BIWEIGHTED HAM SANDWICH SOFTWARE
Directions for Use

DESCRIPTION. BHS is software designed to perform quick and accurate partitioning of geometric graphs, that is, graphs whose vertices have specific locations in 2-space.

This software makes use of the Ham Sandwich Theorem: a theorem from algebraic topology that stipulates that a single straight line can always be found to bisect two weights simultaneously on a set of points in the plane. The software was written by Andrew A. Poe, Northern Michigan University, Marquette, Michigan, USA, as part of a collaborative project with Quentin F. Stout, The University of Michigan, Ann Arbor, Michigan, USA.

DOWNLOADING AND COMPILING. The BHS software consists of a single source file, and can be downloaded simply by accessing the BHS website at http://euclid.nmu.edu/~apoe/BHS and clicking the appropriate field.

This file, bhs.c, is self-consciously written in ANSI C, and should be compiled appropriately. This is to say the program corresponds fully with the ANSI C specification. No system-specific feature is used in this code. In fact, no feature exclusive to C++ appears in this code, either. You should have no difficulty compiling and executing this code on any system you care to use, provided that your compiler is fully compatible with ANSI C (which, nowadays, is just about all of them).

The only caveat you may need to consider is that the source code is presently in the form used by the Windows environment: the code is written in the ASCII character set, and end-of-line's are represented with the two-byte sequence <CR><LF>. (Unix systems use <LF> alone and Mac systems use <CR> alone.) Depending on your platform, you may need to run your source code through a converter. However, most compilers these days will correctly compile a text file, even if it originated on a system with a slightly different encoding.

EXECUTING. bhs takes four command-line arguments and an optional fifth:

bhs <# of input points> <# of output pieces> <input filename> {<coarsening size>}
If no arguments are present on the command line, the user is prompted for this information.

<# of input points>: the number of points in your data set.
<# of output pieces>: the number of pieces in your partition.
<input filename>: the name of the input file containing the information relating to the points. The input file should consist of a number of lines equivalent to the number of input points specified. Each line will have four floating-point numbers. The first two are the x- and y-coordinates of the corresponding point, and the last two are the two weights on that point. Weights need not be integral, but they should be nonnegative.
<coarsening size>: the grid size for coarsening. The default is 650. Larger grid sizes result in faster execution time; smaller grid sizes result in more accurate partitions.

The output file is named "ham.out.dualcr.<# of output pieces>". It consists of a number of lines equal to the number of input points. Each line contains a single integer inclusively between 0 and <# of output pieces>−1, indicating to which piece of the partition its corresponding point in the input file belongs.

CONTACT. If you have any questions or comments about this software, please direct them to:

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