



MEDCOUPLING Projection methods

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Outline

Agenda

Interpolation, extrapolation or projection?

Spatial Discretization & Nature Of A Field

Functionalities





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What MEDCoupling can do for you

Parallelism in MEDCoupling

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Illustration

Code coupling

Introduction: A typical use case: code coupling

- Different numerical codes simulate different physics
 - And hence (might) use different numerical schemes
 - E.g. temperature computed on nodes in code A and on elements in code B
 - And/or different spatial discretization (i.e. different meshing of the same geometrical domain)
 - A cylinder meshed with hexahedrons in code A, and with tetrahedrons in code B
 - Or even worse, use different dimensions
 - A heat flux on a 2D surface for code A and a 3D source term (e.g. fuel rode) for code B
- How do you “transfer” information from one to the other?
 - I need to provide code B with the temperature computed by code A
 - Solution A: ad-hoc solution. For each pair (code A, code B), write a mapper ... good luck
 - Solution B: use generic projection methods thanks to MEDCoupling



Projection, Interpolation?

- Normally
 - Interpolation: computing a function's value at a given point inside a domain where the function's values are known at discrete points
 - Extrapolation: computing a function's value outside a domain, but in relationship with points where the function's values are known: hazardous!
 - Projection: from linear algebra, expression of a function (a vector) into a new basis of a (another) vector space (often with a smaller dimension)
- In MEDCoupling, we do not take sides, and hence we
 - Prepare the operation (given the two meshes)
 - Transfer one or several fields (but apologies, sometimes you will still see interpolate or project)
- Fields on cells are called P0 fields
- Fields on nodes are called P1 fields (don't ask me why)
- Two meshes are overlapping if they cover exactly the same spatial domain
- Temporal interpolation is not covered!



A Trivial python example

- Transfer a field on cells onto a new field on cells

```
import medcoupling as mc
remap = mc.MEDCouplingRemapper()
remap.setPrecision(1.e-12) # setting general of
remap.prepare(srcMesh,trgMesh,"POP0") # cells to cells
srcField.setNature(mc.IntensiveConservation) # nature of the field
trgField = remap.transferField(srcField,1e+300) # default value to
```

- srcField is a MEDCouplingFieldDouble
- srcMesh and trgMesh are MEDCouplingMesh-S

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Spatial discretization of a Field

Where are the discrete values defined?

- A field can be supported by:
 - The nodes (or vertices) of the mesh: ON_NODES also called P1
 - The cells (or elements) of the mesh: ON_CELLS also called P0
 - By more complex reference locations:
 - Gauss Points (ON_GAUSS_PT, ON_GAUSS_NE),
 - Kriging points (ON_NODES_KR)
- Obviously the projection methods will differ according to the localization
- Generally P0-P0 projection is the best supported option
 - Source field is defined on cells
 - Desired result: a target field expressed on cells
 - Very common case
- Not all combinations are possible
 - See the reference table at the end of the presentation
 - If you don't find what you need, ask for it!



Field Nature (1/2)

Where physics comes into play

- A meaningful projection needs to know whether the physical quantity being projected is:
 - Extensive: mass, power ... quantity that scales with the volume of a cell
 - Intensive: density, temperature ... quantity that do not scale with the volume
- For each of the two above, two sub-methods are available, governing the behavior in case of non-overlapping meshes
 - “Maximum” value preserved in the result
 - “Integral” value preserved in the result
- See detailed formula in the documentation
- Invoke method: `setNature()` on the field
 - If you don't call it, no projection will be possible
- Possible argument values (warning different names prior to V8)



Field Nature (2/2)

Example of non-overlapping mesh

- Understanding the problem of non-overlapping meshes:
- Take a look at the illustration right
 - Mesh A in blue
 - Mesh B in green
- For a projection from B to A, should:
 - the full volume (here surface) of the cell from mesh A be taken into account?
 - Knowing that only part of it coincides with the two cells in mesh B
 - or only the volume covering both mesh A and mesh B?
 - Letting aside what is not overlapping
 - Depends on the nature of the physical quantity you're handling
- Again, take a look at the full formulas + exercises:
 - `${MEDCOUPLING_ROOT_DIR}/share/doc/developer/InterpKerRemapGlobal.html`

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Projection Methods

General principle

To project one field onto a new target mesh, one has to:

- 1** Prepare (required only once): The weight matrix is internally computed Ratios of the volumes between source cells and target cells From the source mesh and the target mesh only W_{ij} : how much from source cell (i) will contribute to target cell (j) API: prepare(source, target, method)
- 2** The source field must have a valid nature set!
- 3** Transfer (can be done several times): A field on the source mesh can be transferred to the target mesh API: transfer(srcField, tgtField, defaultValue) Default value covers non-overlapping cases

Supported configurations

- Mesh combination (U: unstructured, C: cartesian, E: extruded) U - U U - C C - U C - C E - E
- Dimensions 1D 2D curve, full 2D 3D surface, full 3D
- Spatial discretization P0 - P0 P1 - P0 P0 - P1 P1 - P1 P1 - P0Bary PG - PG