CONF-8709192--3

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DE88 002941

A TECHNIQUE FOR COMPUTING BOWING REACTIVITY FEEDBACK IN LMFBR'S

by

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*Work supported by the U.S. Department of Energy, Nuclear Energy Programs under Contract W-31-109-ENG-38.

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A TECHNIQUE FOR COMPUTING BOWING REACTIVITY FEEDBACK IN LMFBR'S

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During normal or accidental transients occurring in a LMFBR core, the assemblies and their support structure are subjected to important thermal gradients which induce differential thermal expansions of the walls of the hexcans and differential displacement of the assembly support structure.

These displacements, combined with the creep and swelling of structural materials, remain quite small, but the resulting reactivity changes constitute a significant component of the reactivity feedback coefficients used in safety analyses[1].It would be prohibitive to compute the reactivity changes due to all transients. Thus, the usual practice is to generate reactivity gradient tables.

The purpose of the work presented here is twofold:

1. develop and validate an efficient and accurate scheme for computing these reactivity tables
2. qualify this scheme

Development and Validation

The method used in prior work within the U. S. is conceptually simple[1]:

- each assembly is assumed to consist of a homogenized duct (hexcan, pins, sodium) and an interassembly gap.
- for neutronics purposes, each assembly is divided into six triangular meshes. The smeared number densities in each mesh are obtained from a standard volume weighting procedure, first for the non-moved and then for the moved cases.
- the worth of each assembly motion is obtained from a specific eigenvalue difference calculation.

This requires many eigenvalue calculations (one for each assembly and each direction), thus making this process lengthy and expensive. Furthermore, we contend that this method is systematically biased.

To make that point, let us consider a 1D unit cell of thickness 2ℓ, consisting of a homogenized duct surrounded by a thin sodium gap of thickness 2e. The duct within the unit cell is displaced by $\varepsilon(\varepsilon \ll e)$.

The first order term of the perturbation corresponding to event α (capture, fission, scattering...) is:

$$\left(\Sigma_\alpha^{Duct} - \Sigma_\alpha^{Na}\right)\left[\psi(\ell-e)\psi^*(\ell-e) - \psi(e-\ell)\psi^*(e-\ell)\right]\varepsilon$$

For the homogenization technique, using 2 meshes per unit cell, this perturbation becomes:

$$\left(\Sigma_\alpha^{Duct} - \Sigma_\alpha^{Na}\right) \quad \frac{\varepsilon}{\ell}\left[\int_0^{\ell} \psi\psi^*(x)dx - \int_{-\ell}^{0} \psi\psi^*(x)dx\right]$$

When assuming that the flux and adjoint are linear functions of x, the ratio of homogenized to explicit perturbations becomes $\ell/2(\ell-e)$. Similarly, for hexagonal geometries, this ratio is $2\ell/3(\ell-e)$.

This ratio indicates the origin of the systematic error in the homogenization scheme: whereas the actual perturbation displaces some mass from the left duct edge (at $e-\ell$) to the right duct edge (at $\ell-e$), the homogenized scheme, by spreading this mass evenly over each mesh, displaces it from the center of mass of the left mesh (at $-\frac{\ell}{2}$ or $-\frac{2}{3}\ell$ for square and hexagonal geometries) to the symmetric position: the homogenized scheme does not conserve mass displacements.

Consequently, it is proposed that the results of the homogenization scheme be multiplied by a Systematic Correction Factor equal to the ratio of the mass displacements; this new scheme (the Corrected Triangular Homogenization Scheme = CTHS) was implemented in the RHOBOW computer code.

It is not clear whether existing schemes[2] which attempt to account for this bias (using R-Z results) would be accurate for azimuthally asymmetric cores such as the radially heterogeneous cases currently being developed for advanced LMR designs[3,4,5].

CTHS was validated against a series of explicit geometry benchmarks in 2D and 3D, transport and diffusion theory, with explicit representation of sodium gaps. Results are indicated in Table 1.

The worths predicted by CTHS are within 12% of the benchmark value for driver assembly motions. This is an important improvement over the accuracy of the standard method (error up to 50%). For blanket assemblies, the CTHS worths are in error by as much as 44%. Nevertheless, it should be noted that these assemblies have a small worth and a highly non-linear behavior. For global core motions, linearity and additivity are verified within a few percentage points: this confirms the validity of the use of reactivity gradients tables.

Qualification

Experimental results are not yet available. Nevertheless some of the assumptions made in the benchmarks used for the validation of CTHS have been investigated by comparison with more accurate schemes. Results are the following:

- geometrical effects: the use of a homogenized duct region instead of a pin by pin representation introduces errors of 6% or less
- group structure effects: the use of a few group structure introduces errors of 3% or less
- transport vs. diffusion (excluding streaming): the use of diffusion theory instead of higher order Sn calculations introduces errors up to 16% for very severe benchmarks.
- streaming effects: for a realistic core, neutron streaming in the sodium between the fuel pins has a very small influence on individual assembly motion worths (less than 1%). Inter assembly gap streaming was given special consideration: this gap is a privileged streaming path [6] and a small core radial expansion can result in a large gap thickness increase. By making use of Monte

Carlo generated Benoist D's, it was shown that the increase of neutron streaming in that gap contributes 5 to 10% of the total reactivity worth during a uniform expansion or free flowering.

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Table 1. Results for Assemblies Motions.

Benchmark	Motion	Neutronics Formalism	Worth	Non-linearity[4]	Additivity[7]	Perturbation Formulation	THS[5] Error	CTHS[6] Error
TFM2[8]	U.M.[1] Driver Only	Transport S4	3.743E-3	--	--	Exact	-47%	2.5%
DFM3[9]	U.M.[1] Driver Only	Diffusion	5.735E-3	1.7%	--	F.O.P.	-50%	-3.1%
PAFR[10]	U.E.[2]	Diffusion	4.648E-3	7.4%	3%	F.O.P.	-20%	7.9%
PAFR	Singular[3]	Diffusion	6.029E-4	1.7%	--	F.O.P.	-17%	12.0%
PRISME[11]	U.E.[2]	Diffusion	6.000E-3	3.5%	--	F.O.P.	-29%	-4.3%
PRISME	U.M.[1] Driver Only	Diffusion	5.640E-3	2.5%	--	F.O.P.	-28%	-3.1%
PRISME	U.M.[2] Blanket Only	Diffusion	7.372E-4	46.1%	--	F.O.P.	-59%	-44.4%

Notes:

[1] U.M. = uniform movement of all assemblies

[2] U.E. = uniform expansion

[3] All drivers were moved one by one. The values indicated correspond to the case with the highest errors for CTHS.

[4] The non-linearity of a perturbation is the half-width of the worth interval obtained when computing a perturbation and its opposite.

[5] THS = Triangular Homogenization Scheme

[6] CTHS = Corrected Triangular Homogenization Scheme

[7] The additivity of a benchmark is the difference between a global core perturbation and the sum of each single assembly perturbation.

[8] TFM2 is a 2D transport theory benchmark, with square assemblies. It comprises an inner ring of moving driver assemblies, surrounded by rings of blanket and reflector material (see Figure 2).

[9] DFM3 is a 3D diffusion benchmark: it is a vertical extension of TFM2, with added axial reflectors (see Figure 2).

[10] PAFR is a 2D diffusion benchmark with 6 rings of moving driver and blanket assemblies (see Figure 3).

[11] PRISME is a 2D diffusion benchmark, typical of current LMFBR designs (see Figure 4).

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