ASEN 5331 - HW4

James Wright

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0.1 Meaning of `n...`

Term	Definition	Source/Relevant Reference
`nsd`	number of spacial dimensions	`common/common.h#343`
`nflow`	number of flow variables (ie. size of $\boldsymbol{Y}$)	?
`nshape`	number of interior element shape functions	`common/common.h#444`
`ngauss`	number of interior element integration points	`common/common.h#447`
`npro`	number of elements processed in a single call of `e3.f`	Jansen lecture
`npro`	number of virtual processors for the current block	`common/common/h#586`
`nen`	maximum number of element nodes	`common/common.h#341`
`nQpt`	number of quadrature points per element	`common/shp4t.f#14`
`nshl`	number of shape functions per element	`common/genblkPosix.f#70`
`nshg`	global number of shape functions	`common/common.h#354`
`nenl`	number of element nodes for current block	`common/common.h#382`
`nedof`	total number of degrees of freedom	`common/e3.f#35,344`

1 Essential Boundary Conditions

1.1 Setting BC Values

In `compressible/itrbc.f`
$\boldsymbol{Y} =$ `y`
$g(x) =$ `BC` on a per node basis

The essential boundary conditions are set in `/compressible/itrbc.f#59-198`. The `iBC` variable contains bit-wise information on what specific boundary conditions are going to be set. `BC` contains the BC data ($g(x)$ in the notes) for each individual node. `iBC` is set in `common/genibc.f` and `BC` is set in `common/genbc.f`, which takes `iBC` as an input.

Essentially, the code checks `iBC` for which values of $\boldsymbol{Y}$ should be set. This logical check is done via the `ibits()` function. If a given $\boldsymbol{Y}$ chosen, then $\boldsymbol{Y}$ is set to the corresponding value in `BC`.

So `common/gendat.f->gendat()` calls `common/genibc.f->geniBC()` to create the `iBC` vector. `common/gendat.f` then calls `common/genbc.f->genBC()` to create the `BC` vector which contains the values that should then be substituted into the `y` array in `compressible/itrbc.f`.

1.2 Applying $\boldsymbol{S}$ Matrices

The application of the $\boldsymbol{S}$ matrices applied in two different locations: `compressible/b3res.f` and `compressible/b3lhs.f`, which apply $\boldsymbol{S}$ to the residual (`res`, RHS) and mass matrix (`EGMass`, LHS) respectively.

For the residual, the values of `res` are replaced based on the logical output from the same `ibits()` operation on `iBC` as before, similar to when `BC` values were set in `common/genbc.f->genBC()`. This process occurs in `compressible/b3res.f#28-163`.

Applying $\boldsymbol{S}$ on the LHS operates in a nearly identical way.