ONERA
THE FRENCH AEROSPACE LAB

Distributor2 Documentation

Release 3.2

/ELSA/MU-12016/V3.2

Feb 09, 2021

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ONE

PREAMBLE

This module provides functions to distribute blocks on a given number of processors. At the end of the process, each block will have a number corresponding to the processor it must be affected to for a balanced computation, depending on given criterias. This module doesn't perform splitting (see the Transform module for that).

This module is part of Cassiopee, a free open-source pre- and post-processor for CFD simulations.

For use with the array interface, you have to import Distributor2 module:

```python
import Distributor2 as D2
```

For use with the pyTree interface:

```python
import Distributor2.PyTree as D2
```

TWO

LIST OF FUNCTIONS

– Automatic load balance

`Distributor2.distribute`(arrays, NProc[, ...])	Distribute zones over NProc processors.
`Distributor2.PyTree.distribute`(t, NProc[, ...])	Distribute a pyTree over processors.

– Various operations

`Distributor2.PyTree.addProcNode`(t, proc)	Add a "proc" node to zones with the given proc value.
`Distributor2.PyTree.getProc`(t)	Return the value of proc node.
`Distributor2.PyTree.getProcDict`(t[, ...])	Return the proc of a zone in a dictionary proc['zoneName'].
`Distributor2.PyTree.getProcList`(t[, NProc, sort])	Return the list of zones for each proc.
`Distributor2.PyTree.copyDistribution`(a, b)	Copy distribution of a in b.
`Distributor2.PyTree.printProcStats`(t[, ...])	Print stats dictionary.
`Distributor2.Mpi.redispatch`(t[, graph])	Redistribute tree from graph.

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Distributor2.**distribute**(*A, NProc, prescribed=[], perfo=[], weight=[], com=[],*
algorithm='graph', mode='nodes', nghost=0)
Distribute automatically the blocks amongst NProc processors.

- prescribed is a list of blocks that are forced to be on a given processor.

For instance, prescribed[2] = 0 means that block 2 MUST be affected to processor 0.

- perfo is a tuple or a tuple list for each processor.

Each tuple describes the relative weight of solver CPU time regarding the communication speed and latence (solverWeight, latenceWeight, comSpeedWeight).

- weight is a list of weight for each block indicating the relative cost for solving each block.
- com is a ixj matrix describing the volume of points exchanged between bloc i and bloc j.
- algorithm can be chosen in: 'gradient', 'genetic', 'fast', 'graph'
- mode='node', 'cells': optimize distribution of block considering node (cells) numbers.
- nghost: take into account ghost cells (only for structured grids)

    Parameters

    - **a** (`[array, list of arrays]`) – Input data
    - **N** (`int`) – number of processors
    - **prescribed** (`list of ints`) – list of prescribed blocks
    - **perfo** (`list of tuples`) – list of performance for each processor
    - **weight** (`list of ints`) – list of weight for each block
    - **algorithm** (`string`) – ['gradient', 'genetic', 'fast', 'graph']
    - **nghost** (`int`) – number of ghost cells present in the mesh

The function output is a stats dictionary. stat['distrib'] is a vector describing the attributed processor for each block, stats['meanPtsPerProc'] is the mean number of points per proc, stats['varMin'] is the minimum variation of number of points, stats['varMax'] is the maximum variation of number of points, stats['varRMS'] is the mean variation of number of points, stats['nptsCom'] is the number of points exchanged between processors for communication, stats['comRatio'] is the ratio between the number of points exchanged between processors in this configuration divided by the total number of matching/overlap boundary points, stats['adaptation'] is the value of the optimized function.

Example of use:

- Distribute arrays (array):

```
# - distribute (array) -
import Generator as G
import Distributor2 as D2
import numpy

# Distribution sans communication entre blocs
N = 11
arrays = []
for i in range(N):
    a = G.cart( (0,0,0), (1,1,1), (10+i, 10, 10) )
    arrays.append(a)
out = D2.distribute(arrays, NProc=5); print(out)

# Distribution avec des perfos differentes pour chaque proc
out = D2.distribute(arrays, NProc=3, perfo=[(1,0,0), (1.2,0,0), (0.2,0,0)]);␣
↪print(out)

# Distribution avec forcage du bloc 0 sur le proc 1, du bloc 2 sur le proc 3
# -1 signifie que le bloc est a equilibrer
prescribed = [-1 for x in range(N)]
prescribed[0] = 1; prescribed[2] = 3
out = D2.distribute(arrays, NProc=5, prescribed=prescribed); print(out)

# Distribution avec communications entre blocs, perfos identique pour tous
# les procs
volCom = numpy.zeros( (N, N), numpy.int32 )
volCom[0,1] = 100; # Le bloc 0 echange 100 pts avec le bloc 1
out = D2.distribute(arrays, NProc=5, com=volCom, perfo=(1,0.,0.1)); print(out)

# Distribution avec des solveurs differents pour les blocs (le solveur est 2
# fois plus couteux pour les bloc 2 et 4)
out = D2.distribute(arrays, weight=[1,2,1,2,1,1,1,1,1,1,1], NProc=3); print(out)
```

Distributor2.PyTree.**distribute**(*A, NProc, prescribed={}, perfo=[], weight=[], useCom='match', algorithm='graph', mode='nodes', nghost=0*)

Distribute automatically the blocks amongst NProc processors.

With the pyTree interface, the user-defined node .Solver#Param/proc is updated with the attributed processor number.

If useCom=0, only the grid number of points is taken into account. If useCom='match', only match connectivities are taken into account. if useCom='overlap', only overlap connectivities are taken into account. if useCom='bbox', overlap between zone bbox is taken into account. if useCom='ID', ID (interpolation or match) and IBCD (IBM points) are taken into account. If useCom='all', matching and overlap communications are taken into account.

When using distributed trees, prescribed must be a dictionary containing the zones names as key, and the prescribed proc as value. weight is also a dictionary where the keys are the zone names and the weight as the value. It is not mandatory to assign a weight to all the zones of the pyTree. Default value is assumed to be 1, only different weight values can be assigned to zones. t can be either a skeleton or a loaded skeleton pyTree for useCom=0 or useCom='match', but must be a loaded skeleton tree only for the other settings.

> **Parameters**
>
> - **a** ([pyTree, base, zone, list of zones]) – Input data
>
> - **N** (int) – number of processors
>
> - **prescribed** (dictionary) – dictionary of prescribed block (optional)
>
> - **perfo** (list of tuples) – list of perfo for each processor (optional)
>
> - **weight** (dictionary) – dictionary of weights for block (optional)
>
> - **useCom** (['0', 'all', 'match', 'overlap', 'bbox', 'ID']) – tell what to use to measure communication volumes
>
> - **algorithm** (string) – ['gradient', 'genetic', 'fast', 'graph']
>
> - **nghost** (int) – number of ghost cells present in the mesh

Example of use:

- Distribute zones (pyTree):

```
# - distribute (pyTree) -
import Generator.PyTree as G
import Distributor2.PyTree as D2
import Converter.PyTree as C
```

```
import Connector.PyTree as X

N = 11
t = C.newPyTree(['Base'])
pos = 0
for i in range(N):
    a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
    pos += 10 + i - 1
    t[2][1][2].append(a)
t = X.connectMatch(t)

# Distribute on 3 processors
t, stats = D2.distribute(t, 3)
C.convertPyTree2File(t, 'out.cgns')
```

3.1 Various operations

Distributor2.PyTree.**addProcNode**(*a*, *NProc*)

Add a "proc" node to all zones of a with given value. Exists also as in place version (_addProcNode) that modifies a and returns None.

> **Parameters**
>
> > - **a** ([pyTree, base, zone, list of zones]) – input data
> > - **NProc** (int) – proc to be set
>
> **Returns** reference copy of a
>
> **Return type** identical to input

Example of use:

> - Add a proc node (pyTree):

```
# - addProcNode (pyTree) -
import Converter.PyTree as C
import Generator.PyTree as G
import Distributor2.PyTree as D2

a = G.cart((0,0,0), (1,1,1), (10,10,10))
a = D2.addProcNode(a, 12)
C.convertPyTree2File(a, 'out.cgns')
```

Distributor2.PyTree.**getProc**(*a*)

> Return the proc value of a zone or a list of zones.
>
> > **Parameters a** ([pyTree, base, zone, list of zones]) – input data
> >
> > **Returns** the affected proc of zone
> >
> > **Return type** int or list of ints (for multiple zones)
>
> *Example of use:*
>
> - Get proc of a zone (pyTree):

```
# - getProc (pyTree) -
import Generator.PyTree as G
import Distributor2.PyTree as D2

a = G.cart((0,0,0), (1,1,1), (10,10,10))
a = D2.addProcNode(a, 12)
proc = D2.getProc(a); print(proc)
#>> 12
```

Distributor2.PyTree.**getProcDict**(*a*, *prefixByBase=False*)

> Return a dictionary where procDict['zoneName'] is the no of proc affected to zone 'zoneName'.
>
> > **Parameters**
> >
> > - **a** ([pyTree, base, zone, list of zones]) – input data
> >
> > - **prefixByBase** (boolean) – if true, add base prefix to zone name
> >
> > **Returns** the dictionary of zone/proc.
> >
> > **Return type** dictionary
>
> *Example of use:*
>
> - Return the dictionary of zones/proc (pyTree):

```
# - getProcDict (pyTree) -
import Generator.PyTree as G
import Distributor2.PyTree as D2
import Converter.PyTree as C
import Connector.PyTree as X

N = 11
t = C.newPyTree(['Base'])
pos = 0
for i in range(N):
```

```
        a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
        pos += 10 + i - 1
        t[2][1][2].append(a)

t = X.connectMatch(t)
t, stats = D2.distribute(t, 3)

proc = D2.getProcDict(t)
zoneNames = C.getZoneNames(t, prefixByBase=False)
for z in zoneNames: print(z, proc[z])

# - or with base prefix -
proc = D2.getProcDict(t, prefixByBase=True)
zoneNames = C.getZoneNames(t, prefixByBase=True)
for z in zoneNames: print(z, proc[z])
```

Distributor2.PyTree.**getProcList**(*a*, *NProc=None*)

> Return procList where procList[proc] is a list of zone names attributed to the proc processor.

>> **Parameters a** ([pyTree, base, zone, list of zones]) – input data

>> **Returns** the affected proc of zone

>> **Return type** int or list of ints

> *Example of use:*

> - Return the list of zones affected to a proc (pyTree):

```
# - getProcList (pyTree) -
import Generator.PyTree as G
import Distributor2.PyTree as D2
import Converter.PyTree as C
import Connector.PyTree as X

N = 11
t = C.newPyTree(['Base'])
pos = 0
for i in range(N):
    a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
    pos += 10 + i - 1
    t[2][1][2].append(a)

t = X.connectMatch(t)
t, stats = D2.distribute(t, 3)
```

```
procList = D2.getProcList(t)
print(procList)
```

Distributor2.PyTree.**copyDistribution**(a, b)

> Copy the distribution from b to a matching zones by their name. Exists also as in place version (_copyDistribution) that modifies a and returns None.

> > **Parameters**
> >
> > - **a** ([pyTree, base, zone, list of zones]) – input data
> >
> > - **b** ([pyTree, base, zone, list of zones]) – original data
> >
> > **Returns** modifie reference copy of a
> >
> > **Return type** same as input data

> *Example of use:*

> - Copy proc distribution from one tree to another (pyTree):

```python
# - copyDistribution (pyTree) -
import Converter.PyTree as C
import Distributor2.PyTree as D2
import Generator.PyTree as G

# Case
N = 11
t = C.newPyTree(['Base'])
pos = 0
for i in range(N):
    a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
    a[0] = 'cart%d'%i
    pos += 10 + i - 1
    D2._addProcNode(a, i)
    t[2][1][2].append(a)

t2 = C.newPyTree(['Base'])
for i in range(N):
    a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
    a[0] = 'cart%d'%i
    pos += 10 + i - 1
    t2[2][1][2].append(a)
t2 = D2.copyDistribution(t2, t)
C.convertPyTree2File(t2, 'out.cgns')
```

Distributor2.Mpi.**redispatch**(*a*)

> Redispatch a tree where a new distribution is defined in the node 'proc'.

>> **Parameters a** ([pyTree, base, zone, list of zones]) – input data

>> **Returns** modifie reference copy of a

>> **Return type** same as input data

> *Example of use:*

>> • Redispatch a tree (pyTree):

```python
# - redispatch (pyTree) -
import Converter.PyTree as C
import Distributor2.PyTree as D2
import Distributor2.Mpi as D2mpi
import Converter.Mpi as Cmpi
import Connector.PyTree as X
import Converter.Internal as Internal
import Generator.PyTree as G

# Case
N = 11
t = C.newPyTree(['Base'])
pos = 0
for i in range(N):
    a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
    pos += 10 + i - 1
    t[2][1][2].append(a)
t = X.connectMatch(t)
if Cmpi.rank == 0: C.convertPyTree2File(t, 'in.cgns')
Cmpi.barrier()

# lecture du squelette
a = Cmpi.convertFile2SkeletonTree('in.cgns')

# equilibrage 1
(a, dic) = D2.distribute(a, NProc=Cmpi.size, algorithm='fast', useCom=0)

# load des zones locales dans le squelette
a = Cmpi.readZones(a, 'in.cgns', rank=Cmpi.rank)

# equilibrage 2 (a partir d'un squelette charge)
(a, dic) = D2.distribute(a, NProc=Cmpi.size, algorithm='gradient1',
                         useCom='match')

a = D2mpi.redispatch(a)
```

```python
# force toutes les zones sur 0
zones = Internal.getNodesFromType(a, 'Zone_t')
for z in zones:
    nodes = Internal.getNodesFromName(z, 'proc')
    Internal.setValue(nodes[0], 0)

a = D2mpi.redispatch(a)

# Reconstruit l'arbre complet a l'ecriture
Cmpi.convertPyTree2File(a, 'out.cgns')
```

Distributor2.PyTree.**printProcStats**(*a*, *stats=None*, *NProc=None*)
    Print statistics for each processor: number of points and list of zones names.

> **Parameters**
>
> - **a** ([pyTree, base, zone, list of zones]) – input data
>
> - **stats** (Python dictionary) – dictionary obtained from Distributor2.distribute
>
> - **NProc** (integer) – number of processors
>
> **Returns** None

Example of use:

- Print procs statistics after distribution of a tree (pyTree):

```python
# - printProcStats (pyTree) -
import Generator.PyTree as G
import Distributor2.PyTree as D2
import Converter.PyTree as C
import Connector.PyTree as X

N = 11
t = C.newPyTree(['Base'])
pos = 0
for i in range(N):
    a = G.cart((pos,0,0), (1,1,1), (10+i, 10, 10))
    pos += 10 + i - 1
    t[2][1][2].append(a)
t = X.connectMatch(t)

# Distribute on 3 processors
t, stats = D2.distribute(t, 3)
```

```
# With stats and NProc
D2.printProcStats(t, stats, NProc=3)
# NProc is guessed from stats
D2.printProcStats(t, stats)
# All are guessed from t
D2.printProcStats(t)

C.convertPyTree2File(t, 'out.cgns')
```

Note: new in version 2.7.

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