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Authors
Merrill, D.W.
Selvin, S.
Mohr, M.S.

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D.W. Merrill, S. Selvin, and M.S. Mohr

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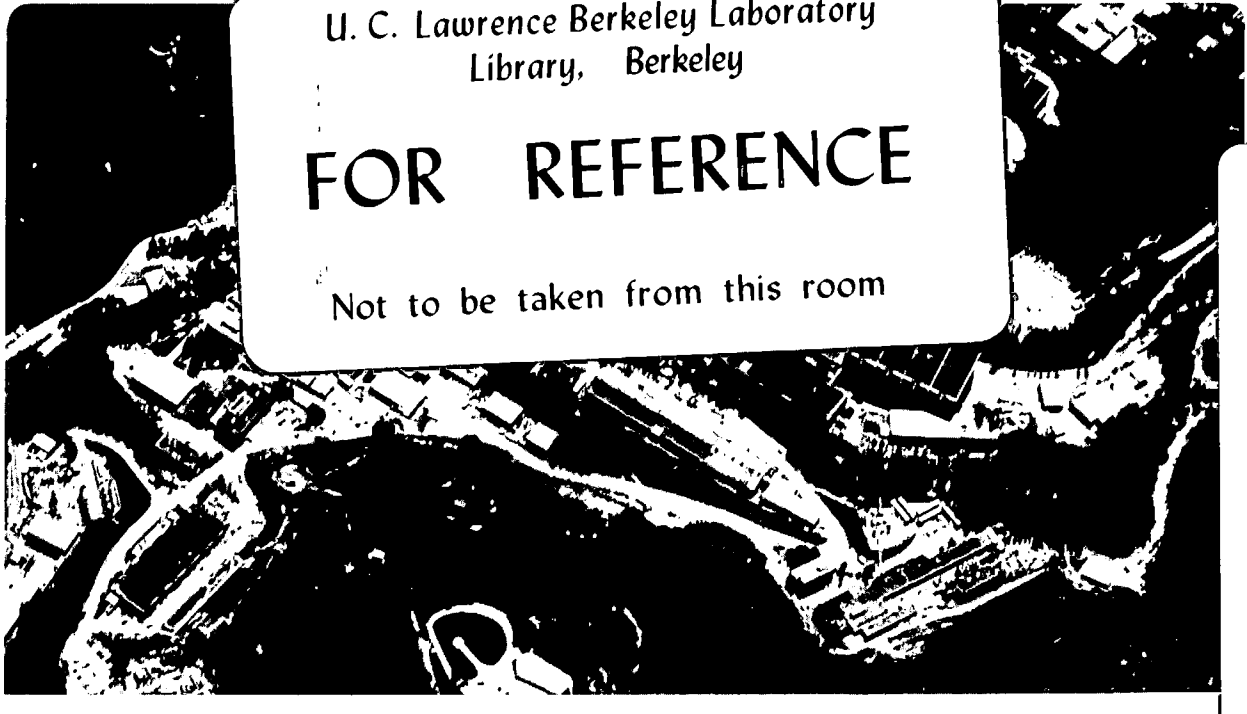

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Density Equalizing Map Projections: A New Algorithm

by

Deane W. Merrill, Steve Selvin and Michael S. Mohr

Information and Computing Sciences Division
Lawrence Berkeley Laboratory
University of California
Berkeley, California 94720

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DENSITY EQUALIZING MAP PROJECTIONS: A NEW ALGORITHM

DEANE W. MERRILL, STEVE SELVIN AND MICHAEL S. MOHR

Information and Computing Sciences Division
Lawrence Berkeley Laboratory
1 Cyclotron Road
University of California
Berkeley, California, USA 94720

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ABSTRACT

In the study of geographic disease clusters, an alternative to traditional methods based on rates is to analyze case locations on a transformed map in which population density is everywhere equal. Although the analyst's task is thereby simplified, the specification of the density equalizing map projection (DEMP) itself is not simple and continues to be the subject of considerable research. Here a new DEMP algorithm is described, which avoids some of the difficulties of earlier approaches.[2-6] The new algorithm (a) avoids illegal overlapping of transformed polygons; (b) finds the unique solution that minimizes map distortion; (c) provides constant magnification over each map polygon; (d) defines a continuous transformation over the entire map domain; (e) defines an inverse transformation; (f) can accept optional constraints such as fixed boundaries; and (g) can use commercially supported minimization software. Work is continuing to improve computing efficiency and improve the algorithm.

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INTRODUCTION

In analyzing the geographic distribution of disease one needs to adjust for variations in population density. Calculation of rates is unsuitable if the number of cases in individual geographic subareas is small, and aggregation of subareas leads to loss of geographic detail. An alternate approach is to adjust geographic boundaries so that population density is everywhere equal; then on the density-equalized map projection (DEMP), cases will be randomly distributed if disease risk is constant. Here we describe a new algorithm for producing the density-equalized map, which has significant advantages relative to earlier approaches.[2-6]

PRE-DEMP MAP PROCESSING

The DEMP requires a map file with geographic regions described as polygons, whose vertices are specified by x and y coordinates. Also required is a specification of the variable whose density is to be equalized, for example the population of each geographic region. In order to shorten computation time, unnecessary geographic detail is removed from the map by a point removal algorithm. The algorithm preserves nodes, i.e. points that cannot be removed without altering the map topology. Next, each polygon in the map is subdivided into triangles. The Delaunay triangulation is used because it is unique for a given polygon, and produces triangles that are as equi-angular as possible.[7]

DEMP ALGORITHM

Piecewise linear transformations

In the density equalizing map projection (DEMP), we require that the transformation within each Delaunay triangle be constant and linear, so that each triangle maps into another triangle. All points (x,y) within a given triangle i are mapped into points (u,v) by a linear transformation

$$\begin{pmatrix} u \\ v \\ 1 \end{pmatrix} = \begin{pmatrix} a_i & b_i & e_i \\ c_i & d_i & f_i \\ 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} x \\ y \\ 1 \end{pmatrix}$$

Suppose j,k,l (in counterclockwise order) are the vertices of triangle i. Prior to the DEMP its coordinates are (x_j,y_j), (x_k,y_k), (x_l,y_l) and its area is

$$A_i = \tfrac{1}{2} (x_j y_k - x_k y_j + x_k y_l - x_l y_k + x_l y_j - x_j y_l)$$

After the DEMP its coordinates are (u_j,v_j), (u_k,v_k), (u_l,v_l) and its area is

$$B_i(u,v) = \tfrac{1}{2} (u_j v_k - u_k v_j + u_k v_l - u_l v_k + u_l v_j - u_j v_l)$$

The DEMP is defined by specifying $a_i,b_i,\ldots f_i$ for every triangle in the map. More economically, one can specify the transformed (u,v) coordinates of every triangle vertex in the map, thus automatically guaranteeing that adjacency of triangles be preserved in the DEMP; $a_i,b_i,\ldots f_i$ are expressed as linear functions of (u,v).

The linearity of the DEMP transformation guarantees constant area magnification within each triangle and avoids spurious variation of population density in the transformed map. Such

variation, if present, could be erroneously interpreted as evidence for disease clustering. The assumed transformation is continuous over the domain of the original map. Except for regions with zero population, the inverse transformation is defined and is also continuous.

Area constraints

To equalize population density over the entire transformed map, we require that (a) transformed polygon areas be proportional to population; and (b) areas of triangles within each polygon be in the same proportion before and after the DEMP. Furthermore, we specify that (c) total map area be unchanged by the DEMP. Conditions (a), (b) and (c) together determine the *target* area B_{i0} of every triangle i in the transformed map. For population density to be correctly equalized, every triangle i in the map must satisfy a quadratic relation

$$H_i(u,v) \equiv B_i(u,v) - B_{i0} = 0$$

The imposition of separate area constraints on each triangle i and not only on the polygons prevents the occurrence of negative-area (upside-down) triangles, which would produce overlapping polygons and self-intersecting polygon boundaries.

Map distortion

The area constraint functions $H_i(u,v)=0$ are necessary but not sufficient to uniquely define the DEMP. Tobler recommends that a unique optimum solution be defined by making the DEMP as nearly conformal as possible.[8] Conformal transformations locally preserve the shape (but not necessarily the size, location, or orientation) of each infinitesimal portion of the map. We define the non-conformal distortion of triangle i as

$$G_i(u,v) = (a_i - d_i)^2 + (b_i + c_i)^2$$

where a_i, b_i, c_i and d_i are linear functions of the transformed coordinates (u,v). The overall distortion $G(u,v)$ is calculated as the sum of $G_i(u,v)$ over all triangles i, weighted by area.

In principle, three additional constraints are required to prevent overall rotation or translation of the final (u,v) coordinates. In practice these constraints have no effect.

The convergence of multiple runs from different starting points increases our confidence in the final solution, although the uniqueness and optimality of the solution cannot be proven.

POST-DEMP MAP PROCESSING

In analyzing the geographic distribution of disease, the purpose of the DEMP is to plot cases on a transformed map where population density has been equalized. In addition one may wish to transform geographic features such as the locations of environmental hazards.

The DEMP solution determines the values of transformed coordinates (u,v) which minimize overall map distortion $G(u,v)$, subject to the triangle area constraints $H_i(u,v)=0$. From these one obtains $a_i,b_i,\ldots f_i$ for each triangle i. From the pre-DEMP triangle coordinates (x,y) one determines in which triangle i the coordinates (x_m,y_m) of each case or geographic feature m are located. Then the appropriate $a_i,b_i,\ldots f_i$ are used to transform the point (x_m,y_m) into density-equalized coordinates (u_m,v_m).

PRELIMINARY RESULTS

In preliminary tests we used the NAG (Numerical Algorithms Group) Fortran library routine E04VDF, minimizing the quadratic objective function $G(u,v)$ subject to a fourth order constraint function $H(u,v) = 0$. The latter is a sum of the squares of the individual area constraints $H_i(u,v)=0$.

With E04VDF convergence is slow and the speed of computation is a serious obstacle to further progress. Maps of only 100 triangles require 30 minutes of calculation on a Sun SPARCstation 1, and processing time increases as the third power of the number of triangles. E04VDF is poorly suited to the DEMP algorithm because the sparseness of the problem is ignored. Future implementations will use more appropriate minimization techniques.[9]

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