NONLINEAR SUPERELEMENT ANALYSIS TO MODEL ASSEMBLY PROCESSES

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Abstract:

It is often desirable to know the residual effect of assembly processes on the final product. Although only a linear static analysis may be desired, the changes in loads and constraints throughout the assembly process prevent the use of a simple linear solution. If the product is fairly complex, it is often necessary to use a large finite element model. This paper describes the use of a single nonlinear solution (MSC/NASTRAN V66A SOL 66) using superelements to analyze a large model subjected to varying loads and constraints. As the load and support change in each subcase, the structural deflection changes by adding to or subtracting from the previous deformation state. The model used represents the High Resolution Mirror Assembly (HRMA) for NASA's Advanced X-Ray Astrophysics Facility (AXAF). The process represented is the alignment and assembly of the AXAF mirrors to the support structure.

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Acronyms:

AXAF	Advanced X-Ray Astrophysics Facility
HRMA	High Resolution Mirror Assembly
CAP	Center Aperture Plate
MPC	Multi-Point Constraint
SPC	Single Point Constraint
OD	Outer Diameter
CG	Center of Gravity

1.0 Introduction

Finite element models are commonly used by analysts to determine the linear static or modal solutions to engineering parts and assemblies. It is sometimes desirable, but not convenient, to determine the residual effects on the structure from the assembly process that was used to construct it. Residual stresses and strains can be built into an assembly because each step in the process involves a previously deformed shape that undergoes further deformation. The structure has a changing stiffness which is unique at each stage in the assembly process. A sequential solution of this type is clearly nonlinear although each assembly step on its own is a linear solution. Changes in the assembly supports throughout the process likewise demand a nonlinear algorithm due to the resulting changes to the stiffness matrix.

The task is further complicated if a large finite element model is required, where the use of superelements may be necessary or highly recommended. The use of superelements demands more care from the analyst, and the combination of superelements in a nonlinear solution requires some additional model organization.

This paper describes and provides an example of a technique that can be used to model manufacturing and assembly processes where changes in loads as well as boundary conditions exist within a single large model solution. Assembly stresses and strains can be analyzed in a solution that mimics the assembly environment with changes in loads and constraints from one subcase to the other. After a description of the analysis problem to be solved, the nonlinear method will be explained and illustrated with a simple example. Finally, the technique will be applied to the analysis problem for which it was developed. Other relevant examples will be identified to demonstrate the application of this technique to virtually any process. The nonlinear techniques discussed in this paper were derived from a concept originally described in a MSC/NASTRAN Application Manual note [1].

2.0 Analysis Problem Background

The performance of an optical instrument like any highly sensitive structure is susceptible to degradation due to residual strains left in the structure from assembly. Whether residual stresses or strains are of interest, small amounts can have drastic consequences. In many structures, residual stresses and strains may be insignificant compared to the operational stresses and strains. For sensitive structures, such as the Advanced X-Ray Astrophysics Facility (AXAF) High Resolution Mirror Assembly (HRMA), typical displacements might be measured in units of microinches. Therefore, residual strains are of critical importance.

2.1 **AXAF HRMA Structure**

NASA's Advanced X-Ray Astrophysics Facility is one of the four large orbital telescopes collectively known as the the Great Observatories for Space Astrophysics. AXAF along with the Gamma-Ray Observatory, Hubble Space Telescope, and Space Infrared Telescope Facility serve to gather information about the origin of the universe, fundamental laws of physics, and the birth of stars, planets, and life by imaging astronomical objects across the entire electromagnetic spectrum [2]. AXAF is a high-resolution telescope which reflects X-rays off of the mirrors in the HRMA and focuses the image onto detectors in the science instrument module (Figure 1). The HRMA consists of four nested, confocal Wolter Type-I grazing incidence mirror pairs bonded to an elaborate support structure (Figure 2).

NASA awarded the AXAF contract to the TRW Space and Technology Group on 19 August 1988. As AXAF's prime contractor, TRW is responsible for systems engineering and the integration of the entire AXAF observatory, including the design and development of the AXAF spacecraft. The TRW team includes the Eastman Kodak Company as the telescope system

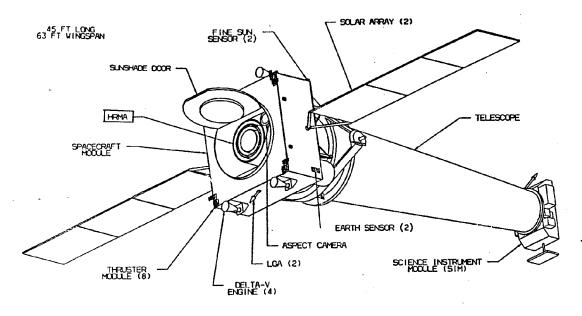


FIGURE 1. AXAF Telescope Configuration. Forward section of HRMA is exposed to incoming X-rays.

subcontractor. Kodak will design and integrate the x-ray telescope, including assembly and alignment of the HRMA, the x-ray imaging portion of the telescope. Other TRW subcontractors include Hughes Danbury Optical Systems, who will grind and polish the HRMA optics, and Ball Aerospace, who is responsible for the star tracking aspect camera and science instrument accommodation hardware. The AXAF program is managed by the Marshall Space Flight Center with technical support from the Harvard College Smithsonian Astrophysical Observatory [3].

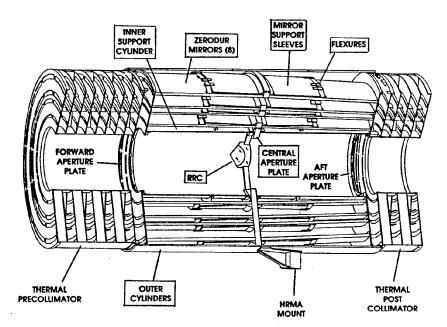


FIGURE 2. HRMA Configuration. Structures included in FE model are indicated with a box around label.

2.2 Nominal Assembly Residual Strain

One of the major areas of concern during the assembly process of the HRMA is the residual impact of the mirror supports during the alignment and bonding of the mirrors to the support structure assembly. The mirror residual strains that are added from this assembly process can be described by the combination of nominal and variation residuals. The nominal residual is the strain resulting from a perfect, flawless assembly process. The variation residual is the strain resulting from all the imperfections and tolerances that lead to net force and moment differences between mirror support points. The example analysis used to illustrate the method discussed in this paper deals with the nominal residual errors which are present despite the assumption of a perfect assembly process due to the strain resulting from the change of loads and boundary conditions throughout the assembly flow (Figure 3).

The nominal assembly residual strain is a direct result of the assembly process which is simplified as three steps per mirror:

STEP 1 Structure: Mirror & HRMA sub-assembly -- not bonded

Load: 1g axial gravity

Support: mirror supports (12 points), HRMA tower support

STEP 2 Structure: Mirror & HRMA sub-assembly -- bonded

Load: 1g axial gravity
Support: HRMA tower support

STEP 3 Structure: Mirror & HRMA sub-assembly -- bonded

Load: none (0g)

Support: HRMA telescope support

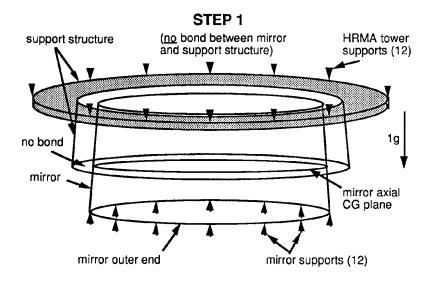
The mirrors are assembled in this manner one at a time in a specified mirror sequence. At each stage in the assembly process there is a change of load and/or boundary conditions. The mirror is initially held at twelve equally spaced locations along the circumference of the outer end of the optic. The mirror is then aligned and bonded in place at twelve locations along the mirror OD at the mirror axial CG plane. The mirror supports at the outer end of the optic are then released, and the next mirror undergoes the same process. During these assembly steps, the HRMA sub-assembly is supported at discrete locations where it interfaces with the assembly tower, the structure which is the ground in the system. The final step in this process is the removal of the 1g load to simulate the relaxation of the structure when in earth orbit (zero g). This step occurs while the complete HRMA assembly is supported by the rest of the telescope at three discrete interface points. When the load is removed in the final step, some of the structural deflection will be recovered and some will be locked in the structure as residual deformation. This remaining deformation is referred to as the residual strain from the nominal assembly process.

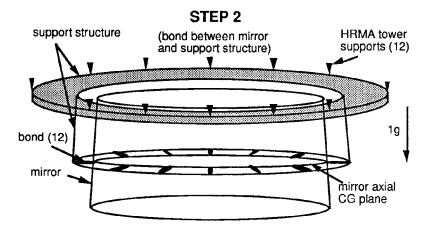
3.0 Nonlinear Solution Method

The nonlinear method developed for this analysis requires the manipulation of multi-point constraint (MPC) sets and single point constraint (SPC) sets during the solution process. The assembly process is modelled through the use of these constraint changes and load changes from subcase to subcase. These changes between subcases simulate the addition or subtraction of parts to the assembly as well as changes in the environment (loading and support).

3.1 Multi-Point Constraints

The MPC as defined in MSC/NASTRAN [4] is a constraint equation of the form





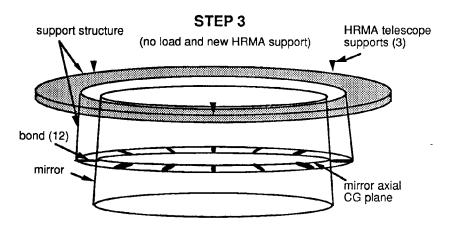


FIGURE 3. AXAF HRMA mirror assembly process. Loads and supports change between steps.

$$\Sigma_{\mathbf{j}} A_{\mathbf{j}} u_{\mathbf{j}} = 0 \tag{1}$$

where u_j represents the displacement of the j^{th} grid point in a specified degree of freedom scaled by the coefficient, A_j . The MPC equations for this technique require the values of A_j to be +1 or -1 so that the displacements for a degree of freedom at the connected grid points sum to zero, the desired relative displacement. Consider the two nodes, Node 1 and Node 2:

$$A_1 u_1 + A_2 u_2 = 0 (2)$$

$$u_1 - u_2 = 0$$
 (3)

$$\mathbf{u}_1 = \mathbf{u}_2 \tag{4}$$

where A_1 and A_2 are equal to +1 and -1, respectively, and the relative displacement of Node 1 and Node 2 is therefore zero.

If two nodes in a model are linked with an MPC in the form of equation 3, then the additional relative displacement of the two nodes in the specified degree of freedom is constrained to zero. In other words, there is no change in the relative displacement of the two points, although they may change displacement identically in the form of rigid body motion. It does not matter if the two nodes linked together have already displaced or not. If the MPC is turned on, connecting two undeformed nodes, then the displacements of the two nodes are identical. If the MPC is instead turned on after the nodes have deformed, then the additional displacement of the two nodes is identical. This use of the MPC will be referred to as 'MPC type I'.

MPC equations in the manner just described can be used to simulate the connection (bond, weld, etc.) of parts in an assembly. If, however, Node 2 in equation 3 was already constrained to zero with an SPC, then the effect of the MPC is to add a fixed constraint to Node 1. From Equation 4, the displacement of Node 1 is set to zero. Therefore, when an MPC equation of this type is turned on, the dependent node, Node 1, is effectively constrained in its current (deformed or undeformed) position. This use of the MPC will be referred to as 'MPC type II'

Both types of MPC equations described can be used in an analysis as needed depending on the type of process modelled. In order to connect nodes in a model, the MPC type I can be used. However, if constraints are to be added to nodes in the model at any point during the solution, then the MPC type II must be used for this additional constraint. Constraints cannot be added to the model at deformed grid point locations using only an SPC card. Using just an SPC card on the deformed node would force the node back to its initial position as defined on the GRID card instead of fixing the node at its deformed position. The example problem in section 3.4 illustrates the use of both types of MPC equations.

3.2 Single Point Constraints

SPC's are used in this application to zero the displacements of nodal degrees of freedom at symmetry points as well as points that are supported from outside structures not included in the analysis, but assumed to be rigid. SPC sets can be removed from the structure as the analysis proceeds, but the addition of SPC's must be handled in conjunction with the MPC type II described in the previous section. It is recommended that even when the MPC type II is used, the fixed node (Node 2 from Equation 3) should be constrained with a SPC that is active throughout the entire analysis solution.

3.3 Nonlinear Structure

Since a nonlinear solution sequence is required for this analysis, it is also required that the

data deck appear nonlinear when the cards are interpreted by MSC/NASTRAN (Version 66A, Solution 66). This requirement can be satisfied by including a nonlinear element, a dummy structure, that is present in the data deck, but has no connection or affect on the actual structure of interest. For the examples presented in this paper a nonlinear gap element, CGAP, is used. Note that any other nonlinear structure, such as a beam with a nonlinear material card, can be used. The choice is completely arbitrary. This requirement may not be necessary with more recent versions of MSC/NASTRAN.

3.4 Example Problem

It would be helpful at this point to develop a simple example to illustrate and verify the nonlinear method to be implemented. Consider the two simple processes, Process #1 and Process #2, applied to the sets of cantilevered beams as illustrated in Figure 4 and Figure 5, respectively.

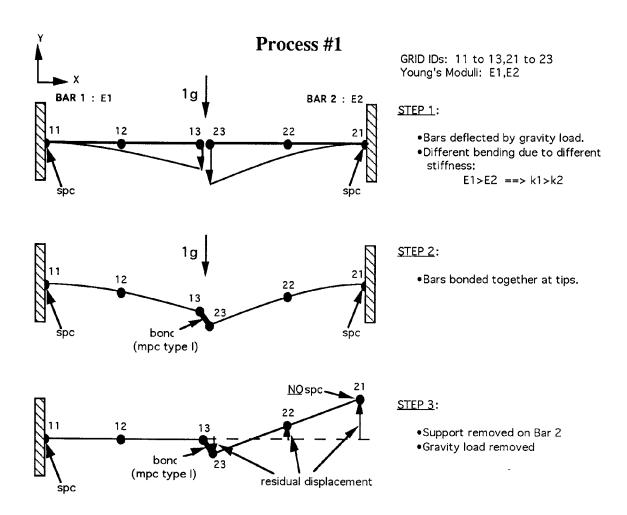


FIGURE 4. Example Problem, Process #1. Two cantilevered bars with a change in load and constraint. Only MPC type I is used. Figure not to scale.

Process #1: 1.) beams are deformed by gravity (initial deformation) 2.) beam tips are bonded rigidly together (MPC addition) 3.) support is removed at the base of one of the beams (SPC change) gravity is removed (Load change) Process #2: 1.) beams are deformed by gravity (initial deformation) beam tips are bonded rigidly together 2.) (MPC addition) support is removed at the bases of both beams (SPC change) support is added at the bonded joint (SPC change) gravity is removed (Load change)

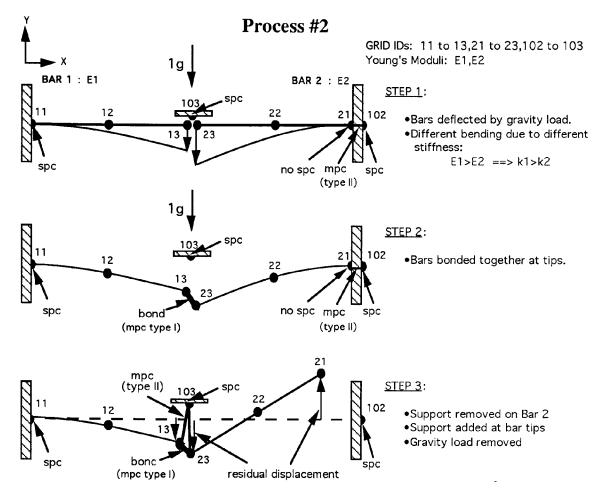


FIGURE 5. Example Problem, Process #2. Two cantilevered bars with a change in load and constraint. Both MPC type I and MPC type II are used. Figure not to scale.

Since only the final residual is of interest in the two example processes, each can be analyzed with a two step (subcase) structure by combining the changes in steps two and three into

one step. The steps combined only involve a MPC addition, a SPC change, and a change in load within one subcase of the nonlinear solution. Thus the subcase involves a linear deformation, with the nonlinearity occurring in the change between the subcases. Therefore, the combination of these changes in one subcase is identical to the individual changes one at a time. The brute force approach also confirms that this combination of steps is valid. The MSC/NASTRAN data decks for the two processes are included in Appendix A.

EXAMPLE PROBLEM, PROCESS #1:				DISPLACEMENT				VECTOR		
SUBCASE 1	POINT ID	. TYPE	T1	Т2	т3	R1	R2	R3		
GRAVITY LOAD FOR INITIAL DEFORMATION	11	G	0.0	0.0	0.0	0.0	0.0	0.0		
	12	G	0.0	-3.477614E-08	0.0	0.0	0.0	-5.796023E-08		
	13	G	0.0	-1.004644E-07	0.0	0.0	0.0	-6.955228E-08		
	21	G	0.0	0.0	0.0	0.0	0.0	0.0		
	22	G	0.0	-3.477614E-07	0.0	0.0	0.0	5.796023E-07		
	23	G	0.0	-1.004644E-06	0.0	0.0	0.0	6.955228E-07		
	POINT ID	. TYPE	T1	T2	Т3	R1	R2	R3		
RESIDUAL EFFECTS AFTER BARS ATTACHED	11	G	0.0	0.0	0.0	0.0	0.0	0.0		
	12	G	0.0	6.617445E-23	0.0	0.0	0.0	1.455838E-22		
	13	G	0.0	2.514629E-22	0.0	0.0	0.0	2.117582E-22		
	21	G	0.0	6.259705E-07	0.0	0.0	0.0	7.650751E-07		
	22	G	0.0	-1.391046E-07	0.0	0.0	0.0	7.650751E-07		
	23	G	0.0	-9.041796E-07	0.0	0.0	0.0	7.650751E-07		
EXAMPLE PROBLEM, PROCESS #2:				DISPLACEMENT VECTOR						
SUBCASE 1	POINT ID	. TYPE	Tl	т2	т3	R1	R2	R3		
GRAVITY LOAD FOR INITIAL DEFORMATION	11	G	0.0	0.0	0.0	0.0	0.0	0.0		
	12	G	0.0	-3.477614E-08	0.0	0.0	0.0	-5.796023E-08		
	13	G	0.0	-1.004644E-07	0.0	0.0	0.0	-6.955228E-08		
	21	G	0.0	0.0	0.0	0.0	0.0	0.0		
	22	G	0.0	-3.477614E-07	0.0	0.0	0.0	5.796023E-07		
	23	G	0.0	-1.004644E-06	0.0	0.0	0.0	6.955228E-07		
SUBCASE 2	POINT ID	TYPE	т1	Т2	т3	R1	R2	R3		
RESIDUAL EFFECTS AFTER BARS ATTACHED	11	G	0.0	0.0	0.0	0.0	0.0	0.0		
	12	G	0.0	-3.284413E-08	0.0	0.0	0.0	-5.796023E-08		
	13	G	0.0	-1.004644E-07	0.0	0.0	0.0	-6.955228E-08		
	21	G	0.0	3.864016E-07	0.0	0.0	0.0	6.955228E-07		
	22	G	0.0	-3.091212E-07	0.0	0.0	0.0	6.955228E-07		
	23	G	0.0	-1.004644E06	0.0	0.0	0.0	6.955228E-07		

FIGURE 6. Example Problems output data. For use in equations 5 to 8.

In order to draw conclusions from the output data, consider the following formulas which are used to calculate some of the residual deformations that are expected in the beams. Each can be derived with reference to Figures 4 and 5. Equations 5 and 6 give the residual displacement (translation and rotation) of Node 23 for each process. Equation 7 determines the residual displacement of Node 21 for either process.

Process #1:
$$\delta_{23}^2 = \delta_{23}^1 - \delta_{13}^1$$
, $\Theta_{23}^2 = \Theta_{23}^1 - \Theta_{13}^1$ (5)

Process #2:
$$\delta_{23}^2 = \delta_{23}^{11}, \quad \Theta_{23}^2 = \Theta_{23}^{11}$$
 (6)

Process #1 & #2:
$$\delta_{21}^2 = \delta_{23}^2 + \Theta_{23}^2(L)$$
, $\Theta_{21}^2 = \Theta_{23}^2$ (7)

The transverse deflection, δ , and nodal rotation, Θ , are written in terms of node number (subscript) and subcase (superscript). The length, L, refers to the bar length, 2 inches.

Application of Equations 5 through 7 to the output data in Figure 6 verifies that the analytical model gives the expected residual displacement data for both processes. In both examples it is assumed that there is only elastic deformation, so when the load is removed all of the deformation is recovered unless prevented by the change in constraint. The output data (Figure 6) uses the standard MSC/NASTRAN output format where (for these examples) T2 corresponds to transverse deflection, δ , and R3 refers to nodal rotation, Θ . Note that in the model for Process #2, the addition of the constraint at Nodes 13 and 23 require the use of a MPC (type II) with the constrained (SPC) Node 103. The data file for Process #2 shows the use of MPC type II on Nodes 13 and 103 as well as 23 and 103. It would also be acceptable to replace these two MPC sets with one equivalent set that links all three nodes.

4.0 Nonlinear Superelement Analysis of the Nominal Assembly Residual Strain

The nominal assembly residual strain analysis is set up using the nonlinear method developed in the previous section. Since this analysis does not involve the addition of any constraints, only MPC type I is used. Due to the large size of the model, superelements are recommended, and as a result there are some additional requirements that the model must meet in order to comply with both nonlinear and superelement rules. The following sections describe the model that has been developed to analyze the residual strain problem.

4.1 Finite Element Model

Most of the HRMA structure can be effectively modelled as plates and shells. Therefore, the model is constructed of QUAD4 elements, with some BAR and HEX elements as well. The model consists of eight conical mirrors and an elaborate sub-assembly all of which was created using MSC/NASTRAN MSGMESH [4]. The sub-assembly consists of a Center Aperture Plate (CAP), Outer and Inner Cylinders, Flanges, Sleeves, and Flexures. Figure 7 shows the model of the complete HRMA assembly after all mirrors are in place, and Figure 2 identifies each of the components that make up the FE model. Since all loads are axially symmetric, structural symmetry can be taken advantage of as Figure 7 indicates. The structure is symmetric every 120°, but other analyses of the model not discussed here require the 180° model segment shown.

The CAP is the base of the complete assembly and is the interface to the components of the telescope not in the model (Figure 2). Thus the CAP connects to ground. The Cylinders add weight and deformation to the CAP structure at the inner and outer diameters. The flanges are small protrusions that extend from the CAP surface and bond to the ends of the sleeves where they overlap. The sleeves connect to twelve flexures at equally spaced circumferential locations at the other end of the sleeve. Finally, each flexure bonds to the mirror once the mirror is in place and aligned. There are eight mirrors and sleeves in the complete HRMA, with a set of twelve flexures connecting each of the eight. All elements of the model are present at all stages in the analysis, however the bonds between mirrors and the sub-assembly are not established until the corresponding MPC's are turned on.

The MSC/NASTRAN data file used for this analysis is included in Appendix B. The data file contains the executive and case control sections as well as the bulk data loads and constraints. The remaining bulk data of the model are entered as included files. The case control section combined with the load and constraint sets show the manipulation of the load and support in order to model the assembly flow.

4.2 Multi-Point Constraints

Multi-point constraint sets are required at the interface points between each set of flexures and the mirror which is bonded to them. A duplicate node is included as part of each flexure at the

interface point with the mirror. The MPC is therefore the equation linking the two duplicate nodes together at each flexure/mirror interface. One MPC set is defined as all the MPC cards needed to connect one mirror to its twelve supporting flexures. Thus there are eight sets of MPC cards in the complete analysis. When an MPC set is turned on, or added to the active list of MPC sets, the relative displacements of the constrained node pairs are fixed, and the bond is established for that mirror. As the MPC case control card changes from subcase to subcase, the bulk data MPCADD card changes resulting in the sequential bonding of mirrors to the sub-assembly structure.

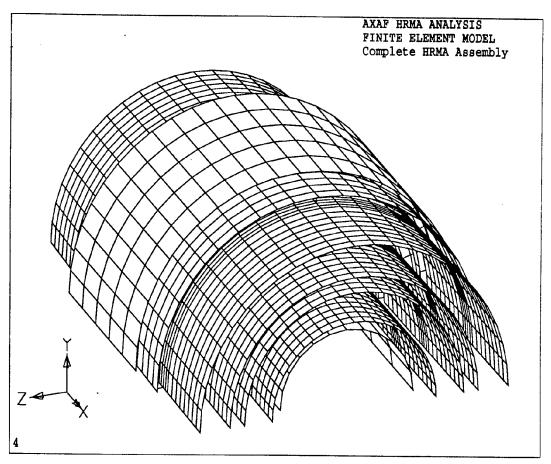


FIGURE 7. AXAF HRMA Finite Element Model used for this analysis.

4.3 Single Point Constraints

SPC's are used at all cuts of symmetry as well as external points of support. At the onset of the analysis all of the SPC sets are active through the use of the SPCADD card. SPC sets are removed as the analysis proceeds from one subcase to another.

SPC set 10 is used for symmetry constraints and is therefore active throughout the entire analysis. Sets 11 through 26 are used for mirror supports and are therefore turned off in sequence according to the mirror assembly order. These SPC sets are turned off one at a time until none are active when all mirrors have been bonded. The remaining SPC sets correspond to the support of the sub-assembly at the interface to the external structure (the tower or telescope). These SPC sets apply constraint to the CAP structure to support it during assembly on earth (set 20) as well as in

orbit (set 30). The constraints of SPC set 20 reflect the external supports applied to the structure while assembly occurs in the assembly tower at Kodak. SPC set 30 models the external support from the telescope interface—where the HRMA connects to the rest of the AXAF structure.

All of the SPC set changes between subcases involve the removal of SPC's; an SPC is never added to a deformed node. Thus the usage of MPC's (type I) and SPC's is valid.

4.4 Nonlinear Structure

The nonlinear structure previously explained (section 3.3) is again used. The gap element allows the nonlinear solution to be executed, but does not in any way affect the structure of interest.

4.5 Superelement Implementation

Superelements are extremely helpful in this analysis due to the large size of the model and the nature of the nonlinear iteration process. The model has 9,337 nodes and 9,452 elements. If superelements were not used, the stiffness matrix of the whole structure (the residual) would have to calculated in every subcase. Through the use of superelements as indicated below, the residual structure can be reduced to only 387 nodes.

The model is easily divided into upstream superelements as indicated by the division of the structure into parts in the discussion of section 4.1. Each of the eight mirrors is a superelement, as well as each of the eight groups of flanges, sleeves, and flexures. The CAP, outer cylinder, and inner cylinder are all unique superelements. The only difficulty in assigning superelement sets occurs in selecting the residual (superelement 0) structure. The superelements are being used in a nonlinear routine which will iteratively solve the structure stiffness matrix for the residual. Since the nonlinear iterations occur on the residual only, any part of the model that will have a change in constraint must be in the residual. At the same time, the residual should be made as small as possible to minimize the amount of time to solve the stiffness matrix in each subcase. A simple solution to these two requirements is to assign nodal points to the residual structure only if the point has a SPC or MPC attached to it at any time during the analysis. Thus the residual structure is a group of scattered nodes on the model. The stiffness matrix for the upstream superelements (most of the model nodes) only solves once.

The method of assigning loads to the structure is also affected by using superelements in a nonlinear solution sequence. It is necessary to have a case control LOADSET card to call a set of bulk data LSEQ cards. The LSEQ cards link the DAREA set identification number to the load set identification number (SID) on the actual bulk data load cards (FORCE, MOMENT, etc.). It is also required that a CLOAD card be used in the case control load selections to call the bulk data loads. This analysis uses the case control CLOAD cards to call bulk data CLOAD cards which linearly combine the specified load sets (FORCE, GRAV, etc.). Appendix B illustrates the above card usage more clearly.

5.0 Conclusions

The solution for the nominal assembly residual strain was calculated in MSC/NASTRAN V66A using the method described in this paper. The assembly process of the mirror alignment and bonding was modelled in the fashion described, and the resulting mirror deformations at each stage in the process were determined. The final on-orbit residual strain that can be expected from a nominal assembly was also determined as well as a performance estimate from the resulting mirror strains. The conclusion is that nominal residual strain errors have negligible performance impact on the HRMA structure (0.0006 arcsec of image error out of a total 1.0 arcsec error budget). The explanation for the low impact of this error source is the compliant nature of the HRMA flexures which allow the mirror strains to be relieved when the system is on-orbit.

The nonlinear techniques described in this paper can be used on a wide variety of analysis problems. Whether or not superelements are required, the technique can be used to determine residual stresses or strains resulting from assembly processes where loads and/or supports change throughout the process. The nominal assembly residual strain is an example of a residual resulting from the addition of parts to an assembly deformed by gravity. In addition to this example, the following problems are appropriate for the nonlinear technique.

One typical class of problems frequently analyzed are thermal analyses. Consider a thermal change that occurs during the assembly process. The structure may have a different isothermal temperature each time another piece is assembled to the sub-assembly. This example is the case for the referenced document, "Analysis of the Electronic Chip Manufacturing Process" [1]. Other

analyses could involve a gradient or CTE variation instead.

Another class of problems involve change in constraints within the structure without the addition of new parts to the assembly. Consider a structure that has an initial deformation from any load, and then is bonded or welded together at several points before the load changes. Residuals could be significant in these problems as well.

Regardless of the specific details of the process to be analyzed, as long as the analysis requires a change in loads and/or constraints on the deformed structure, the techniques presented herein are applicable.

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Arthur Buettner (Eastman Kodak Company) for his concurrent development of the nonlinear method with application to another assembly process.

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APPENDIX A.

Process #1

```
ID STONE, MARK
TIME 100
SOL 66
CEND
TITLE = AXAF HRMA ANALYSIS
SUBTITLE = EXAMPLE PROBLEM. PROCESS #1
LABEL = MJS -- 01/17/92
DISP = ALL
SEALL = ALL
NLPARM = 100
SUBCASE 1
   LABEL = GRAVITY LOAD for initial deformation
   LOAD = 100
   SPC = 1
SUBCASE 2
   LABEL = RESIDUAL EFFECTS after bars attached
    LOAD = 200
   SPC = 10
MPC = 100
BEGIN BULK
PARAM, GROPNT, 0
PARAM, POST, 0
PARAM, BAILOUT,-1
GRID.11.0.0..0..0.
GRID,12,0,1.,0.,0.
GRID,13,0,2.,0.,0.
GRID, 23, 0, 2., 0., 0.
GRID, 22, 0, 3., 0., 0.
GRID,21,0,4.,0.,0.
CBAR, 14, 31, 11, 12, 0., 1., 0.
CBAR, 15, 31, 12, 13, 0., 1., 0.
CBAR, 24, 32, 23, 22, 0., 1., 0.
CBAR, 25, 32, 22, 21, 0., 1., 0.
PBAR, 31, 41, 1., 0.083333, 0.083333, 0.1406
PBAR, 32, 42, 1., 0.083333, 0.083333, 0.1406
MAT1,41,1.+7,,0.3,1.-4
MAT1,42,1.+6,,0.3,1.-4
SPCADD, 1, 10, 20
SPC1,10,123456,11
SPC1,20,123456,21
MPC,100,13,1,1.,23,1,-1.
MPC,100,13,2,1.,23,2,-1.
MPC,100,13,3,1.,23,3,-1.
MPC,100,13,4,1.,23,4,-1.
MPC,100,13,5,1.,23,5,-1.
MPC,100,13,6,1.,23,6,-1.
GRAV,100,0,386.4,0.,-1.,0.
NLPARM, 100,1
GRID,1,0,0.,0.,0.,0,123456
GRID, 2, 0, 0., 1., 0., 0, 2345
GRID,3,0,0.,1.,0.,0,123456
CBAR,1,1,1,2,1.,0.,0.
PBAR,1,41,1.,0.1,0.1,0.1
CGAP,2,2,2,3,0.,1.,0.,0
PGAP, 2, 1., 0., 1.+6
FORCE, 200, 2, 0, -1., 1., 0., 0.
ENDDATA
```

Process #2

```
ID STONE MARK
TIME 100
SOT. 66
CEND
TITLE = AXAF HRMA ANALYSIS
SUBTITLE = EXAMPLE PROBLEM, PROCESS #2
LABEL = MJS - 01/17/92
DISP = ALL
SEALL = ALL
NLPARM = 100
SUBCASE 1
   LABEL = GRAVITY LOAD for initial deformation
   LOAD = 100
   SPC = 1
MPC = 200
SUBCASE 2
   LABEL = RESIDUAL EFFECTS after bars attached
   LOAD = 200
   SPC = 1
   MPC = 100
BEGIN BULK
PARAM, GRDPNT, 0
PARAM, POST, 0
PARAM, BAILOUT, -1
GRID,11,0,0.,0.,0.
GRID,12,0,1.,0.,0.
GRID,13,0,2.,0.,0.
GRID,23,0,2.,0.,0.
GRID,22,0,3.,0.,0.
GRID,21,0,4.,0.,0.
CBAR,14,31,11,12,0.,1.,0.
CBAR, 15, 31, 12, 13, 0., 1., 0.
CBAR, 24, 32, 23, 22, 0., 1., 0.
CBAR, 25, 32, 22, 21, 0., 1., 0.
PBAR, 31, 41, 1., 0.083333, 0.083333, 0.1406
PBAR, 32, 42, 1., 0.083333, 0.083333, 0.1406
MAT1,41,1.+7,,0.3,1.-4
MAT1,42,1.+6,,0.3,1.-4
GRID,102,0,4.,0.,0.
GRID,103,0,2.,0.,0.
SPC1,1,123456,11,102,103
MPC,100,13,1,1.,103,1,-1.
MPC,100,13,2,1.,103,2,-1.
MPC,100,13,3,1.,103,3,-1.
MPC,100,13,4,1.,103,4,-1.
MPC,100,13,5,1.,103,5,-1.
MPC,100,13,6,1.,103,6,-1.
MPC,100,23,1,1.,103,1,-1.
MPC,100,23,2,1.,103,2,-1.
MPC,100,23,3,1.,103,3,-1.
                                NLPARM, 100,1
MPC,100,23,4,1.,103,4,-1.
MPC,100,23,5,1.,103,5,-1.
                                GRID,1,0,0.,0.,0.,0,123456
MPC,100,23,6,1.,103,6,-1.
                                GRID,2,0,0.,1.,0.,0,2345
MPC,200,21,1,1.,102,1,-1.
                                GRID,3,0,0.,1.,0.,0,123456
                                CBAR,1,1,1,2,1.,0.,0.
MPC,200,21,2,1.,102,2,-1.
                                PBAR,1,41,1.,0.1,0.1,0.1
MPC, 200, 21, 3, 1., 102, 3, -1.
MPC,200,21,4,1.,102,4,-1.
                                 CGAP, 2, 2, 2, 3, 0., 1., 0., 0
MPC, 200, 21, 5, 1., 102, 5, -1.
                                PGAP, 2, 1., 0., 1.+6
MPC,200,21,6,1.,102,6,-1.
GRAV,100,0,386.4,0.,-1.,0.
                                FORCE, 200, 2, 0, -1., 1., 0., 0.
                                 ENDDATA
```

APPENDIX B.

```
NASTRAN REAL=0, HICORE=2000000, BUFFSIZE=9217, BUFFPOOL=0
                                                                                   $ H4 ALIGNMENT; P6,P4,H6,P3 ON HRMA
                                                                  SUBCASE 50
INIT DBALL, LOGICAL=(DB1(40000), DB2(40000))
                                                                     LABEL = 1G AXIAL, GSE SUPPORT - H4 ALIGN
                                                                     DISP(PRINT, PUNCH) = 24
ID STONE .MARK
                                                                     SPCF = 30
TIME 10000
                                                                     CLOAD = 1001
SOL 66
                                                                     SPC = 124
CEND
                                                                     MPC = 113
                                                                  SUBCASE 60
                                                                                   $ P1 ALIGNMENT; P6,P4,H6,P3,H4 ON HRMA
TITLE = AXAF HRMA-I MODEL
                                                                     LABEL = 1G AXIAL, GSE SUPPORT -- P1 ALIGN
SUBTITLE = NOMINAL TOWER CELL SUPPORT RESIDUAL
                                                                     DISP(PRINT, PUNCH) = 11
LABEL = MJS - 05/29/92; last rev. 06/12/92
                                                                     SPCF = 30
                                                                     CLOAD = 1002
SUPER=ALL
                                                                     SPC = 111
SEALL=ALL
                                                                     MPC = 124
NLPARM=100
LOADSET = 1000
                                                                                   $ H3 ALIGNMENT; P6,P4,H6,P3,H4,P1 ON HRMA
                                                                  SUBCASE 70
                                                                     LABEL = 1G AXIAL, GSE SUPPORT --- H3 ALIGN
ECHO = PUNCH
                                                                     DISP(PRINT, PUNCH) = 23
                                                                     SPCF = 30
SET 11 = 11000 THRU 11999,24000 THRU 24999,13000 THRU 13999,
                                                                     CLOAD = 1001
          26000 THRU 26999,14000 THRU 14999,16000 THRU 16999
                                                                     SPC = 123
SET 13 = 13000 THRU 13999,26000 THRU 26999,14000 THRU 14999,
          16000 THRU 16999
SET 14 = 14000 THRU 14999,16000 THRU 16999
SET 16 = 16000 THRU 16999
SET 21 = 21000 THRU 21999,23000 THRU 23999,11000 THRU 11999,
          24000 THRU 24999,13000 THRU 13999,26000 THRU 26999,
          14000 THRU 14999,16000 THRU 16999
SET 23 = 23000 THRU 23999,11000 THRU 11999,24000 THRU 24999,
          13000 THRU 13999,26000 THRU 26999,14000 THRU 14999,
          16000 THRU 16999
SET 24 = 24000 THRU 24999,13000 THRU 13999,26000 THRU 26999,
          14000 THRU 14999,16000 THRU 16999
SET 26 = 26000 THRU 26999,14000 THRU 14999,16000 THRU 16999
SET 30 = 1103,1115,1127,1139,1151,1163,1175,1801,1817,1833,1849,
          11021,11105,11189,11273,11357,11441,11525,
13021,13105,13189,13273,13357,13441,13525,
14021,14105,14189,14273,14357,14441,14525,
          16021,16105,16189,16273,16357,16441,16525,
          21021,21105,21189,21273,21357,21441,21525,
          23021,23105,23189,23273,23357,23441,23525,
          24021,24105,24189,24273,24357,24441,24525
          26021,26105,26189,26273,26357,26441,26525
                 $ P6 ALIGNMENT
                                                           SUBCASE 80
                                                                           $ H1 ALIGNMENT; P6, P4, H6, P3, H4, P1, H3 ON HRMA
   LABEL = 1G AXIAL, GSE SUPPORT - P6 ALIGN
                                                              LABEL = 1G AXIAL, GSE SUPPORT --- H1 ALIGN
   DISP(PRINT, PUNCH) = 16
                                                              DISP(PRINT, PUNCH) = 21
   SPCF = 30
                                                              SPCF = 30
   CLOAD = 1001
                                                              CLOAD = 1002
   SPC = 116
                                                              SPC = 121
   MPC = 100
                                                              MPC = 123
                 $ P4 ALIGNMENT: P6 ON HRMA
                                                           SUBCASE 90
                                                                            $ IN-TOWER HRMA: P6, P4, H6, P3, H4, P1, H3, H1
   LABEL = 1G AXIAL, GSE SUPPORT - P4 ALIGN
                                                              LABEL = 1G, IN-TOWER HRMA
   DISP(PRINT, PUNCH) = 14
                                                              DISP(PRINT, PUNCH) = 21
   SPCF = 30
                                                              SPCF = 30
   CLOAD = 1002
                                                              CIOAD = 1001
   SPC = 114
MPC = 116
                                                              SPC = 100
                                                              MPC = 121
SUBCASE 30
                 $ H6 ALIGNMENT; P6,P4 ON HRMA
                                                           SUBCASE 100
                                                                           $ ON-ORBIT RESIDUAL
   LABEL = 1G AXIAL, GSE SUPPORT - H6 ALIGN
                                                              LABEL = 0G, ON-ORBIT RESIDUAL
   DISP(PRINT, PUNCH) = 26
                                                              DISP(PRINT, PUNCH) = 21
   SPCF = 30
                                                              SPCF = 30
   CLOAD = 1001
                                                              CLOAD = 0
   SPC = 126
                                                              SPC = 200
   MPC = 114
                                                              MPC = 121
   BCASE 40 $ P3 ALIGNMENT; P6,P4,H6 ON HRMA
LABEL = 1G AXIAL, GSE SUPPORT — P3 ALIGN
SUBCASE 40
                                                           SUBCASE 200
                                                                           $ CYLFIT OLOAD
                                                              LABEL = 1# CYLFIT PRESSURE LOAD
   DISP(PRINT, PUNCH) = 13
                                                              OLOAD(PUNCH) = 21
   SPCF = 30
                                                              CLOAD = 1003
   CLOAD = 1002
                                                              SPC = 200
   SPC = 113
                                                              MPC = 121
   MPC = 126
ŝ
                                                           REGIN BULK
```

```
$ CAPA supports (SPC's)
                                                                   SPC1,20,23,1103,1115,1127,1139,1151,1163,+SPC
$ Parameters for analysis
                                                                    +SPC,1175
                                                                   SPC1,20,3,1801,1817,1833,1849
PARAM, POST, 0
PARAM, GRDPNT, 0
                                                                   SPC1,30,23,1103,1151
PARAM, K6ROT, 1
                                                                   $ Mirror supports (SPC's)
SPC1,11,3,11021,11105,11189,11273,11357,11441,+SPC11
PARAM, BAILOUT, -1
$ Included files for HRMA-I
                                                                   +SPC11,11525
INCLUDE 'cells/hrma-I/misc/seset-I.bulk'
                                                                   SPC1,13,3,13021,13105,13189,13273,13357,13441,+SPC13
INCLUDE 'cells/hrma-I/capa/cap-I.pch'
                                                                   +SPC13,13525
INCLUDE 'cells/hrma-I/capa/cap-fit-I.pch'
                                                                   SPC1,14,3,14021,14105,14189,14273,14357,14441,+SPC14
INCLUDE 'cells/hrma-I/misc/oshell-grep-I.pch'
                                                                   +SPC14,14525
INCLUDE 'cells/hrma-I/misc/oshell-cap-I.pch'
                                                                   SPC1,16,3,16021,16105,16189,16273,16357,16441,+SPC16
INCLUDE 'cells/hrma-I/misc/ishell-cap-c.pch'
                                                                   +SPC16,16525
INCLUDE 'cells/hrma-I/misc/pi-shell-c.pch'
                                                                   SPC1,21,3,21021,21105,21189,21273,21357,21441,+SPC21
INCLUDE 'cells/hrma-I/misc/hi-shell-c.pch'
                                                                   +SPC21.21525
INCLUDE 'cells/hrma-I/fitting/plfit-I-mod.pch'
                                                                   SPC1,23,3,23021,23105,23189,23273,23357,23441,+SPC23
INCLUDE 'cells/hrma-I/fitting/p3fit-I-mod.pch'
                                                                   +SPC23, 23525
INCLUDE 'cells/hrma-I/fitting/p4fit-I-mod.pch'
INCLUDE 'cells/hrma-I/fitting/p6fit-I-mod.pch'
                                                                   SPC1,24,3,24021,24105,24189,24273,24357,24441,+SPC24
                                                                   +SPC24,24525
INCLUDE 'cells/hrma-I/fitting/hlfit-I-mod.pch'
                                                                   SPC1,26,3,26021,26105,26189,26273,26357,26441,+SPC26
INCLUDE 'cells/hrma-I/fitting/h3fit-I-mod.pch'
                                                                   +SPC26,26525
INCLUDE 'cells/hrma-I/fitting/h4fit-I-mod.pch'
                                                                   SPC1,11,2,11021,11441
INCLUDE 'cells/hrma-I/fitting/h6fit-I-mod.pch'
                                                                   SPC1,13,2,13021,13441
INCLUDE 'cells/hrma-I/sleeve/plslv-I.pch'
                                                                   SPC1,14,2,14021,14441
INCLUDE 'cells/hrma-I/sleeve/p3slv-I.pch'
                                                                   SPC1,16,2,16021,16441
INCLUDE 'cells/hrma-I/sleeve/p4slv-I.pch'
                                                                   SPC1,21,2,21021,21441
INCLUDE 'cells/hrma-I/sleeve/p6slv-I.pch'
                                                                   SPC1,23,2,23021,23441
INCLUDE 'cells/hrma-I/sleeve/hlslv-I.pch'
                                                                   SPC1,24,2,24021,24441
INCLUDE 'cells/hrma-I/sleeve/h3slv-I.pch'
                                                                   SPC1,26,2,26021,26441
INCLUDE 'cells/hrma-I/sleeve/h4slv-I.pch'
INCLUDE 'cells/hrma-I/sleeve/h6slv-I.pch'
                                                                   $ Single-point constraint sets (SPC's)
INCLUDE 'cells/hrma-I/flexure/plflx-I.pch'
                                                                   SPCADD, 100, 10, 20
INCLUDE 'cells/hrma-I/flexure/p3flx-I.pch'
                                                                   SPCADD, 111, 10, 20, 11, 23, 21
INCLUDE 'cells/hrma-I/flexure/p4flx-I.pch'
                                                                   SPCADD,113,10,20,13,24,11,23,21
INCLUDE 'cells/hrma-I/flexure/p6flx-I.pch'
                                                                   SPCADD, 114, 10, 20, 14, 26, 13, 24, 11, +SPC114
INCLUDE 'cells/hrma-I/flexure/hlflx-I.pch'
                                                                   +SPC114,23,21
INCLUDE 'cells/hrma-I/flexure/h3flx-I.pch'
                                                                   SPCADD,116,10,20,16,14,26,13,24,+SPC116
INCLUDE 'cells/hrma-I/flexure/h4flx-I.pch'
                                                                   +SPC116,11,23,21
SPCADD,121,10,20,21
INCLUDE 'cells/hrma-I/flexure/h6flx-I.pch'
INCLUDE 'cells/ra/mirror/plmirror-dbl-rbe.pch'
                                                                   SPCADD,123,10,20,23,21
INCLUDE 'cells/ra/mirror/p3mirror-dbl-rbe.pch'
                                                                   SPCADD, 124, 10, 20, 24, 11, 23, 21
INCLUDE 'cells/ra/mirror/p4mirror-dbl-rbe.pch'
                                                                   SPCADD, 126, 10, 20, 26, 13, 24, 11, 23, +SPC126
INCLUDE 'cells/ra/mirror/p6mirror-dbl-rbe.pch'
                                                                   +SPC126,21
INCLUDE 'cells/ra/mirror/h1mirror-dbl-rbe.pch'
                                                                   SPCADD, 200, 10, 30
INCLUDE 'cells/ra/mirror/h3mirror-dbl-rbe.pch'
INCLUDE 'cells/ra/mirror/h4mirror-dbl-rbe.pch'
                                                                   $ Multi-point constraint sets
INCLUDE 'cells/ra/mirror/h6mirror-dbl-rbe.pch'
                                                                   MPCADD, 100, 71, 73, 74, 76, 81, 83, 84, +MPC100
INCLUDE 'cells/props/flex-props-0131.bulk
                                                                   +MPC100,86
INCLUDE 'cells/props/material-0602.bulk'
                                                                   MPCADD, 111, 71, 73, 74, 76, 81, 83, 84, +MPC111
                                                                   +MPC111,86,36,34,46,33,44,31
MPCADD,113,71,73,74,76,81,83,84,+MPC113
$ Load Combinations (for nonlinear superelement analysis)
CLOAD, 1001, 1., 1., 2, 0., 3
                                                                   +MPC113,86,36,34,46,33
CLOAD, 1002, 1., 1., 2, 1., 3
                                                                   MPCADD, 114, 71, 73, 74, 76, 81, 83, 84, +MPC114
CLOAD,1003,1.,1.,1
                                                                   +MPC114,86,36,34
LSEQ,1000,1,10
                                                                   MPCADD, 116, 71, 73, 74, 76, 81, 83, 84, +MPC116
LSEQ,1000,2,20
                                                                   +MPC116,86,36
LSEQ,1000,3,30
                                                                   MPCADD, 121, 71, 73, 74, 76, 81, 83, 84, +MPC121
                                                                   +MPC121,86,36,34,46,33,44,31,43,+MPC121B
$ Axial Gravity Load (1g)
                                                                   +MPC121B.41
GRAV,20,0,386.4,1.,0.,0.
                                                                   MPCADD, 123, 71, 73, 74, 76, 81, 83, 84, +MPC123
$ Load for nonlinear element
                                                                   +MPC123,86,36,34,46,33,44,31,43
MPCADD,124,71,73,74,76,81,83,84,+MPC124
FORCE, 30, 2, 0, -1., 1., 0., 0.
$ Cylfit Oloads (1#)
                                                                   +MPC124,86,36,34,46,33,44
PLOAD4,10,11001,1.,,,THRU,11480,+PLP1
                                                                   MPCADD, 126, 71, 73, 74, 76, 81, 83, 84, +MPC126
+PLP1,1100,1.,0.,0.
                                                                   +MPC126,86,36,34,46
PLOAD4,10,13001,1.,,,THRU,13480,+PLP3
+PLP3,1300,1.,0.,0.
                                                                   $ Nonlinear structure & parameter
PLOAD4,10,14001,1.,,,THRU,14480,+PLP4
                                                                   NLPARM, 100, 1
+PLP4,1400,1.,0.,0.
                                                                   GRID,1,0,0.,0.,0.,0,123456
PLOAD4,10,16001,1.,,,THRU,16480,+PLP6
                                                                   GRID,2,0,0.,1.,0.,0,2345
GRID,3,0,0.,1.,0.,0,123456
+PLP6,1600,1.,0.,0.
PLOAD4,10,21001,1.,,,THRU,21480,+PLH1
                                                                   CBAR, 1, 1, 1, 2, 1., 0., 0.
+PIH1,2100,1.,0.,0.
                                                                   PBAR,1,101,1.,0.1,0.1,0.1
PLOAD4,10,23001,1.,,,THRU,23480,+PLH3
                                                                   CGAP, 2, 2, 2, 3, 0., 1., 0., 0
+PLH3,2300,1.,0.,0.
                                                                   PGAP, 2, 1., 0., 1.+6
PLOAD4,10,24001,1.,,,THRU,24480,+PLH4
+PLH4,2400,1.,0.,0.
PLOAD4,10,26001,1.,,,THRU,26480,+PLH6
                                                                   ENDDATE
+PLH6,2600,1.,0.,0.
```