`chroGPS`: navigating though the epigenome.

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1 Introduction

The `chroGPS` package provides tools go generate intuitive maps to visualize the association between genetic elements, with emphasis on epigenetics. The approach is based on Multi-Dimensional Scaling. We provide several sensible distance metrics, and adjustment procedures to remove systematic biases typically observed when merging data obtained under different technologies or genetic backgrounds.

Many routines are designed to perform computations in parallel by specifying an argument `mc.cores`, which uses package `multicore`. As this package is not available in all platforms, currently only Unix/Linux and Mac OS X versions of the package are supported. Please see the help page for each function for more details.

You will find the full vignette for the chroGPS package with detailed examples in the chroGPS-manual.pdf file included in the inst/doc folder.

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