

Overview of the Eirene versions

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Branches

- master
- develop
- hlst_openmp
- develop_nhorst_Wbundling
- forks/iter/branches

forks/iter/master
forks/iter/develop
forks/iter/BGK_bugfix
forks/iter/suggested_changes
forks/iter/ADAS_bundled_files
forks/iter/fort.13-14-15_safeties
forks/iter/safe_develop
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forks/iter/istream_in_parmmod
forks/iter/species_rescaling
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Overview of the Eirene versions today (Nov. 2022)

Branches

- master
- develop
- hlst_openmp
- develop_nhorst_Wbundling
- forks/iter/branches
- compiling_issues_JSON8.2.5_gfortran
- SOLEDGE3X_changes
- eirene_unified

forks/iter/master
forks/iter/develop
forks/iter/BGK_bugfix
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forks/iter/species_rescaling_DR3
forks/iter/species_rescaling_dr3_PB_AMU
forks/iter/master
forks/iter/develop

A short look onto the new branches

- › forks/iter/species_rescaling_dr3_PB_AMU
effort to remove SOLPS-ITER specific coding from main code
- › forks/iter/master
Eirene master from SOLPS-ITER version 3.0.8
- › forks/iter/develop
New developments in SOLPS-ITER since release of version 3.0.8
- › compiling_issues_JSON8.2.5_gfortran
string type issues fixed at AMU
- › SOLEDGE3X_changes
Small correction to EIRENE_SHEATH

Eirene_unified

Started from branches “eirene_develop” combined with “hlst_openmp”

All forks/iter branches up to “species_rescaling_dr3_PB_AMU” have been incorporated.

All SOLPS-ITER specific coding has been shifted into interface or user specific routines.

Some SOLPS-ITER specific parts have become part of the main code:

- Subroutine EIRENE_INIT_EION has been moved from EIRMOD_EXTRAB25 into the main code as EION is need to calculate the radiation tallies.
- Arrays LKINDI, LKINDP, LKINDM have been moved from EIRMOD_EXTRAB25 into EIRMOD_COMUSR as these arrays are read in block 4 of the Eirene input.
- The parallelization schemes introduced by T.Feher into SOLPS-ITER are available for all cases now (still need testing)

Eirene_unified continued

The species specific rescaling option has been implemented
- but differently from what had been done in SOLPS-ITER

The option can be switched on and off using NLSPCSCL read in input block 1.

In the original implementation additional arrays were introduced for the species resolved tallies.

In current implementation the original tallies are expanded when NLSPCSCL=T

Example: tally PMAT (part. source from molecules to atoms)

Originally:

```
real :: pmat(natm,nrad)
```

Scoring:

```
pmat(iatm,icell) = ....
```

SOLPS-ITER:

```
real :: pmat(natm,nrad)
```

```
real :: pmat2(natm,nmol,nrad)
```

Scoring:

```
pmat(iatm,icell) = ....
```

```
pmat2(iatm,imol,icell) = ....
```

Eirene_unified:

```
real :: pmat(natm,nrad)
```

```
if NLSPCSCL = F
```

```
real :: pmat(natm*(nmol+1),nrad)
```

```
if NLSPCSCL = T
```

```
real, pointer :: PMAT2(:,:)
```

Scoring

Either:

```
pmat (iatm,icell) = ...
```

```
iad = eirene_indirect_address(iatm,imol,natm)
```

```
pmat (iad,icell) = ...
```

Or:

```
pmat (iatm,icell) = ...
```

```
pmat2 (1:natm,0:nmol) => pmat(:,icell)
```

```
pmat2 (iatm,imol) = ...
```

At the moment the species specific scaling is being tested.

The new branches will be merged into Eirene_unified next. The aim is to incorporate the branches until beginning of 2023.

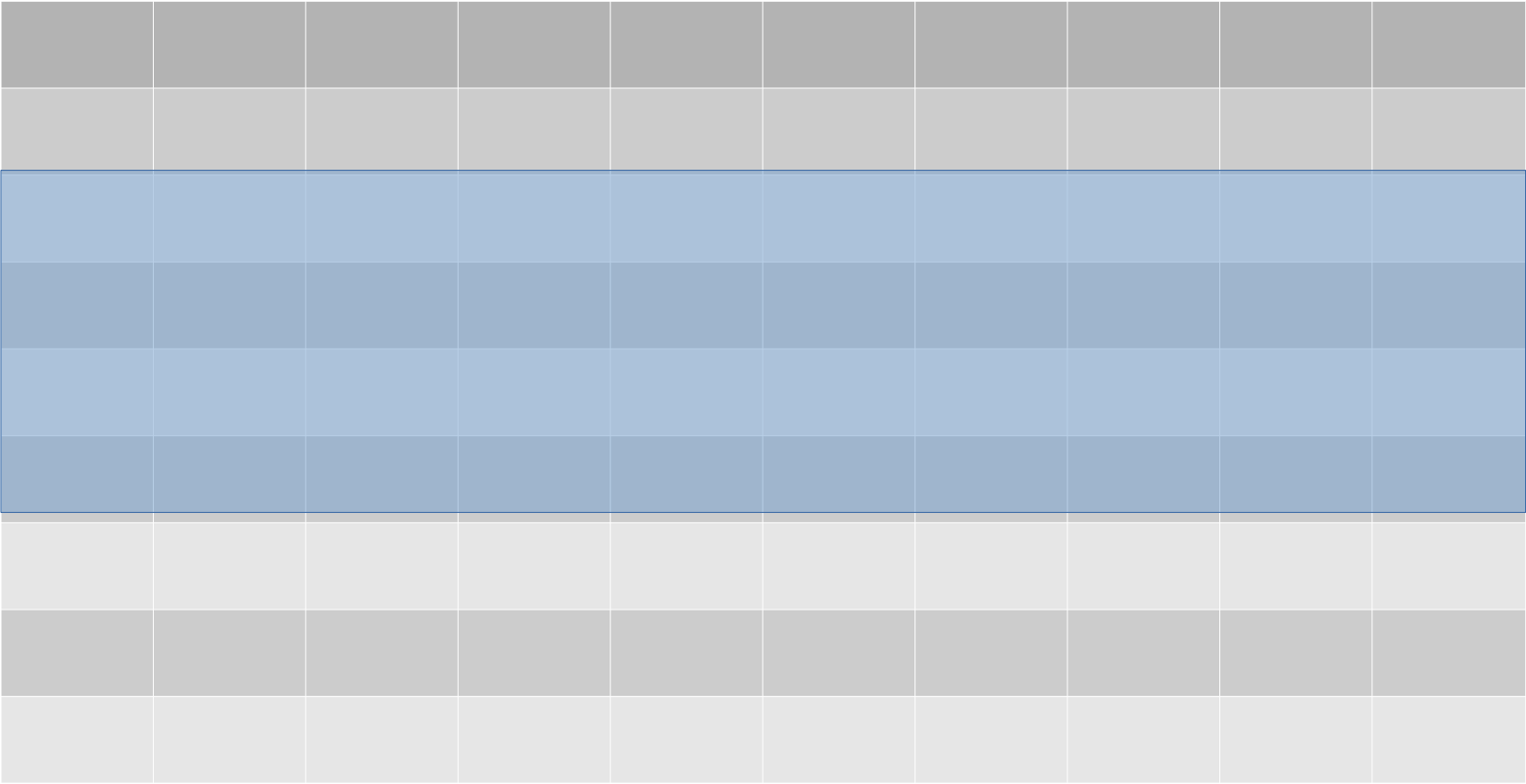
Up to now test are only carried out without parallelization.

Tests for use of MPI and OpenMP need to be done.

I would like to do tests putting Eirene_unified into SOLPS-ITER and run cases against the latest version of SOLPS-ITER.

Tally matrix ESTIMV(NVOLTL,NRAD)

PMAT



Tally index

Cell index