Python tools for computational molecular biology and bioinformatics. Bioinformatics. 25(11):1422–1423. eng. doi:10.1093/bioinformatics/btp163.

Cohen N, Dagan T, Stone L, Graur D. 2005. GC composition of the human genome: in search of isochores. Mol Biol Evol. 22(5):1260–1272. eng. doi:10.1093/molbev/msi115.

Costantini M, Clay O, Auletta F, Bernardi G. 2006. An isochore map of human chromosomes. Genome Res. 16(4):536–541. eng. doi:10.1101/gr.4910606.

Cozzi P, Milanesi L, Bernardi G. 2015. Segmenting the Human Genome into Isochores. Evol Bioinform Online. 11:253–261. eng. doi:10.4137/EBO.S27693.

Cuny G, Soriano P, Macaya G, Bernardi G. 1981. The major components of the mouse and human genomes. 1. Preparation, basic properties and compositional heterogeneity. Eur J Biochem. 115(2):227–233. eng. doi:10.1111/j.1432-1033.1981.tb05227.x.

Delage W, Thevenon J, Lemaitre C. 2020. Towards a better understanding of the low discovery rate of short-read based insertion variant callers. In: JOBIM 2020. [place unknown]: [publisher unknown].

Elhaik E, Graur D. 2014. A comparative study and a phylogenetic exploration of the compositional architectures of mammalian nuclear genomes. PLoS Comput Biol. 10(11):e1003925. eng. doi:10.1371/journal.pcbi.1003925.

Elhaik E, Graur D, Josic K. 2010. Comparative testing of DNA segmentation algorithms using benchmark simulations. Mol Biol Evol. 27(5):1015–1024. eng. doi:10.1093/molbev/msp307.

Elhaik E, Graur D, Josić K, Landan G. 2010. Identifying compositionally homogeneous and nonhomogeneous domains within the human genome using a novel segmentation algorithm. Nucleic Acids Res. 38(15):e158. eng. doi:10.1093/nar/gkq532.

Fimmel E, Gumbel M, Karpuzoglu A, Petoukhov S. 2019. On comparing composition principles of long DNA sequences with those of random ones. Biosystems. 180:101–108. eng. doi:10.1016/j.biosystems.2019.04.003.

Fukagawa T, Sugaya K, Matsumoto K, Okumura K, Ando A, Inoko H, Ikemura T. 1995. A boundary of long-range G + C% mosaic domains in the human MHC locus: pseudoautosomal boundary-like sequence exists near the boundary. Genomics. 25(1):184–191. eng. doi:10.1016/0888-7543(95)80124-5.

Graur D, Sater AK, Cooper TF. 2016. Molecular and genome evolution. Sunderland, Massachusetts: Sinauer Associates. ISBN: 9781605354699.

Lander ES, and 254 others. 2001. Initial sequencing and analysis of the human genome. Nature. 409(6822):860–921. eng. doi:10.1038/35057062.

Li W, Bernaola-Galván P, Carpena P, Oliver JL. 2003. Isochores merit the prefix 'iso'. Comput Biol Chem. 27(1):5–10. eng. doi:10.1016/s1476-9271(02)00090-7.

Macaya G, Thiery JP, Bernardi G. 1976. An approach to the organization of eukaryotic genomes at a macromolecular level. J Mol Biol. 108(1):237–254. eng. doi:10.1016/s0022-2836(76)80105-2.

Michaux J, Reyes A, Catzeflis F. 2001. Evolutionary history of the most speciose mammals: molecular phylogeny of muroid rodents. Mol Biol Evol. 18(11):2017–2031. eng. doi:10.1093/oxfordjournals.molbev.a003743.

Mourad R. 2020. Studying 3D genome evolution using genomic sequence. Bioinformatics. 36(5):1367–1373.

Nacheva E, Mokretar K, Soenmez A, Pittman AM, Grace C, Valli R, Ejaz A, Vattathil S, Maserati E, Houlden H, et al. 2017. DNA isolation protocol effects on nuclear DNA analysis by microarrays, droplet digital PCR, and whole genome sequencing, and on mitochondrial DNA copy number estimation. PLoS One. 12(7):e0180467.

Schmidt T, Frishman D. 2008. Assignment of isochores for all completely sequenced vertebrate genomes using a consensus. Genome Biol. R104. eng. doi:10.1186/gb-2008-9-6-r104.

Thiery JP, Macaya G, Bernardi G. 1976. An analysis of eukaryotic genomes by density gradient centrifugation. J Mol Biol. 108(1):219–235. eng. doi:10.1016/s0022-2836(76)80104-0.

Wickham H. 2016. ggplot2: Elegant Graphics for Data Analysis. [place unknown]: Springer-Verlag New York. ISBN: 978-3-319-24277-4. https://ggplot2.tidyverse.org/.