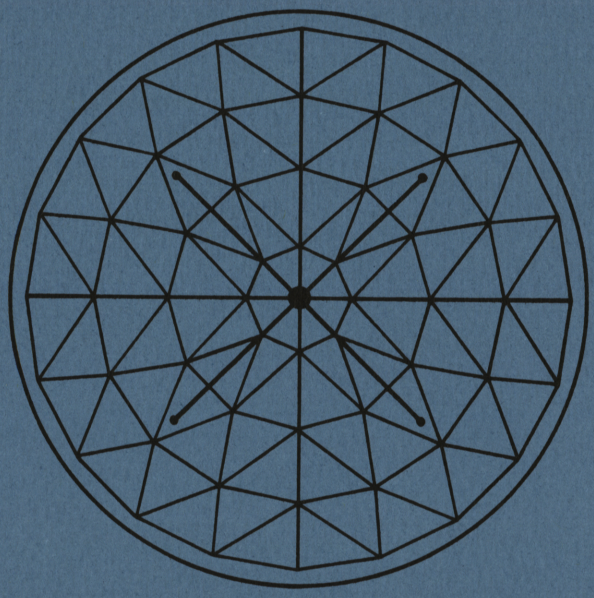

REPORT 4

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REPORT NO. 4
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PROJECT: LFSP
SUBJECT: Homology Program

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Calculating Method for Homology Solutions of Telescope Structures

The following is a mathematical method, written in such a way that it can be applied most directly for a computer program. As a first approach, it treats each joint as a pin joint, and each member as a single shape or pipe. It does not make use of symmetries, neither in the structure nor in the deformation matrix. (The use of symmetries will shorten the calculation time, but would complicate the formulae; it should be introduced while writing the program.)

I. Introduction

In general, we have three types of degrees of freedom for a homologous structure:

cross sections of members,
geometrical size and shape of the structure,
homology parameters (for example: change of focal length).

The following approach solves for cross sections and homology parameters, but considers the geometry as being given.

The conditions of homology deformation lead to algebraic equations of high order for the cross sections (the order can be as high as the number of members). A direct solution seems impossible, and the only way left is iteration: we start with a "first guess" for all cross sections, and improve them with an iterative method until homology is reached. If the changes are small, all equations then can be linearized. We thus need a fairly good first guess to start with, but I feel confident that a good first guess will be possible even in case of a complicated structure, if the structure consists only of cells for which the single-cell homology solutions already are found.

In my antenna paper I have shown that mathematical solutions must exist for every structure. But a "physical" solution is much more narrow a selection: all cross sections must be real, positive and finite. Should our program yield a solution which is not physical, we have to try another first guess, or we must change the geometrical shape.

Since the number of cross sections is larger than the number of conditions, there is

no unique solution, and the problem is not defined. We thus need some further demand for making it defined. I have choosen the following:

> from all possible homology solutions, take the one which
> is most similar to the first guess (or to the last iteration).

This has two advantages. First, all changes will be as small as possible which gives the best hope that the linearized approach converges. Second, since the first guess will be a physical structure, we have the best hope that also the result will be a physical solution.

The solution thus obtained will, hopefully, be a physical solution, but not neccessarily the best one. The best solution we might define as the one (from all physical solutions) which meets as well the rigidity condition (wind deflections during observation) as the strength condition (survival) with a minimum total mass. But this is a minimum problem and cannot be solved with a linear approach. The linear approach can only yield a gradient, meaning the direction in which to go to the best solution; but it cannot tell how far to go, which ought to be found by a second-order method. Whether this can be done in a rigorous way, or just by a few trials, will depend on calculating times.

II. Miscellaneous

A few things, partly needed for preparing the main sections, partly looking more like appendices, are somewhat heterogeneously grouped together in the present section.

1. Some numbers and their relations

Call:

p = number of structural points (pin-joints)
N = " " surface points to be kept homologous
m = " " members in the structure
m_ν = " " members meeting at point P_ν
c = " " homology conditions + 1 (for keeping weight constant)
h = " " homology parameters
f = " " free parameters for cross sections

Then:

PROJECT: LFSP
SUBJECT: Homology Program

$$3\,(p-2) \leq m \leq p\,(p-1)/2 \qquad (1)$$

$$3 \leq m_\nu \leq p-1 \qquad (2)$$

$$6 - \frac{12}{p} \leq \overline{m_\nu} \leq p-1 \qquad (3)$$

$$c = 2N + 1 \qquad (4)$$

$$f = m + h - c \qquad (5)$$

2. Input data

The program should be given, as input data:

1. The x,y,z coordinates of all p points (telescope looking in negative z-direction, no deformations), in the following order:

   First, the N surface points
   Second, all p-N-3 intermediate points
   Third, three holding points (two bearings, one drive).

2. The number N of surface points, and the instruction which of the coordinates are fixed at the holding points.

3. A first guess for the cross sections of all members, in form of a matrix of size p by p. A zero in this matrix means "No member" between the two points.

4. Material constants:

   ρ = density

   E = modulus of elasticity

   S_o = maximum allowed stress

5. Surface loads (in kg per surface point):

   w_o = simulation of an antenna surface (including panels, etc.)
   w_s = survival load (storm, snow, ice)
   w_w = maximum wind load during observation (for, say, 25 mph)

6. Shortest wavelength, λ, for observation

7. Accuracy, ΔH_o, wanted for "end of iteration".

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PROJECT: LFSP
SUBJECT: Homology Program

3. Outline of over-all program

1. Take coordinates, calculate lengths and projected lengths of all members. Set up matrices described in section "derivatives".

2. Take first guess of cross sections, set up deformation matrix A and force vectors F; calculate inverse, A^{-1}, calculate all deformations.

3. Find deviations from homology, using "best-fitting" homology parameters.

4. Keep weight W constant, find nearest homology solution with iterative method, until accuracy wanted is reached. Check for negative cross sections and for non-convergence (indicate failures).

5. Apply survival 1 oad, calculate total weight W_s as defined by survival. Find shortest wavelength λ_s for structure defined by survival.

   Apply maximum observational wind load, calculate total weight W_w as defined by wind deflections.

   Regard $\max(W_s, W_w)$ as final weight, give all cross sections.

6. Calculate sensitivity S of structure (deviations from homology due to small inaccuracies of cross sections).

7. Calculate direction in which to go to "best" solution. (= gradient)

Up to here, all is completely computerized. From here on, it might be done manually or computerized, depending on the calculation times required.

8. If $W_w > W_s$, change all cross sections in direction of gradient, repeat 2. to 7. until minimum weight is approached closely enough.

9. If $W_s > W_w$, find number of member with highest stress; increase this cross section only, for a new first guess. Repeat, until as many members as possible are close to highest stress.

10. The whole procedure might be repeated with various geometrical shapes.

4. Inverse of a matrix after small changes are added

Suppose we have a matrix A and its inverse A^{-1}. We add to A a matrix, a, whose elements are small as compared to those of A :

$$B = A + a . \tag{6}$$

We want a good approximation for the inverse, B^{-1}, written in the following form:

$$B^{-1} = A^{-1} + b. \tag{7}$$

We multiply (7) from the right side by (6) and obtain, with E = unit matrix,

$$E = (A^{-1} + b)(A + a) = E + bA + A^{-1}a + ba .$$

For a linear approximation, we neglect ba and have $bA = -A^{-1}a$. We multiply from the right side by A^{-1}, and finally obtain the wanted correction, b, in terms of quantities already known:

$$b = - A^{-1}a\, A^{-1} \tag{8}$$

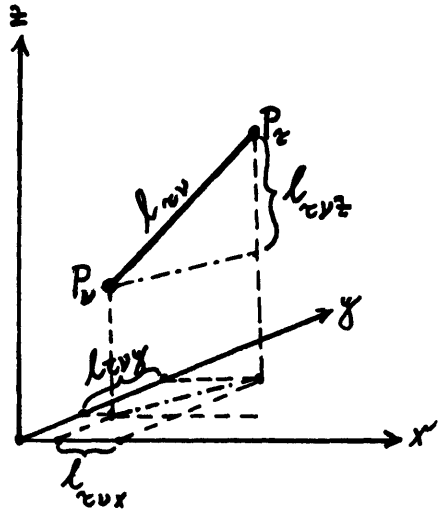
or, in index notation:

$$b_{ij} = - \sum_k \sum_l A^{-1}_{ik}\, a_{kl}\, A^{-1}_{lj} \tag{9}$$

III. Deformation Matrix

1. Equilibrium of forces

We consider the member connecting points P_ν and P_τ. From the input data, we calculate its length, $l_{\tau\nu}$, and the projection of this length on the coordinate axes, $l_{\tau\nu x}$, $l_{\tau\nu y}$ and $l_{\tau\nu z}$. If the x-coordinate of point P_τ is deformed by amount Δx_τ, and so on, the resulting elongation of member $\tau\nu$ is given by



$$\Delta l_{\tau\nu} = \frac{l_{\tau\nu x}}{l_{\tau\nu}} (\Delta x_\tau - \Delta x_\nu) + \frac{l_{\tau\nu y}}{l_{\tau\nu}} (\Delta y_\tau - \Delta y_\nu) + \frac{l_{\tau\nu z}}{l_{\tau\nu}} (\Delta z_\tau - \Delta z_\nu). \tag{10}$$

Letting $\alpha = x, y, z$ (and later also $\beta = x, y, z$) we rewrite (10) as

PROJECT: LFSP
SUBJECT: Homology Program

$$\Delta l_{\tau\nu} = \sum_{\alpha=x}^{z} \frac{l_{\tau\nu\alpha}}{l_{\tau\nu}} (\Delta\alpha_\tau - \Delta\alpha_\nu) \ . \qquad (11)$$

Calling $Q_{\tau\nu}$ the cross section of member $\tau\nu$, and E the modulus of elasticity, the force along member $\tau\nu$ is (positive for tension, negative for compression)

$$F_{\tau\nu} = \frac{\Delta l_{\tau\nu}}{l_{\tau\nu}} E\, Q_{\tau\nu} \ , \qquad (12)$$

and its projection on axis α is

$$F_{\tau\nu\alpha} = E\, Q_{\tau\nu} \frac{l_{\tau\nu\alpha}}{l_{\tau\nu}^3} \sum_{\beta=x}^{z} l_{\tau\nu\beta} (\Delta\beta_\tau - \Delta\beta_\nu) \ . \qquad (13)$$

This is the α-component of the force acting on point P_τ, resulting from the deformation of member $\tau\nu$.

In addition to the "deformation forces" (13), we have, if gravitation has direction α, the "weight forces" on all points P_τ resulting from the weight of all members joining in P_τ; and, on surface points only, the "load forces" resulting from the loads applied to surface points, for various cases which we indicate by index Ω:

Ω	direction g of gravity	surface load	case
1	z	w_o	observing zenith
2	x	w_o	observing horizon
3	z	w_w	max. wind for obs.
4	z	$w_o + w_s$	survival condition

(14)

where the loads are defined in section "Input data". To be on the safe side and for simplicity, we have applied the survival force in the same direction as gravity. These additional forces, acting in α-direction on point τ in case Ω, then can be written as (divided by E in order to rid (13) from this constant factor):

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PROJECT: LFSP
SUBJECT: Homology Program

$$F^{\Omega}_{\tau\alpha} = \delta_{\alpha g}\frac{1}{E}\left\{(1-\delta_{\Omega 3})\left[\frac{\rho}{2}\sum_{\nu=1}^{p} Q_{\tau\nu}\, l_{\tau\nu} + \vartheta_{\tau N}(w_o + \delta_{\Omega 3} w_w + \delta_{\Omega 4} w_s)\right]\right\} \qquad (15)$$

where

$$\delta_{ij} = \begin{cases} 1 & \text{for } i=j \\ 0 & \text{for } i\neq j \end{cases} \quad \text{and} \quad \vartheta_{ij} = \begin{cases} 1 & \text{for } i\leq j \\ 0 & \text{for } i>j \end{cases} . \qquad (16)$$

In order to have equilibrium at point τ in direction α for case Ω, we must add (13) for all members $\tau\nu$ coming to point τ from various points ν, and let this sum be equal to the additional forces (15):

$$\sum_{\nu=1}^{p} Q_{\tau\nu}\frac{l_{\tau\nu\alpha}}{l^3_{\tau\nu}}\sum_{\beta=x}^{z} l_{\tau\nu\beta}(\Delta\beta^{\Omega}_{\tau} - \Delta\beta^{\Omega}_{\nu}) = F^{\Omega}_{\tau\alpha} \qquad \begin{array}{l}\tau=1 \ldots p-3\\ \alpha=x,y,z\\ \Omega=1 \ldots 4\end{array} \qquad (17)$$

For simplicity, we have assumed that the three holding points are fixed in all three directions, thus $\tau = 1 \ldots p-3$.

2. Rearrangement

Formula (17) is arranged in order of the cross sections. We rearrange it in order of the deformations: (keeping in mind that the last three points do not deform)

$$\sum_{\beta=x}^{z}\left\{\Delta\beta^{\Omega}_{\tau}\sum_{\varphi=1}^{p}\frac{l_{\tau\varphi\alpha}}{l^3_{\tau\varphi}}Q_{\tau\varphi} - \sum_{\substack{\nu=1\\ \nu\neq\tau}}^{p-3}\Delta\beta^{\Omega}_{\nu}\frac{l_{\tau\nu\alpha}\, l_{\tau\nu\beta}}{l^3_{\tau\nu}}Q_{\tau\nu}\right\} = F^{\Omega}_{\tau\alpha} \qquad (18)$$

which can be written as

$$\sum_{\beta=x}^{z}\sum_{\nu=1}^{p-3} A_{\tau\alpha,\nu\beta}\,\Delta\beta^{\Omega}_{\nu} = F^{\Omega}_{\tau\alpha} \qquad \begin{array}{l}\tau = 1 \ldots p-3\\ \alpha = x,y,z\\ \Omega = 1 \ldots 4\end{array} \qquad (19)$$

We call A the "deformation matrix" and F^{Ω} the "force vectors". Matrix A is of box-type: it is divided into $(p-3)^2$ boxes of size 3 by 3 . It has two types of symmetry: each box is symmetrical in itself (exchange of α and β), and matrix A is symmetrical with respect to the boxes (exchange of τ and ν). If points τ and ν are not connected by a member, both boxes $\tau\nu$ and $\nu\tau$ contain 9 zeros each. Matrix A

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TELEPHONE ARBOVALE 456-2011

PROJECT: LFSP
SUBJECT: Homology Program

looks as shown below:

		ν	1			2			3			.....	p-3		
τ	α	β	x	y	z	x	y	z	x	y	z	.....	x	y	z
	x		s	s	s	0	0	0	-	-	-		-	-	-
1	y		s	s	s	0	0	0	-	-	-		-	-	-
	z		s	s	s	0	0	0	-	-	-		-	-	-
	x		0	0	0	s	s	s	-	-	-		0	0	0
2	y		0	0	0	s	s	s	-	-	-		0	0	0
	z		0	0	0	s	s	s	-	-	-		0	0	0
	x		-	-	-	-	-	-	s	s	s		-	-	-
3	y		-	-	-	-	-	-	s	s	s		-	-	-
	z		-	-	-	-	-	-	s	s	s		-	-	-
	⋮														
	x		-	-	-	0	0	0	-	-	-		s	s	s
p-3	y		-	-	-	0	0	0	-	-	-		s	s	s
	z		-	-	-	0	0	0	-	-	-		s	s	s

$= A_{\tau\alpha,\nu\beta}$

where, as an example, we have assumed that point P_1 is connected with points P_3 and P_{p-3}, but not with point P_2; P_3 is connected with all points shown; and P_{p-3} is connected with all points except P_2. The marks "s" and "-" mean:

$$\text{s)} \quad A_{\tau\alpha,\tau\beta} = \sum_{\substack{\varphi=1 \\ \varphi\neq\tau}}^{p} \frac{l_{\tau\varphi\alpha}\, l_{\tau\varphi\beta}}{l^3_{\tau\varphi}}\, Q_{\tau\varphi} \qquad (20)$$

$$\text{-)} \quad A_{\tau\alpha,\nu\beta} = -\frac{l_{\tau\nu\alpha}\, l_{\tau\nu\beta}}{l^3_{\tau\nu}}\, Q_{\tau\nu} \quad \text{for} \quad \tau\neq\nu \qquad (21)$$

The sum in (20) actually has only so many terms as members join in point P_τ. With $Q_{ii} = 0$ we summarize:

$$A_{\tau\alpha,\nu\beta} = \delta_{\tau\nu} \sum_{\varphi=1}^{p} \frac{l_{\tau\varphi\alpha}\, l_{\tau\varphi\beta}}{l^3_{\tau\varphi}}\, Q_{\tau\varphi} - \frac{l_{\tau\nu\alpha}\, l_{\tau\nu\beta}}{l^3_{\tau\nu}}\, Q_{\tau\nu} \qquad \begin{vmatrix} \tau=1 \ \ldots \ p-3 \\ \nu=1 \ \ldots \ p-3 \\ \alpha=x,y,z \\ \beta=x,y,z \end{vmatrix} \quad (22)$$

PROJECT: LFSP
SUBJECT: Homology Program

3. Derivatives

Matrix A, as well as the force vectors F, are both linear in the cross sections; this means their derivatives, with respect to the Q's, do not depend on the Q's, they are constant for a given geometrical shape. We thus should start our program, for a given shape, by first building up the derivatives of A and F. Those of A are:

$$a_{\tau\alpha,\tau\beta,\pi\varphi} = \frac{\partial A_{\tau\alpha,\tau\beta}}{\partial Q_{\pi\varphi}} = \delta_{\tau\pi} L_{\tau\alpha,\varphi\beta} \qquad (22)$$

$$a_{\substack{\tau\alpha,\nu\beta,\pi\varphi \\ \tau\neq\nu}} = \frac{\partial A_{\tau\alpha,\nu\beta}}{\partial Q_{\pi\varphi}} = -\delta_{\tau\pi}\delta_{\nu\varphi} L_{\tau\alpha,\varphi\beta} \qquad (23)$$

$\tau = 1 \ldots p-3$
$\nu = 1 \ldots p-3$
$\pi = 1 \ldots p-3$
$\varphi = 1 \ldots p$
$\alpha = x,y,z$
$\beta = x,y,z$ (24)

with

$$L_{\tau\alpha,\varphi\beta} = \frac{l_{\tau\nu\alpha}\, l_{\tau\nu\beta}}{l^3_{\tau\nu}}$$

which, if wanted, can be summarized into

$$a_{\tau\alpha,\nu\beta,\pi\varphi} = \delta_{\tau\pi}\left\{\delta_{\tau\nu} - (1-\delta_{\tau\nu})\delta_{\nu\varphi}\right\} L_{\tau\alpha,\varphi\beta} \,. \qquad (25)$$

The derivatives of the F^{Ω} are, from (15):

$$f^{\Omega}_{\tau\alpha,\pi\varphi} = \frac{\partial F^{\Omega}_{\tau\alpha}}{\partial Q_{\pi\varphi}} = \delta_{\alpha g}\,\delta_{\tau\pi}\,\frac{\varrho}{2E}\, l_{\tau\varphi} \qquad (26)$$

but for the F^{Ω}, we have in addition to the Q-dependent terms also a constant term, which we call

$$f^{\Omega}_{\tau\alpha,o} = \delta_{\alpha g}\,\vartheta_{\tau N}\,\frac{1}{E}\,(w_o + \delta_{\Omega 3} w_w + \delta_{\Omega 4} w_s) \qquad (27)$$

with $g = g(\Omega)$ from (14), and ϑ as defined in (16).

Actually, we do not have to store these derivatives; we store only matrix L and matrix l. L is of same size and symmetry as matrix A, and l is symmetrical and of size p by p. The derivatives, whenever needed, are formed from (25) and (26).

PROJECT: LFSP
SUBJECT: Homology program

For better convenience, we now change our index notation, combining two in one:

$$\left.\begin{matrix}\tau\\ \alpha\end{matrix}\right\}\longrightarrow i \qquad \left.\begin{matrix}\nu\\ \beta\end{matrix}\right\}\longrightarrow j \qquad \left.\begin{matrix}\pi\\ \varphi\end{matrix}\right\}\longrightarrow \gamma \qquad \left|\begin{matrix} i = 1 \dots d \\ j = 1 \dots d \\ \gamma = 1 \dots m \end{matrix}\right. \tag{28}$$

with

$$d = 3(p-3). \tag{29}$$

The notation of the various quantities, then, changes as

$$\begin{matrix} A_{\tau\alpha,\nu\beta} \longrightarrow A_{ij} & a_{\tau\alpha,\nu\beta,\pi\varphi} \longrightarrow a_{ij,\gamma} & Q_{\pi\varphi} \longrightarrow Q_{\gamma} \\ F^{\Omega}_{\tau\alpha} \longrightarrow F^{\Omega}_{i} & f^{\Omega}_{\tau\alpha,\pi\varphi} \longrightarrow f^{\Omega}_{i,\gamma} & f^{\Omega}_{\tau\alpha,o} \longrightarrow f^{\Omega}_{i,o} \end{matrix} \tag{30}$$

Written in this notation, matrix A is built up from the derivatives as

$$A_{ij} = \sum_{\gamma=1}^{m} a_{ij,\gamma}\, Q_{\gamma} \qquad \left|\begin{matrix} i = 1 \dots d \\ j = 1 \dots d \end{matrix}\right. \tag{31}$$

and the force vectors are built up as

$$F^{\Omega}_{i} = f^{\Omega}_{i,o} + \sum_{\gamma=1}^{m} f^{\Omega}_{i,\gamma}\, Q_{\gamma} \qquad \left|\begin{matrix} i = 1 \dots d \\ \Omega = 1 \dots 4 \end{matrix}\right. \tag{32}$$

4. The deformations

Applying the change of notations also to the deformations, by combining

$$\left.\begin{matrix}\Delta x^{\Omega}_{\nu}\\ \Delta y^{\Omega}_{\nu}\\ \Delta z^{\Omega}_{\nu}\end{matrix}\right\}\longrightarrow \Delta\beta^{\Omega}_{j} \qquad \left|\begin{matrix} j = 1 \dots d \end{matrix}\right. \tag{33}$$

we write (19) as

$$\sum_{j=1}^{d} A_{ij}\, \Delta\beta^{\Omega}_{j} = F^{\Omega}_{i} \qquad \left|\begin{matrix} i = 1 \dots d \\ \Omega = 1 \dots 4 \end{matrix}\right. \tag{34}$$

PROJECT: LFSP
SUBJECT: Homology Program

Finally, we caculate the inverse matrix of A and call it A^{-1}, and obtain the deformations as

$$\Delta\beta_j^\Omega = \sum_{i=1}^{d} A_{ji}^{-1} F_i^\Omega \qquad \left| \begin{array}{l} j = 1 \ldots d \\ \Omega = 1 \ldots 4 \end{array} \right. \qquad (35)$$

IV. Small Changes of the Cross Sections

Suppose we have already calculated A, A^{-1} and all $\Delta\beta$ for a given set of Q's. Now, we change each Q_γ by a small amount into $Q_\gamma + dQ_\gamma$, and we want to know the resulting changes $d\Delta\beta$ of the $\Delta\beta$'s. We ask only for a linear approximation. Instead of (34) we have now

$$\sum_{j=1}^{d} \left\{ A_{ij} + \sum_{\gamma=1}^{m} a_{ij,\gamma}\, dQ_\gamma \right\} \left\{ \Delta\beta_i^\Omega + d\Delta\beta_i^\Omega \right\} = F_i^\Omega + \sum_{\gamma=1}^{m} f_{i,\gamma}^\Omega\, dQ_\gamma \qquad \left| \begin{array}{l} i = 1 \,..\, d \\ \Omega = 1 \,..\, 4 \end{array} \right. \qquad (36)$$

and instead of (35) we get, with help of approximation (9)

$$\Delta\beta_j^\Omega + d\Delta\beta_j^\Omega = \sum_{i=1}^{d} \left\{ A_{ji}^{-1} - \sum_{k=1}^{d} \sum_{l=1}^{d} \sum_{\gamma=1}^{m} A_{jk}^{-1} a_{kl,\gamma}\, dQ_\gamma\, A_{li}^{-1} \right\} \left\{ F_i^\Omega + \sum_{\gamma=1}^{m} f_{i,\gamma}^\Omega\, dQ_\gamma \right\} \qquad (37)$$

and, neglecting second-order terms,

$$\Delta\beta_j^\Omega + d\Delta\beta_j^\Omega = \sum_{i=1}^{d} A_{ji}^{-1} F_i^\Omega + \sum_{i=1}^{d} \sum_{\gamma=1}^{m} A_{ji}^{-1} f_{i,\gamma}^\Omega\, dQ_\gamma - \sum_{i=1}^{d} \sum_{k=1}^{d} \sum_{l=1}^{d} \sum_{\gamma=1}^{m} A_{jk}^{-1} a_{kl,\gamma}\, dQ_\gamma A_{li}^{-1} F_i^\Omega \qquad (38)$$

We use (35) for the first and the last term on the right side, we exchange k and i in the last term, and we call

$$B_{j\gamma}^\Omega = \sum_{i=1}^{d} A_{ji}^{-1} \left\{ f_{i,\gamma}^\Omega - \sum_{l=1}^{d} a_{il,\gamma}\, \Delta\beta_l^\Omega \right\} \qquad \left| \begin{array}{l} j = 1 \,..\, d \\ \gamma = 1 \,..\, m \\ \Omega = 1 \,..\, 4 \end{array} \right. \qquad (39)$$

The changes $d\Delta\beta$ of the deformations $\Delta\beta$, as caused by the changes dQ, then are given by

$$d\Delta\beta_j^\Omega = \sum_{\gamma=1}^{m} B_{j\gamma}^\Omega\, dQ_\gamma \,. \qquad \left| \begin{array}{l} j = 1 \,..\, d \\ \Omega = 1 \,..\, 4 \end{array} \right. \qquad (40)$$

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TELEPHONE ARBOVALE 456-2011

PROJECT: LFSP
SUBJECT: Homology Program

V. Homology

1. Homology conditions

The equation for an undeformed paraboloid of focal length f, looking in negative z-direction, is

$$z = -\frac{x^2 + y^2}{4f} . \tag{41}$$

If gravity has z-direction (telescope looking at zenith, $\Omega=1$, g=z), we allow two homologous changes:

1. Parallel translation down, amount dz; call $dz = h_1$ (42)
2. Increase of focal length, amount df; call $2df = h_2$ (43)

If gravity has x-direction (telescope looking at horizon, $\Omega=2$, g=x), we allow again two homologous changes:

3. Parallel translation down, same amount $dx = dz = h_1$
4. Rotation around y-axis, angle $d\varphi$, call $2f d\varphi = h_3$. (44)

We call

$$h_1, \quad h_2, \quad h_3 = \text{homology parameters.}$$

Let a surface point P_ν, under the forces of case Ω, deform its coordinate x_ν by Δx_ν^Ω, and similar to the other two coordinates. We demand that the deformed point then is situated (somewhere) on a paraboloid defined by the three homology parameters. In case of only small deformations, one can show that the deformations of point P_ν must fulfill the following condition:

$$\frac{x_\nu}{2f}\Delta x_\nu^\Omega + \frac{y_\nu}{2f}\Delta y_\nu^\Omega + \Delta z_\nu^\Omega = \begin{cases} h_1 - \dfrac{z_\nu}{2f} h_2 & \text{for } \Omega = 1 \\ \dfrac{x_\nu}{2f} h_1 + \dfrac{x_\nu}{2f}\left(1 - \dfrac{z_\nu}{2f}\right) h_3 & \text{for } \Omega = 2 \end{cases} \tag{45}$$

or, written in general terms:

$$\sum_{\beta=x}^{z} c_{\beta\nu}\,\Delta\beta_\nu^\Omega = \sum_{k=1}^{3} g_{\nu k}^\Omega\, h_k \,, \qquad \begin{array}{l} \nu = 1 \ldots N \\ \Omega = 1, 2. \end{array} \tag{46}$$

PROJECT: LFSP
SUBJECT: Homology Program

where the coefficients have the following values:

	$\beta=x$	$\beta=y$	$\beta=z$
$c_{\beta\nu}$ =	$\frac{x_\nu}{2f}$	$\frac{y_\nu}{2f}$	1

$\nu = 1 \ldots N$ (47)

and

	$k=1$	$k=2$	$k=3$	
$g^{\Omega}_{\nu k}$ =	1	$-\frac{z_\nu}{2f}$	0	$\Omega=1$
	$\frac{x_\nu}{2f}$	0	$\frac{x_\nu}{2f}(1-\frac{z_\nu}{2f})$	$\Omega=2$

$\nu = 1 \ldots N$ (48)

From the left side of (46) we define a vector, b,

$$b^{\Omega}_{\nu} = \sum_{\beta=x}^{z} c_{\beta\nu}\, \Delta\beta^{\Omega}_{\nu} \,. \qquad \begin{matrix}\nu = 1 \ldots N \\ \Omega = 1, 2.\end{matrix} \qquad (49)$$

We change again the index notation, and let

$$b^{\Omega}_{\nu} \longrightarrow b_i \quad \text{and} \quad g^{\Omega}_{\nu k} \longrightarrow g_{ik}\,. \qquad \begin{matrix}i = 1 \ldots 2N \\ k = 1 \ldots 3\end{matrix} \qquad (50)$$

The conditions of homology, (46), then, can be written finally as

$$\sum_{k=1}^{3} g_{ik}\, h_k = b_i \,. \qquad i = 1 \ldots 2N \qquad (51)$$

2. Deviations from homology

Equations (51) will not be fulfilled as long as homology is not reached, and we need a measure for the deviations. From (51) we can derive the best-fitting values of the homology parameters, h_k, by a least-squares method. We define the transposed, $g^{T}_{li} = g_{il}$, and call

PROJECT: LFSP
SUBJECT: Homology Program

$$K_{lk} = \sum_{i=1}^{2N} g_{li}^{T} g_{ik} \qquad (52)$$

$$I_l = \sum_{i=1}^{2N} g_{li}^{T} b_i \qquad (53)$$

$l = 1 \ldots 3$, $k = 1 \ldots 3$

Matrices g and g^T are rectangular, but K is a square matrix (symmetric and positive definite) of size 3 by 3. We calculate the inverse of K, K^{-1}, call h^* the best-fitting values of the homology parameters, and obtain

$$h_k^* = \sum_{l=1}^{3} K_{kl}^{-1} I_l \,. \qquad (54)$$

$k = 1 \ldots 3$

These best-fitting values we insert into (51); we square and add the residuals, and as the measure of deviation, which we call ΔH, we define the rms residual of (51):

$$\Delta H = \left\{ \frac{1}{2N} \sum_{i=1}^{2N} \left(b_i - \sum_{k=1}^{3} g_{ik} h_k^* \right)^2 \right\}^{1/2} . \qquad (55)$$

This deviation ΔH has the dimension of a length. We calculate ΔH after each step of the iteration, and the structure is satisfactory as soon as $\Delta H \leq \lambda/16$, where λ is the shortest wavelength from the input data. But for a more theoretical interest, we might have decided to iterate to a higher accuracy, and for this case we have given ΔH_o, the accuracy wanted, in the input data. This means we iterate until

$$\Delta H \leq \Delta H_o \,. \qquad (56)$$

3. Corrections dQ needed for homology

As long as homology is not reached, equations (46) are not fulfilled. In order to fulfill (46), we would need changes $d\Delta\beta$ for the deformations $\Delta\beta$, and (46) then reads

$$\sum_{\beta=x}^{z} c_{\beta\nu} \left(\Delta\beta_\nu^\Omega + d\Delta\beta_\nu^\Omega \right) = \sum_{k=1}^{3} g_{\nu k}^{\Omega} h_k \,. \qquad (57)$$

$\nu = 1 \ldots N$, $\Omega = 1, 2.$

We use (40), but change the notation

$$B_{j\gamma}^{\Omega} \longrightarrow B_{\nu\beta,\gamma}^{\Omega} \qquad (58)$$

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TELEPHONE ARBOVALE 456-2011

PROJECT: LFSP
SUBJECT: Homology Program

We call

$$C^{\Omega}_{\nu\gamma} = \sum_{\beta=x}^{z} c_{\beta\nu}\, B^{\Omega}_{\nu\beta,\gamma} \qquad \left| \begin{array}{l} \nu = 1 \ldots N \\ \gamma = 1 \ldots m \\ \Omega = 1,\ 2. \end{array} \right. \qquad (59)$$

with B defined in (39) and c in (48). We change notation:

$$C^{\Omega}_{\nu\gamma} \longrightarrow C_{i\gamma} \,. \qquad \left| \; i = 1 \ldots 2N \right.$$

We use (49) with notation (50), and (57) then takes the following form

$$\sum_{\gamma=1}^{m} C_{i\gamma}\, dQ_{\gamma} - \sum_{k=1}^{3} g_{ik}\, h_k = -\, b_i \,, \qquad \left| \; i = 1 \ldots 2N \right. \qquad (60)$$

Equations (60) we call "homology equations". The right sides of (60) are known; and the left sides contain the changes of all cross sections, dQ, needed for obtaining homologous deformations; the type of deformation is described by the three homology parameters, h_k, which also are contained in the left sides of (60).

In the introduction, we have given reasons for going to a special homology solution (the nearest one), which means that also the three homology parameters, h_k, are unknowns, yielding a total of m+3 unknowns.

Since the total weight does not matter for homology, but still must be defined somehow, we keep it constant, by adding one more equation to system (60):

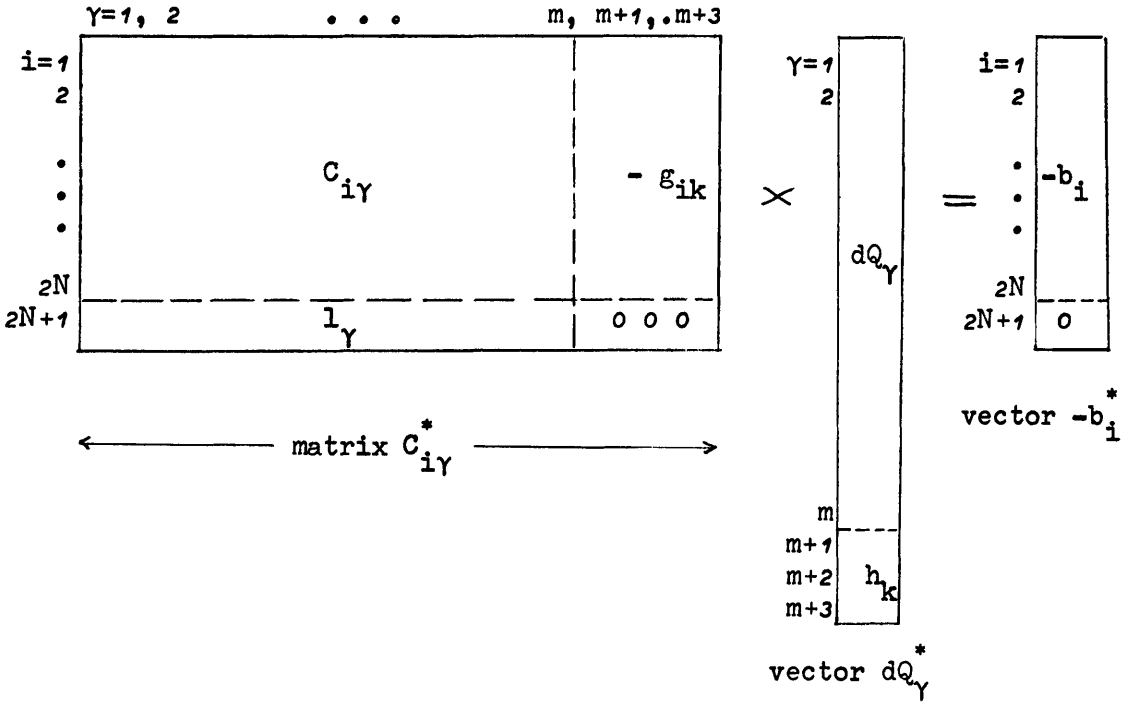
$$\sum_{\gamma=1}^{m} l_{\gamma}\, dQ_{\gamma} = 0 \,. \qquad (61)$$

We thus have 2N+1 equations and m+3 unknowns, and we call

$$c = 2N+1 \qquad \text{and} \qquad n = m+3 \,. \qquad (62)$$

PROJECT: LFSP
SUBJECT: Homology Program

Next, we want a unified way of writing the equations (60) and (61), and of dealing with the unknowns. The system of equations looks as follows:



(63)

As shown above, we define a matrix $C^*_{i\gamma}$, including the g_{ik} and equation (61). We define the vector of unknowns, dQ^*_γ, which includes the homology parameters as

$$dQ^*_{m+k} = h_k \,; \qquad k = 1 \cdots 3 \tag{64}$$

and vector b^*_i is the same as b_i except for an additional zero in the last place. Altogether, the system of homolgy equations then reads

$$\sum_{\gamma=1}^{n} C^*_{i\gamma}\, dQ^*_\gamma = -\, b^*_i \,. \qquad i = 1 \ldots c \tag{65}$$

System (65) has c equations and n unknowns, with $c < n$, and we call

$$\Phi = n-c = m+2-2N = \text{number of free parameters.} \tag{66}$$

PROJECT: LFSP
SUBJECT: Homology Program

VI. The "Nearest" Solution

From the family of all homology solutions, as given by (65) for various choices of the free parameters, we now want to select that solution which requires the smallest possible changes dQ of all cross sections (small as compared to the present values of Q). We thus define a quantity L as the "distance" we have to go to one of the homology solutions, and we require L to be minimum:

$$L = \sum_{\gamma=1}^{m} \left\{\frac{dQ_\gamma}{Q_\gamma}\right\}^2 = \text{Min.} \qquad (67)$$

Equation (67) is required as long as we do not care about the values of the resulting homology parameters $h_1 \cdots h_4$. But actually, it might sometimes be desirable to find structures where $h_1 \cdots h_4$ have only very small values. This means we should include these parameters in the minimum condition (67).

The homology parameters should be given a treatment comparable to that given for the cross section changes. First, we divide $h_1 \cdots h_4$ by twice the focal length f for normalization, just as the dQ are divided by Q in (67). Second, we introduce a weight factor ω (the same for all four parameters), to be given with the input data, which tells how important small homology parameters are; for $\omega = 1$, for example, a 1% change of the focal length is valued the same as a 1% change of a cross section, while $\omega \gg 1$ would try to keep the focal length much more constant, whereas $\omega \ll 1$ makes the change of focal length unimportant. In order to include $h_1 \cdots h_4$ in (67), we use again (64) for the dQ*, and in a similar way we define

$$Q^*_{m+k} = 2f/\omega = \text{const.} \;\Big|\; k = 1 \cdots 4. \qquad (68)$$

Using these definitions, we write instead of (67)

PROJECT: LFSP
SUBJECT: Homology Program

$$L = \sum_{\gamma=1}^{n} \left(\frac{dQ^*_\gamma}{Q^*_\gamma} \right)^2 = \text{Min.} \qquad (69)$$

The task to be solved is a "minimum condition, (69), with a set of constraint equations, (65)". The proper way of solving this task is known as the method of Lagrangean multipliers: in a general case, we have, for n parameters p_j:

1 minimum condition: $L(p_1 \cdots p_n) = \text{Min.}$

c constraint equations: $\varphi_i(p_1 \cdots p_n) = 0 \quad | i = 1 \cdots c.$

We multiply each constraint equation by a multiplier λ_i, add up, and demand

$$L + \sum_{i=1}^{c} \lambda_i \varphi_i = \text{Min.} \qquad (70)$$

Letting all derivatives of (70) with respect to the p_j equal zero, we obtain n equations; together with the c constraints, we then have n + c equations for the n + c unknowns (n values for $p_1 \cdots p_n$, and c values for $\lambda_1 \cdots \lambda_c$).

In our case, the φ_i are represented by the homology equations (65); for L we use (69), dividing by 2 for convenience, and we obtain for (70):

$$\frac{1}{2} \sum_{\gamma=1}^{n} \left(\frac{dQ_\gamma^*}{Q_\gamma^*} \right)^2 + \sum_{i=1}^{c} \lambda_i \left\{ b_i + \sum_{\gamma=1}^{n} C_{i\gamma}^* \, dQ_\gamma^* \right\} = \text{Min.} \qquad (71)$$

We let the derivatives of (71) with respect to all dQ_γ^* equal zero

$$\frac{dQ_\gamma^*}{Q_\gamma^{*2}} + \sum_{i=1}^{c} \lambda_i C_{i\gamma}^* = 0 \quad | \gamma = 1 \cdots n. \qquad (72)$$

Systems (72) and (65) together give n + c equations for the n + c unknowns dQ_γ^* and λ_i. The matrix of the combined system is of size n + c, but because of its

symmetry and incompleteness we do not have to invert the whole matrix. Instead of, we express the dQ_γ^* in terms of the λ from equations (72) as

$$dQ_\gamma^* = - Q_\gamma^{*2} \sum_{j=1}^{c} \lambda_j C_{j\gamma}^* \quad \Big| \quad \gamma = 1 \cdots n, \tag{73}$$

and insert into equations (65):

$$\sum_{\gamma=1}^{n} C_{i\gamma}^* Q_\gamma^{*2} \sum_{j=1}^{c} \lambda_j C_{j\gamma}^* = b_i^* \quad \Big| \quad i = 1 \cdots c. \tag{74}$$

We define a matrix T as a "weighted transposed" of C*

$$T_{\gamma j} = Q_\gamma^{*2} C_{j\gamma}^* \tag{75}$$

and build the product

$$D_{ij} = \sum_{\gamma=1}^{n} C_{i\gamma}^* T_{\gamma j} \quad \Big| \quad \begin{matrix} i = 1 \cdots c, \\ j = 1 \cdots c. \end{matrix} \tag{76}$$

Whereas both matrices C^* and T are rectangular, matrix D is square. We call D^{-1} the inverse of D and have, from equations (74) and (76), for the Lagrangean multipliers λ_j to be inserted into equations (73):

$$\lambda_j = \sum_{i=1}^{c} D_{ji}^{-1} b_i^* . \quad \Big| \quad j = 1 \ldots c \tag{77}$$

We now define a matrix G as

$$G = T (C^* T)^{-1}$$

or

$$G_{\gamma i} = \sum_{j=1}^{c} T_{\gamma j} D_{ji}^{-1} . \quad \Big| \quad \begin{matrix} \gamma = 1 \ldots n \\ i = 1 \ldots c \end{matrix} \tag{78}$$

NATIONAL RADIO ASTRONOMY OBSERVATORY
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TELEPHONE ARBOVALE 456-2011

PROJECT:

SUBJECT:

Equations (73), with help of equations (78) and (77), then finally read

$$dQ_\gamma^* = - \sum_{i=1}^{c} G_{\gamma i}\, b_i^* , \qquad \gamma = 1 \ldots n \qquad (79)$$

where the b_i^* are defined by (63) and (49).

With equations (79), all unknowns now are found, the cross section changes $dQ_1 \ldots dQ_m$ as well as the homology parameters $h_1 \ldots h_4$.

VII. Iteration and Checks

For all cross sections Q, we have now found the corrections dQ, neccessary to bring us (as close as possible with a linear approach) to the homology solution which is most similar to our first guess (or to the result of the previous iteration). We apply these corrections and

replace	by	
Q_γ	$Q_\gamma + dQ_\gamma$	$\gamma = 1 \ldots m$
F_i^Ω	$F_i^\Omega + \sum_{\gamma=1}^{m} f_{i,\gamma}^\Omega\, dQ_\gamma$	$i = 1 \ldots d$ (80)
A_{ij}	$A_{ij} + \sum_{\gamma=1}^{m} a_{ij,\gamma}\, dQ_\gamma$	$j = 1 \ldots d$
		$\Omega = 1,2.$

We check, whether

$$\text{all } Q_\gamma \geq 0 . \qquad \gamma = 1 \ldots m \qquad (81)$$

If not, we replace the negative one by a small positive value and try the next iteration. If it fails again, we print "Negative Cross Section", and stop the calculation. This means trying again with a different first guess, or, more probably, changing the geometrical shape of the structure.

Next, we go through the whole procedure of inverting A and calculating all deflections $\Delta\beta$ until we arrive at the deviations from homology as given in (55). With (56) we check whether the accuracy wanted is already reached; if not, we repeat the iteration. If (56) is fulfilled, we regard (80) as the "Final Result of Iteration".

If, after some iterations, it turns out that the deviations, ΔH, do not decrease but jump or increase, we stop the calculation and print "No Convergence". Most probably, the mathematical solution would call for imaginary or complex cross sections, and we have to change the geometrical shape of the structure.

VIII. Sensitivity

Considering the tolerances in all manufactoring and erection procedures, we ought to know how sensitive our homology solution is with respect to small inaccuracies of the cross sections. We vary each cross section by

$$dQ_\gamma = Q_\gamma \varepsilon_\gamma , \quad \text{with} \quad \varepsilon_\gamma \ll 1, \qquad \gamma = 1 \ldots m \qquad (82)$$

and we regard the ε_γ as being uncorrelated random numbers, with mean zero and rms $\varepsilon_\gamma = \varepsilon$. Suppose we have exact homology before applying the changes (82); in equation (55), then, each single term equals zero. Now, we apply changes (82) and have

$$(\Delta H)^2 = \frac{1}{2N} \sum_{i=1}^{2N} \left\{ \sum_{\gamma=1}^{m} \frac{\partial b_i}{\partial Q_\gamma} dQ_\gamma \right\}^2 . \qquad (83)$$

Since the ε_γ are uncorrelated, only the quadratic terms remain in the average

$$(\Delta H)^2 = \frac{\varepsilon^2}{2N} \sum_{i=1}^{2N} \sum_{\gamma=1}^{m} \left\{ Q_\gamma \frac{\partial b_i}{\partial Q_\gamma} \right\}^2 . \qquad (84)$$

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TELEPHONE ARBOVALE 456-2011

PROJECT: LFSP
SUBJECT: Homology Program

From (60) we find

$$\frac{\partial b_i}{\partial Q_\gamma} = - C_{i\gamma} . \qquad \left| \begin{array}{l} i = 1 \ldots 2N \\ \gamma = 1 \ldots m \end{array} \right. \qquad (85)$$

At present, we go "away" from a homology solution, which means that <u>all</u> cross sections are free for variation (as opposed to (72) and (73), where some parameters were bound by the homology equations). Thus

$$(\Delta H)^2 = \frac{\varepsilon^2}{2N} \sum_{i=1}^{2N} \sum_{\gamma=1}^{m} (C_{i\gamma} Q_\gamma)^2 . \qquad (86)$$

Finally, we define the sensitivity in a dimensionless way as

$$S = \frac{\Delta H}{D\varepsilon} \qquad (87)$$

with

$$D = \text{diameter of the telescope} \qquad (88)$$

and obtain

$$S = \frac{1}{D} \left\{ \frac{1}{2N} \sum_{i=1}^{2N} \sum_{\gamma=1}^{m} (C_{i\gamma} Q_\gamma)^2 \right\}^{1/2} . \qquad (89)$$

Having calculated S, we must demand that the rms deviations from homology, ΔH, are smaller than 1/16 of the shortest wavelength, λ, which leads to the following demand for the structural accuracy

$$\varepsilon \leq \frac{\lambda}{16\, D\, S} . \qquad (90)$$

The accuracy needed will be found properly, from (90), when the calculations are performed. But meanwhile I made a very rough estimate, with help of formulae (59), (39) and (32), which gave

$$\Delta H \approx \varepsilon \Delta\beta, \quad \text{with} \quad \Delta\beta = \text{rms}(\Delta\beta_\nu^\Omega), \quad \nu = 1 \ldots N. \qquad (91)$$

We call λ_g the gravitational limit for a normal telescope of diameter D ($\lambda_g = 8 \text{ cm } (D/100\text{m})^2$, from (8) of my antenna paper, with K = 1.5), and we allow the $\Delta\beta$ for our structure to be three times larger than for the best possible normal telescope, which gives for (90)

$$\varepsilon \leq \frac{\lambda}{3\lambda_g} . \qquad (92)$$

This is a very low demand on the structural accuracy. Even if we want to pass the gravitational limit by a factor 10 in wavelength (or a factor 3 in diameter), we need no better accuracy in the cross sections than three per cent. This eases the manufacturing as well as the calculations: a few iterations will be enough.

IX. The total weight

The total weight was kept constant from the first guess until we reached the nearest homology solution. If we now multiply each cross section (and the surface load w_o) by one and the same factor q, we still have homology. In my antenna paper, I found four items which can define the total weight of a telescope: wind deflections, survival conditions, gravitational deflections, and the minimum stable structure. Now, the gravitational deflections have been made homologous and cannot define the weight; the minimum structure cannot be treated in the present approach, since we have taken the weight of a member as being the product of density times cross section times length, neglecting the passive weight of braces, struts and so on. As to the remaining two items, Fig.6 of my antenna paper shows that we are always in the wind deflection region, if we pass the gravitational limit by an appreciable factor. Thus, the weight will be, most probably, defined by keeping the wind deflections down, but in order to be safe we also check the survival stresses.

1. Survival

We calculate the stress in each member for the survival conditions, case $\Omega = 4$ in (14). The best way seems to be: we calculate all deflections $\Delta\beta$ from (35), find the elongation $\Delta l_{\tau\nu}$ of each member $\tau\nu$ from (11), which gives the stress in member $\tau\nu$ as

$$S_{\tau\nu} = \frac{\Delta l_{\tau\nu}\, E}{l_{\tau\nu}} . \qquad (93)$$

We find the member with the largest stress, S_m, and compare S_m with the maximum allowed stress, S_o, from the input data. If the structure were defined by survival, we had to multiply all cross sections (and w_o, simulating the surface weight) with $q_s = S_m/S_o$. The total weight then is

$$W_s = W\, S_m/S_o = \text{total weight as defined by survival.} \qquad (94)$$

W_s should be printed, in any case.

PROJECT: LFSP
SUBJECT: Homology Program

2. Wind deflections

We apply the maximum wind load for observation, case Ω=3 in (14), and calculate the deformations for all surface points in z-direction from (35); we call Δz the rms value, and we demand

$$\Delta z \leq \lambda/16 \; . \tag{95}$$

This can be done in two ways. First, we ask for the limiting wavelength, λ_s, if the structure were defined by survival, with weight W_s from (94):

$$\lambda_s = 16 \, \Delta z \, S_o/S_m \; . \tag{96}$$

Second, we calculate the total weight, W_w, necessary to fulfill (95) for the shortest wavelength λ as given by the input data:

$$W_w = W \, 16 \, \Delta z/\lambda = \text{total weight as defined by wind deflections.} \tag{97}$$

For the actual weight we finally call

$$q = \max \left(\frac{16 \, \Delta z}{\lambda} , \frac{S_m}{S_o} \right) \tag{98}$$

and we multiply all cross sections with q, and print out the results. The actual total weight then is given by

$$W_a = q \, W \; . \tag{99}$$

X. Approach to Minimum Weight

1. The gradient of the total weight

We assume that the actual weight, W_a, is defined by wind deflections in (97), which, as I think, will always be the case. Our present goal is to decrease this weight while keeping the structure homologous. Within the frame of a linear approach, we cannot solve directly for a minimum weight; but we can find the direction (ratio of cross section changes) in which the weight decreases most rapidly.

Since the actual weight in (97) is proportional to the product of the initial weight W from the firat guess, times the rms wind deflection Δz, our task can be written as:

Change all cross sections Q_γ by dQ_γ,
and all homology parameters h_k by dh_k, such that

(a) Homology still holds,
(b) The initial weight W stays constant,
(c) The wind deformation Δz decreases most rapidly. (100)

Condition (c) means we regard Δz as a function of the n parameters dQ_γ and dh_k, and we ask for the gradient of Δz in this n-dimensional space. But conditions (a) and (b) together are c constraint equations, defining an (n-c)-dimensional hyperplane on which the solution must lie. Thus, we have to project the n-dimensional gradient of Δz on the (n-c)-dimensional hyperplane; this projected gradient, then, points exactly opposite to the direction wanted where Δz decreases most rapidly. Furthermore, the length of the projected gradient can be used as a measure of the distance to the final point of minimum Δz, because at this point the gradient is zero.

The wind deformation Δz is defined as the rms deformation of all surface points in z-direction, under maximum observational wind loads:

$$\Delta z = \left\{ \frac{1}{N} \sum_{\nu=1}^{N} (\Delta\beta_\nu^\Omega)^2 \right\}^{1/2} . \qquad \left| \begin{array}{l} \beta = z \\ \Omega = 3 \end{array} \right. \qquad (101)$$

We apply small changes dQ_γ of all Q_γ, resulting in small changes $d\Delta\beta$ of all $\Delta\beta$, leading to a small change $d\Delta z$ of Δz. Neglecting terms of second order, we then have

$$d\Delta z = \frac{1}{N\,\Delta z} \sum_{\nu=1}^{N} \Delta\beta_\nu^\Omega \, d\Delta\beta_\nu^\Omega . \qquad \left| \begin{array}{l} \beta = z \\ \Omega = 3 \end{array} \right. \qquad (102)$$

Now, we replace the resulting $d\Delta\beta$'s by the causing dQ's with help of equations (40), but we change the notation

$$B_{j\gamma}^\Omega \longrightarrow B_{\beta\nu,\gamma}^\Omega$$

and we define a vector t by

$$t_\gamma = \begin{cases} \dfrac{1}{N\,\Delta z} \displaystyle\sum_{\nu=1}^{N} \Delta\beta_\nu^\Omega \; B_{\beta\nu,\gamma}^\Omega & \left| \begin{array}{l} \gamma = 1 \ldots m \\ \beta = z \\ \Omega = 3 \end{array} \right. \\ 0 \quad \text{for} \quad \gamma = m+1 \ldots m+4, \end{cases} \qquad (103)$$

Equation (102) then reads

$$d\Delta z = \sum_{\gamma=1}^{n} t_\gamma \, dQ_\gamma \qquad (104)$$

and we see that the gradient of Δz in the n-dimensional space is $(\text{grad } \Delta z)_\gamma = t_\gamma$. Next, we must project this gradient on the hyperplane given by the constraint equations, which in our case are given by the homology equations (65) and definitions (63). But in (65), we wanted to reach homology, whereas now we already have homology and just want to keep it; this means that equations (51) hold and can be subtracted from equations (65). Furthermore, we already have a set of homology parameters h_k, but we allow for small changes dh_k. We thus define, instaed of (64):

$$dQ^o_\gamma = \begin{cases} dQ_\gamma \\ dh_k \end{cases} \qquad \begin{array}{l} \gamma = 1 \ldots m \\ \gamma = m+k, \quad k = 1 \ldots 4 \end{array} \qquad (105)$$

and instead of (65) we now have the constraints

$$\sum_{\gamma=1}^{n} C^*_{i\gamma} \, dQ^o_\gamma = 0 . \qquad i = 1 \ldots c \qquad (106)$$

The projection $\overbrace{\gamma}^{g}$ of vector t on the hyperplane given by matrix C^* can be written as

$$g_\gamma = t_\gamma - \sum_{\varphi=1}^{n} H_{\gamma\varphi} \, t_\varphi \qquad \gamma = 1 \ldots n \qquad (107)$$

where matrix H is given by

$$H = C^{*T} (C^* C^{*T})^{-1} C^* . \qquad (108)$$

Or, in detail, we multiply C^* from (63) with its transposed C^{*T}

$$I_{ij} = \sum_{\nu=1}^{n} C^*_{i\nu} \, C^{*T}_{\nu j} . \qquad \begin{array}{l} i = 1 \ldots c \\ j = 1 \ldots c \end{array} \qquad (109)$$

With the inverse, I^{-1}, we get

$$J_{i\varphi} = \sum_{j=1}^{c} I^{-1}_{ij} \, C^*_{j\varphi} \qquad \begin{array}{l} i = 1 \ldots c \\ \varphi = 1 \ldots n \end{array} \qquad (110)$$

and finally have

$$H_{\gamma\varphi} = \sum_{i=1}^{c} C^{*T}_{\gamma i} \, J_{i\varphi} . \qquad \begin{array}{l} \gamma = 1 \ldots n \\ \varphi = 1 \ldots n \end{array} \qquad (111)$$

PROJECT:

SUBJECT:

The length g of the projected gradient, then, is

$$g = \left\{ \sum_{\gamma=1}^{n} g_\gamma^2 \right\}^{1/2} . \qquad (112)$$

The direction of decreasing weight has now been found, as the one opposite to direction (107). If we want to move in this direction by some fraction (or multiple) k of g, we choose k and

$$\text{replace } Q_\gamma \text{ by } Q_\gamma - k g_\gamma \quad \Big| \quad \gamma = 1 \ldots m \qquad (113)$$

by which procedure the homolgy parameters will change from h_j into $h_j - k g_{j+m}$ for $j = 1 \ldots 4$.

2. A two-step procedure

Since a linear approach cannot yield a minimum, it cannot tell us how far we have to go (what value for k we should take). But a quadratic approach, in its full generality, would need $1 + \Phi(\Phi+3)/2$ constants to be defined, which means we had to calculate Δz and grad Δz at $1 + \Phi/2$ points (sets of various Q_γ); this would certainly take much too long a calculation time, and it would give more accuracy than actually needed, because we do not have to find the exact point of minimum weight, we just want to come close to it. The following approach was worked out for a problem in hydrodynamics which lead to a non-linear least-squares fit in many parameters, it gave good results in relatively short calculation times. Applied to our present task, it leads to a two-step procedure: first, we need another homology solution, second, we approach the point of minimum weight.

We call $Q_{\gamma 1}$ the present values of Q_γ, and, similarly, call $g_{\gamma 1}$, g_1, Δz_1 the present values of these quantities. Next, we want to move away from this present point by such a fraction k_1 of g_1, in the direction of decreasing weight, that second-order terms already become appreciable and higher terms still may be neglected. A good choice may be to demand that the largest change of any cross section should be, say, 20 per cent. This means we claculate all

$$k_{\gamma 1} = \left| Q_{\gamma 1} / g_{\gamma 1} \right| \quad \Big| \quad \gamma = 1 \ldots m \qquad (114)$$

and call

$$k_1 = 0.2 \min (k_{11}, k_{21} \ldots k_{m1}). \qquad (115)$$

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TELEPHONE ARBOVALE 456-2011

PROJECT: LFSP
SUBJECT: Homology Program

We change all cross sections according to

$$Q_{\gamma 2} = Q_{\gamma 1} - k_1 g_{\gamma 1} . \qquad \gamma = 1 \ldots m \qquad (116)$$

We use these cross sections as a new first guess, repeat all previous calculations until we arrive again at the gradient of Δz, and we give an index 2 to all new values. We calculate all

$$k_{\gamma 2} = \left| Q_{\gamma 2} / g_{\gamma 2} \right| \qquad \gamma = 1 \ldots m \qquad (117)$$

and call

$$k_2' = \min (k_{12}, k_{22} \ldots k_{m2}) \qquad (118)$$

allowing this time changes up to 100 per cent. We call

$$k_2'' = \frac{k_1}{1 - s} \qquad (119)$$

where s is defined as the scalar product of both gradients, divided by g_1^2:

$$s = \frac{1}{g_1^2} \sum_{\gamma=1}^{m} g_{\gamma 1} g_{\gamma 2} , \qquad (120)$$

and we call

$$k_2 = \min (k_2', k_2'') . \qquad (121)$$

The improved cross sections, then, are given by

$$Q_{\gamma 3} = Q_{\gamma 2} - k_2 g_{\gamma 2} . \qquad \gamma = 1 \ldots m \qquad (122)$$

This holds, if the first step was an improvement, which means if $\Delta z_2 \leq \Delta z_1$. If not, the first step has overshot the minimum point by too large an amount, and we better start the improvement from the first point, which simply means we exchange index 1 and index 2 in all formulae from (117) to (122).

Formula (119) was chosen as to be identical with the general quadratic approach for the two limiting cases, where both gradients are either parallel or antiparallel to each other, and it gives satisfactory results in between. The whole two-step approach might be regarded as a first iteration which could be repeated if calculation times would allow.

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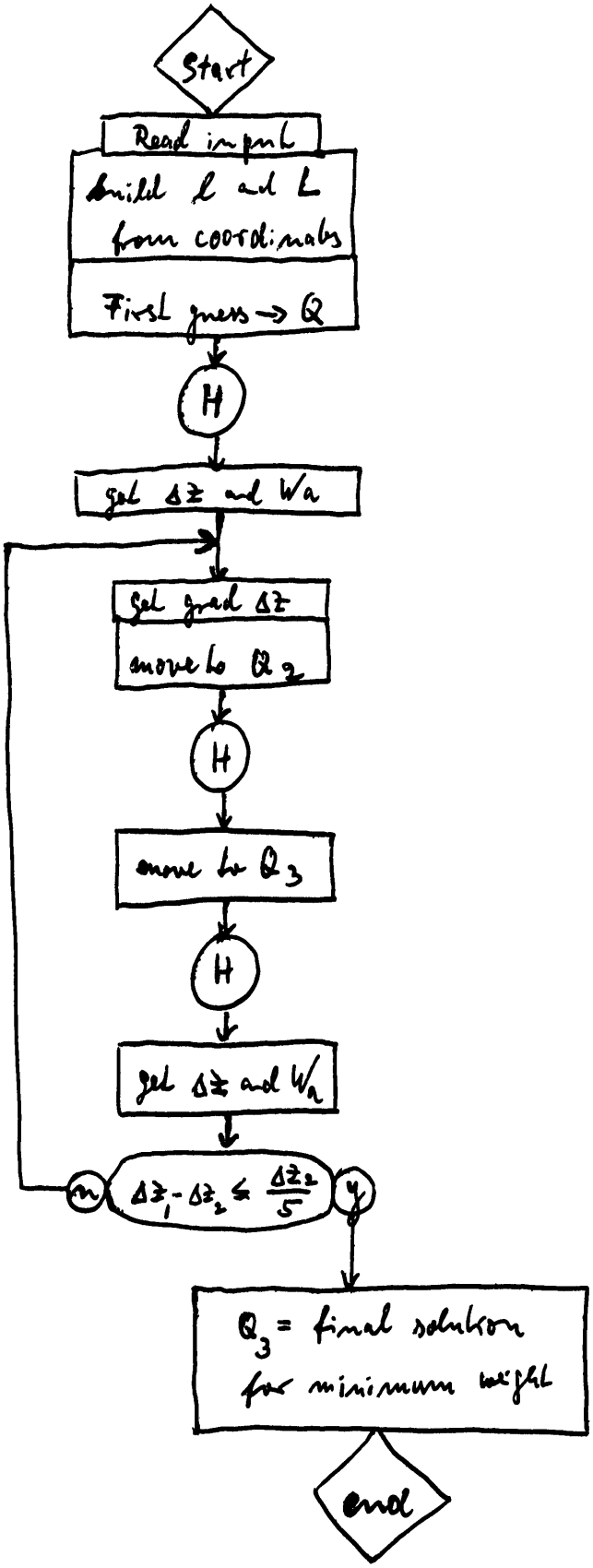
PROJECT:

SUBJECT:

Finally, a possible problem should be mentioned. In equation (101) and (14) we have defined Δz as the deformation in z-direction resulting from a face-on wind in z-direction. This wind direction always yields the largest force on the structure, and our definition of Δz will usually select the largest possible deformation. But if we iterate several times according to (122), we might develop a somewhat unusual structure, being very stiff in z-direction but too soft in the other directions, such that a side wind, although yielding less force, still might result in larger deformations than a face-on wind. If this is the case, we should have changed the definition of Δz and should have included the other cases of side winds in x-direction and in y-direction. But whether or not this complication actually is needed can best be decided after some trial runs of (122) with various model structures have been performed.

General outline:

main program



Subroutine (H), homology