IsoFinder update

IsoFinderC, April 2013

Isochores are long genome segments homogeneous in G+C. The algorithm *IsoFinder* [1] is able to predict isochores at the sequence level. Most of the *IsoFinder* isochores show correlation with biological features such as gene density, SINE and LINE densities, recombination rate or SNP variability.

More recently, the reliability of this algorithm in predicting isochore-like regions at the sequence level has been established through the analysis of large-scale genome patchiness by an independent method: the analysis of the deviations in the power-law behavior of long-range correlations [2,3].

The Online Resource on Isochore Mapping (http://bioinfo2.ugr.es/isochores/) provides access to isochore listings and genome UCSC maps for the best-assembled mammalian genome sequences.

Minor updates to the *IsoFinder* code include:

1. Output file in BED-like format
2. Better identification of chromosome-contigs for recent genome assemblies
3. Increased minimum segment size to improve the reliability of statistical tests

[1] Oliver JL, Carpena P, Hackenberg M, Bernaola-Galván P. 2004. *IsoFinder*: computational prediction of isochores in genome sequences. Nucleic Acids Research 32: W287-W292.
http://dx.doi.org/10.1093/nar/gkh399

[2] Oliver JL, Bernaola-Galván P, Hackenberg M, Carpena P. 2008. Phylogenetic distribution of large-scale genome patchiness. BMC Evolutionary Biology 8: 107.
http://dx.doi.org/10.1186/1471-2148-8-107

[3] Pedro Bernaola-Galván, José L. Oliver, Michael Hackenberg, Ana V. Coronado, Plamen Ch. Ivanov, and Pedro Carpena. 2012. Segmentation of time series with long-range fractal correlations. The European Physical Journal B 85: 211 [PDF]
http://dx.doi.org/10.1140/epjb/e2012-20969-5