NATIONAL RADIO ASTRONOMY OBSERVATORY

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TELEPHONE ARBOVALE 456-2011

REPORT NO. 15

CONTRACT NO. _____

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DATE Sept. 29, 1966

PROJECT: LFST

SUBJECT:

Use of Homology Program

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The following contains several notes for anyone who wants to have a telescope structure investigated for homology with our present program. Detailed descriptions of methods and results are given in Reports 4 and 13.

I. Method

The program leaves the geometry of the structure unchanged. It changes the cross sections of all members simultaneously in each iteration step in such a way, that the deviations of all surface points from a paraboloid of revolution become zero. Since it is a linearized method for a non-linear task, it needs several iteration steps. The task is finding, from all possible homology solutions, that solution which is most similar to the "first guess" as given with the input data.

The parameters defining the best-fit paraboloid of revolution are called homology paramaters; like parallel shifts, change of focal length, and change of pointing direction. The homology parameters are considered unknowns, and are solved for simultaneously with the cross section changes.

Mathematical solutions exist for any stable structure. But if a structure given has no physical solution, the iterations will converge to negative cross sections; or they might not converge at all, meaning imaginary or complex cross sections. Thus, for any structure given, the program either yields an exact solution, or it tells that this structure has none.

II. Limitations

1. The program assumes the structure to be symmetrical in x and y.

2. No surface point can be a holding point or a guiding point.

3. At present, the program handles up to about 100 members, but a change for increasing

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this number is in preparation and should be finished soon.

4. The program treats each joint as a pin-joint, and it neglects any internal sag of the members.

III. Input Data

For investigating a structure we must be given:

1. Coordinates of all structural points (joints of members), such that $x = y = z = o$ at the vertex, that $x = y = o$ and $z < o$ at the focus, and that the axis of tilt is parallel to the x-axis.

   Numbers of points starting with surface points and ending with holding points.

2. Information, which points are surface points (at least seven).

3. Information, which points are restricted in which coordinates (at least two holding points and one guiding point).

4. Additional weights on the surface points, imitating the weight of surface panels.

5. Initial cross sections of all members ("first guess"); detailed description in case of long, built-up members (drawing of geometry, cross sections of chords and struts).

6. Density and modulus of elasticity of material used. Bars can be of different material if wanted.

7. Final accuracy wanted (rms deviation from best-fit paraboloid).

IV. Results

With the values from the input data, and again after each iteration, the program prints the rms and the maximum values of: deviations from best-fit paraboloid, actual deformations from design, and changes of cross sections. It also prints the homology parameters, and the values of all cross sections. Some more values are printed for checking purpose.

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Iterations are stopped when either the accuracy wanted is reached, or in case of no convergence, or if cross sections become negative.

V.   Further Development

The following parts of the method are completely prepared mathematically, but have not yet been programmed:

1.   Sensitivity, investigating the effect of small manufacturing inaccuracies on the resulting deviations from homology.

2.   Total Weight, as defined by survival conditions and by maximum allowed deformation from winds up to, say 25 mph.   This gives a constant factor with which to multiply each cross section of the present solution.

3.   Best Solution.   A method for approaching, out of all possible homology solutions, that solution which fulfils both the survival condition and the wind deformation condition with a minimum amount of total weight.