

Boolean combinations of cellular complexes as chain operations *

Alberto Paoluzzi

August 18, 2014

Contents

1 Introduction

1.1 Preview of the algorithm

1. Embed both cellular complexes A and B in the same space (say, identify their common vertices) by $V_{ab} = V_a \cup V_b$.
2. Build their CDC (Common Delaunay Complex) as the LAR of Delaunay triangulation of the vertex set V_{ab} .
3. Split the (highest-dimensional) cells of CDC crossed by ∂A or ∂B ;
4. With respect to the (split) CDC basis, compute two coordinate chains $\alpha, \beta : CDC \rightarrow \{0, 1\}$, such that:

$$\alpha(cell) = 1 \quad \text{if } |cell| \subset A; \quad \text{else } \alpha(cell) = 0,$$

$$\beta(cell) = 1 \quad \text{if } |cell| \subset B; \quad \text{else } \beta(cell) = 0.$$

5. Extract accordingly the CDC chain corresponding to $AopB$, with $op \in \{\cup, \cap, -\}$.

You may think to the split CDC as a CDT (constrained Delaunay Complex). In part they coincide, but in general, CDC is a polytopal complex (not a simplicial complex).

*This document is part of the *Linear Algebraic Representation with CoChains* (LAR-CC) framework [?].
August 18, 2014

2 Merging arguments

2.1 Reordering of vertex coordinates

A global reordering of vertex coordinates is executed as the first step of the Boolean algorithm, in order to eliminate the duplicate vertices, by substituting duplicate vertex copies (coming from two close points) with a single instance.

Two dictionaries are created, then merged in a single dictionary, and finally split into three subsets of (vertex,index) pairs, with the aim of rebuilding the input representations, by making use of a novel and more useful vertex indexing.

The union set of vertices is finally reordered using the three subsets of vertices belonging (a) only to the first argument, (b) only to the second argument and (c) to both, respectively denoted as V_1, V_2, V_{12} . A top-down description of this initial computational step is provided by the set of macros discussed in this section.

@D Place the vertices of Boolean arguments in a common space @""" First step of Boolean Algorithm """ @i Initial indexing of vertex positions @i @j Merge two dictionaries with keys the point locations @i @j Filter the common dictionary into three subsets @i @j Compute an inverted index to reorder the vertices of Boolean arguments @i @j Return the single reordered pointset and the two d -cell arrays @i @

2.1.1 Re-indexing of vertices

Initial indexing of vertex positions The input LAR models are located in a common space by (implicitly) joining $V1$ and $V2$ in a same array, and (explicitly) shifting the vertex indices in $CV2$ by the length of $V1$. @D Initial indexing of vertex positions @from collections import defaultdict, OrderedDict

""" TODO: change defaultdict to OrderedDefaultdict """

class OrderedDefaultdict(collections.OrderedDict): def *init*(*self*,*args,**kwargs):if not args:*self*.default_factory=Noneelse:if n

def *missing*(*self*,key):if *self*.default_factoryis None:raise KeyError(key)*self*[key]=default=*self*.default_factory()return default

def *reduce*(*self*):optional,for picklesupport args=(*self*.default_factory,)if *self*.default_factoryelsetuple()return *self*.class,args,None,None,*self*.iter

def vertexSieve(model1, model2): from lar2psm import larModelBreak V1,CV1 = larModelBreak(model1) V2,CV2 = larModelBreak(model2) n = len(V1); m = len(V2) def shift(CV, n): return [[v+n for v in cell] for cell in CV] CV2 = shift(CV2,n) @

Merge two dictionaries with point location as keys Since currently $CV1$ and $CV2$ point to a set of vertices larger than their initial sets $V1$ and $V2$, we index the set $V1 \cup V2$ using a Python `defaultdict` dictionary, in order to avoid errors of "missing key". As dictionary keys, we use the string representation of the vertex position vector provided by the `vcode` function given in the Appendix. @D Merge two dictionaries with keys the point

```

locations @ vdict1 = defaultdict(list) for k,v in enumerate(V1): vdict1[vcode(v)].append(k)
vdict2 = defaultdict(list) for k,v in enumerate(V2): vdict2[vcode(v)].append(k+n)
    vertdict = defaultdict(list) for point in vdict1.keys(): vertdict[point] += vdict1[point]
for point in vdict2.keys(): vertdict[point] += vdict2[point] @

```

Example of string coding of a vertex position The position vector of a point of real coordinates is provided by the function `vcode`. An example of coding is given below. The *precision* of the string representation can be tuned at will.

```

>>> vcode([-0.011660381062724849, 0.297350056848685860])
'[-0.0116604, 0.2973501]'

```

Filter the common dictionary into three subsets `Vertdict`, dictionary of vertices, uses as key the position vectors of vertices coded as string, and as values the list of integer indices of vertices on the given position. If the point position belongs either to the first or to second argument only, it is stored in `case1` or `case2` lists respectively. If the position (`item.key`) is shared between two vertices, it is stored in `case12`. The variables `n1`, `n2`, and `n12` remember the number of vertices respectively stored in each repository. @D Filter the common dictionary into three subsets @ `case1, case12, case2 = [],[],[]` for `item` in `vertdict.items()`: `key,val = item` if `len(val)==2`: `case12 += [item]` elif `val[0] != n`: `case1 += [item]` else: `case2 += [item]` `n1 = len(case1)`; `n2 = len(case12)`; `n3 = len(case2)` @

Compute an inverted index to reorder the vertices of Boolean arguments The new indices of vertices are computed according with their position within the storage repositories `case1`, `case2`, and `case12`. Notice that every `item[1]` stored in `case1` or `case2` is a list with only one integer member. Two such values are conversely stored in each `item[1]` within `case12`. @D Compute an inverted index to reorder the vertices of Boolean arguments @ `invertedindex = list(0 for k in range(n+m))` for `k,item` in `enumerate(case1)`: `invertedindex[item[1][0]] = k` for `k,item` in `enumerate(case12)`: `invertedindex[item[1][0]] = k+n1` `invertedindex[item[1][1]] = k+n1` for `k,item` in `enumerate(case2)`: `invertedindex[item[1][0]] = k+n1+n2` @

2.1.2 Re-indexing of d-cells

Return the single reordered pointset and the two *d*-cell arrays We are now finally ready to return two reordered LAR models defined over the same set V of vertices, and where (a) the vertex array V can be written as the union of three disjoint sets of points C_1, C_{12}, C_2 ; (b) the *d*-cell array $CV1$ is indexed over $C_1 \cup C_{12}$; (b) the *d*-cell array $CV2$ is indexed over $C_{12} \cup C_2$.

The `vertexSieve` function will return the new reordered vertex set $V = (V_1 \cup V_2) \setminus (V_1 \cap V_2)$, the two renumbered *s*-cell sets $CV1$ and $CV2$, and the size `len(case12)` of $V_1 \cap V_2$. @D Return the single reordered pointset and the two *d*-cell arrays @ $V =$

[eval(p[0]) for p in case1] + [eval(p[0]) for p in case12] + [eval(p[0]) for p in case2] CV1 = [sorted([invertedindex[v] for v in cell]) for cell in CV1] CV2 = [sorted([invertedindex[v] for v in cell]) for cell in CV2] return V, CV1, CV2, len(case12) @

2.1.3 Example of input with some coincident vertices

In this example we give two very simple LAR representations of 2D cell complexes, with some coincident vertices, and go ahead to re-index the vertices, according to the method implemented by the function `vertexSieve`.

```
@o test/py/bool/test02.py @@i Initial import of modules @i from bool import * V1
= [[1,1],[3,3],[3,1],[2,3],[2,1],[1,3]] V2 = [[1,1],[1,3],[2,3],[2,2],[3,2],[0,1],[0,0],[2,0],[3,0]] CV1
= [[0,3,4,5],[1,2,3,4]] CV2 = [[3,4,7,8],[0,1,2,3,5,6,7]] model1 = V1,CV1; model2 = V2,CV2
VIEW(STRUCT([ COLOR(CYAN)(SKEL1(STRUCT(MKPOLS(model1)))), COLOR(RED)(SKEL1(ST
```

Example discussion The aim of the `vertexSieve` function is twofold: (a) eliminate vertex duplicates before entering the main part of the Boolean algorithm; (b) reorder the input representations so that it becomes less expensive to check whether a 0-cell can be shared by both the arguments of a Boolean expression, so that its coboundaries must be eventually split. Remind that for any set it is:

$$|A \cup B| = |A| + |B| - |A \cap B|.$$

Let us notice that in the previous example

$$|V| = |V_1 \cup V_2| = 12 \leq |V_1| + |V_2| = 6 + 9 = 15,$$

and that

$$|V_1| + |V_2| - |V_1 \cup V_2| = 15 - 12 = 3 = |C_{12}| = |V_1 \cap V_2|,$$

where C_{12} is the subset of vertices with duplicated instances. @D Output from `test/py/boolean/test02.py`
 @V = [[3.0,1.0],[2.0,1.0],[3.0,3.0],[1.0,1.0],[1.0,3.0],[2.0,3.0], [3.0,2.0],[2.0,0.0],[2.0,2.0],[0.0,0.0],[3.0,0.0],[0.0,1.0]]
 CV1 = [[3,5,1,4],[2,0,5,1]] CV2 = [[8,6,7,10],[3,4,5,8,11,9,7]] @ Notice also that V has been
 reordered in three consecutive subsets C_1, C_{12}, C_2 such that CV1 is indexed within $C_1 \cup C_{12}$,
 whereas CV2 is indexed within $C_{12} \cup C_2$. In our example we have $C_{12} = \{3, 4, 5\}$: @D Re-
 ordering of vertex indexing of cells @ `sorted(CAT(CV1))` [0, 1, 1, 2, 3, 4, 5, 5] `sorted(CAT(CV2))` [3, 4, 5, 6, 7, 7, 8, 8, 9, 10, 11] @

Cost analysis Of course, this reordering after elimination of duplicate vertices will allow to perform a cheap $O(n)$ discovering of (Delaunay) cells whose vertices belong both to V1 and to V2. Actually, the *same test* can be now used both when the vertices of the input arguments are all different, and when they have some coincident vertices. The total cost of such pre-processing, executed using dictionaries, is $O(n \ln n)$.

2.1.4 Example

Building a covering of common convex hull @D Building a covering of common convex hull @def covering(model1,model2,dim=2,emptyCellNumber=1): V, CV1, CV2, n12 = vertexSieve(model1,model2) ,EEV1 = larFacets((V,CV1),dim,emptyCellNumber),EEV2 = larFacets((V,CV2),dim,emptyCellNumber)if emptyCellNumber!= 0 : CV1 = CV1[: -emptyCellNumber]if emptyCellNumber!= 0 : CV2 = CV2[: -emptyCellNumber]VV = AA(LIST)(range(len(V)))returnV, [VV,EEV1,EEV2,CV1,CV2],n12@

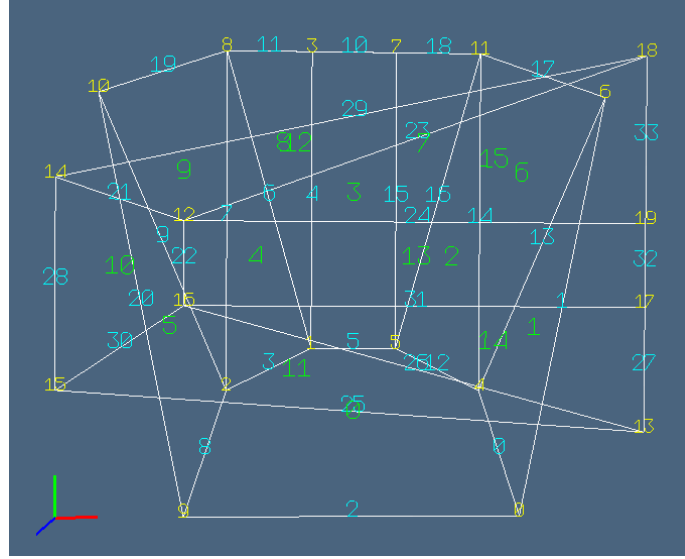


Figure 1: Set covering of the two Boolean arguments.

3 Selecting cells to split

Relational inversion (Characteristic matrix transposition) @D Characteristic matrix transposition @""" Characteristic matrix transposition """ def invertRelation(V,CV): VC = [[] for k in range(len(V))] for k,cell in enumerate(CV): for v in cell: VC[v] += [k] return VC @

@D Look for cells in Delaunay, with vertices in both operands @""" Look for cells in Delaunay, with vertices in both operands """ def mixedCells(CV,CV1,CV2,n12): n0,n1 = 0, max(AA(max)(CV1)) vertices in CV1 (extremes included) m0,m1 = n1+1-n12, max(AA(max)(CV2)) vertices in CV2 (extremes included) return [list(cell) for cell in CV if any([n0j=vj=n1 for v in cell]) and any([m0j=vj=m1 for v in cell])] @

@D Look for cells in cells12, with vertices on boundaries @""" Look for cells in cells12, with vertices on boundaries """ def mixedCellsOnBoundaries(cells12,BV): cells12BV =

```

[cell for cell in cells12 if len(list(set(cell).intersection(BV))) != 0] return cells12BV @
@D Build intersection tasks @""" Build intersection tasks """ def cuttingTest(cuttingHyperplane,polytope,V):
signs = [INNERPROD([cuttingHyperplane, V[v]+[1.]] for v in polytope] signs = eval(vcode(signs))
return any([value<-0.001 for value in signs]) and any([value>0.001 for value in signs])
def splittingTasks(V,pivots,BV,BC,VBC,CV,VC): tasks = [] for pivotCell in pivots:
cutVerts = [v for v in pivotCell if v in BV] for v in cutVerts: cutFacets = VBC[v] cells2cut
= VC[v] for face,cell in CART([cutFacets,cells2cut]): polytope = CV[cell] points = [V[w]
for w in BC[face]] dim = len(points[0]) theMat = Matrix( [(dim+1)*[1.] + [p+[1.] for p
in points] ) cuttingHyperplane = [(-1)**(col)*theMat.minor(0,col).determinant() for col in
range(dim+1)] if cuttingTest(cuttingHyperplane,polytope,V): tasks += [[face,cell,cuttingHyperplane]]
tasks = AA(eval)(set(AA(str)(tasks))) tasks = TrivialIntersection(tasks,V,BC,CV) return
tasks @

```

facet-cell trivial intersection filtering A final filtering is applied to the pairs (`cuttingHyperplane`, `polytope`) in the `tasks` array, in order to remove those facets (pairs in 2D) whose intersection reduces to a single point, i.e. to the common vertex between the boundary $(d-1)$ -face, having `cuttingHyperplane` as affine hull, and the `polytope` d -cell.

For this purpose, it is checked that at least one of the facet vertices, transformed into the common-vertex-based coordinate frame, have all positive coordinates. This fact guarantees the existence of a non trivial intersection between the $(d-1)$ -face and the d -cell.

```

@D Trivial intersection filtering @""" Trivial intersection filtering """ def Trivial-
Intersection(tasks,V,EEV,CV): out = [] for face,cell,affineHull in tasks: faceVerts, cel-
lVerts = EEV[face], CV[cell] v0 = list(set(faceVerts).intersection(cellVerts))[0] v0 = com-
mon vertex transformMat = mat([VECTDIFF([V[v],V[v0]]) for v in cellVerts if v !=
v0]).T.I vects = (transformMat * (mat([VECTDIFF([V[v],V[v0]]) for v in faceVerts if
v != v0]).T)).T.tolist() if any([all([x>0 for x in list(vect)]) for vect in vects]): out +=
[[face,cell,affineHull]] return out @

```

4 Splitting cells traversing the boundaries

In the previous section we computed a set of "slitting seeds", each made by a boundary facet and by a Delaunay cell to be splitted by the facet's affine hull. Here we show how to partition ate each such cells into two cells, according to Figure ??, where the boundary facets of the two boolean arguments are shown in yellow color.

In the example in Figure ??, the set of pairs (`facet`, `cell`) to be used as splitting seeds are given below.

```

[[25, 3], [1, 3], [29, 18], [20, 22], [1, 19], [25, 10], [20, 10], [29, 22]]

```

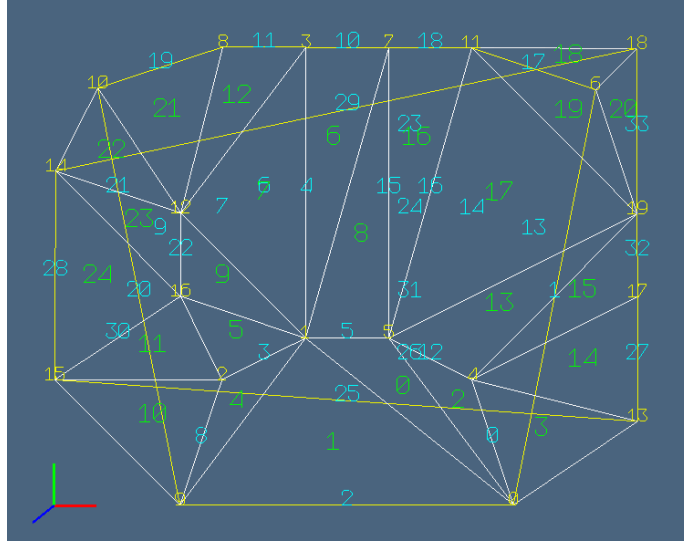


Figure 2: example caption

4.1 Cell splitting

A cell will be split by `pyplasm` intersection with a suitable rotated and translated instance of a (large) d -cuboid with the superior face embedded in the hyperplane $z = 0$.

Splitting a cell with an hyperplane The macro below defines a function `cellSplitting`, with input the index of the `face`, the index of the `cell` to be bisected, the `covector` giving the coefficients of the splitting hyperplane, i.e. the affine hull of the splitting `face`, and the arrays `V`, `EEV`, `CV`, giving the coordinates of vertices, the (accumulated) facet to vertices relation (on the input models), and the cell to vertices relation (on the Delaunay model), respectively.

The actual subdivision of the input `cell` onto the two output cells `cell1` and `cell2` is performed by using the `pyplasm` Boolean operations of intersection and difference of the input with a solid simulation of the needed hyperspace, provided by the `rototranslSubspace` variable. Of course, such `pyplasm` operators return two `Hpc` values, whose vertices will then be extracted using the `UKPOL` primitive.

```
@D Cell splitting @""" Cell splitting in two cells """ def cellSplitting(face,cell,covector,V,EEV,CV):
    dim = len(V[0]) subspace = (T(range(1,dim+1))(dim*[-50])(CUBOID(dim*[100]))) nor-
    mal = covector[:-1] if len(normal) == 2: 2D complex rotatedSubspace = R([1,2])(ATAN2(normal)-
    PI/2)(T(2)(-50)(subspace)) elif len(normal) == 3: 3D complex rotatedSubspace = R()(subspace)
    else: print "rotation error" t = V[EEV[face][0]] rototranslSubspace = T(range(1,dim+1))(t)(rotatedSubspace)
    cellHpc = MKPOL([V,[v+1 for v in CV[cell]]],None)
    cell1 = INTERSECTION([cellHpc,rototranslSubspace]) tolerance=0.0001 use_ctree =
```


Example of face-cell and cell-face dictionaries @D Example of face-cell and cell-face dictionaries @""" Example of face-cell and cell-face dictionaries """ tasks (face,cell) = [[0, 4, [-10.0, 2.0, 110.0]], [31, 5, [3.0, -14.0, 112.0]], [17, 18, [10.0, 2.0, -30.0]], [22, 3, [-1.0, -14.0, 42.0]], [17, 19, [10.0, 2.0, -30.0]], [31, 18, [3.0, -14.0, 112.0]], [22, 19, [-1.0, -14.0, 42.0]], [0, 3, [-10.0, 2.0, 110.0]]

tasks (dict_{fc}) = defaultdict(< type'list' >, 0 : [(4, [-10.0, 2.0, 110.0]), (3, [-10.0, 2.0, 110.0]), 17 : [(18, [10.0, 2.0, -30.0]), (19, [10.0, 2.0, -30.0])], 18 : [(17, [3.0, -14.0, 112.0]), (22, [-1.0, -14.0, 42.0])])

tasks (dict_{cf}) = defaultdict(< type'list' >, 19 : [(17, [10.0, 2.0, -30.0]), (22, [-1.0, -14.0, 42.0]), 18 : [(17, [3.0, -14.0, 112.0]), (22, [-1.0, -14.0, 42.0])])

4.3 Updating the vertex set and dictionary

In any dimension, the split of a d -cell with an hyperplane (crossing its interior) produces two d -cells and some new vertices living upon the splitting hyperplane.

When the d -cell c is contained in only one seed of the CDC decomposition, i.e. when `dict_cf[c]` has cardinality one (in other words: it is crossed only by one boundary facet), the two generated cells `vcell1`, `vcell2` can be safely output, and accommodated in two slots of the `CV` list.

Conversely, when more than one facet crosses c , much more care must be taken to guarantee the correct fragmentation of this cell.

Managing the splitting dictionaries The function `splittingControl` takes care of cells that must be split several times, as crossed by several boundary faces.

If the dictionary item `dict_cf[cell]` has *length* one (i.e. is crossed *only* by one face) the `CV` list is updated and the function returns, in order to update the `dict_fc` dictionary.

Otherwise, the function subdivides the facets cutting `cell` between those to be associated to `vcell1` and to `vcell2`. For each pair `aface`, `covector` in `dict_cf[cell]` and in position following `face` in the list of pairs, check if either `vcell1` or `vcell2` or both, have intersection with the subset of vertices shared between `cell` and `aface`, and respectively put in `alist1`, in `alist2`, or in both. Finally, store `vcell1` and `vcell2` in `CV`, and `alist1`, `alist2` in `dict_cf`.

```
@D Managing the splitting dictionaries @""" Managing the splitting dictionaries """
def splittingControl(face,cell,covector,vcell,vcell1,vcell2,dict_fc,dict_cf,V,BC,CV,VC,CVbits,lenBC1):
    boundaryFacet = BC[face] translVector = V[boundaryFacet[0]] tcovector = [cv+tv*covector[-1]
    for (cv,tv) in zip(covector[:-1],translVector)]+[0.0] print "tcovector =",tcovector
    c1,c2 = cell,cell if not haltingSplitTest(cell,vcell,vcell1,vcell2,boundaryFacet,translVector,tcovector,V)
    :
```

```
    only one facet covector crossing the cell cellVerts = CV[cell] CV[cell] = vcell1 CV +=
    [vcell2] print "llll cell,len(CV) =",cell,len(CV) CVbits += [copy(CVbits[cell])] c1,c2 =
    cell,len(CV)-1
```

```
    firstCell,secondCell = AA(testingSubspace(V,covector))([vcell1,vcell2]) if face ; lenBC1
    and firstCell==-1: face in boundary(op1) CVbits[c1][0] = 0 CVbits[c2][0] = 1 elif face
```

```

i = lenBC1 and firstCell == -1: face in boundary(op2) CVbits[c1][1] = 0 CVbits[c2][1] =
1 else: print "error splitting face,c1,c2 =",face,c1,c2
    dict_fc[face].remove((cell,covector))removethesplitcelldict_cf[cell].remove((face,covector))removethespl
    more than one facet covectors crossing the cell alist1,alist2 = list(),list() for aface,covector
in dict_cf[cell] :
    for each facet crossing the cell compute the intersection between the facet and the cell
faceVerts = BC[aface] commonVerts = list(set(faceVerts).intersection(cellVerts))
    and attribute the intersection to the split subcells if set(vcell1).intersection(commonVerts)
!= set(): alist1.append((aface,covector)) else: dict_fc[aface].remove((cell,covector))
    if set(vcell2).intersection(commonVerts) != set(): alist2.append((aface,covector)) dict_fc[aface] +=
[(len(CV) - 1, covector)]
    dict_cf[cell] = alist1dict_cf[len(CV) - 1] = alist2
    else: dict_fc[face].remove((cell,covector))removethesplitcelldict_cf[cell].remove((face,covector))removethespl
    return V,CV,CVbits, dict_cf, dict_fc, [c1, c2]@

```

4.4 Updating the split cell and the queues of seeds

When a d -cell of the combined Delaunay complex (CDC) is split into two d -cells, the first task to perform is to update its representation as vertex list, and to update the list of d -cells. In particular, as `cell`, and `cell1`, `cell2` are the input d -cell and the two output d -cells, respectively, we go to substitute `cell` with `cell1`, and to add the `cell2` as a new row of the $CSR(M_d)$ matrix, i.e. as the new terminal element of the `CV` array. Of course, the reverse relation `VC` must be updated too.

Updating the split cell First of all notice that, whereas `cell` is given as an integer index to a `CV` row, `cell1`, `cell2` are returned by the `cellSplitting` function as lists of lists of coordinates (of vertices). Therefore such vectors must be suitably transformed into dictionary keys, in order to return the corresponding vertex indices. When transformed into two lists of vector indices, `cell1`, `cell2` will be in the form needed to update the `CV` and `VC` relations.

Updating the vertex set of split cells The code in the macro below provides the splitting of the CDC along the boundaries of the two Boolean arguments. This function, and the ones called by its, provide the dynamic update of the two main data structures, i.e. of the LAR model (V, CV) .

```

@D Updating the vertex set of split cells @""" Updating the vertex set of split cells """
def testingSubspace(V,covector): def testingSubspace0(vcell): inout = SIGN(sum([INNERPROD([V[v]+[1.],co
for v in vcell])) return inout return testingSubspace0
    def splitCellsCreateVertices(vertdict,dict_fc,dict_cf,V,BC,CV,VC,lenBC1) : DEBUG =
False; CVbits = [[-1, -1]forkinrange(len(CV))]nverts = len(V); cellPairs = []; twoCellIndices =

```

```

[]; while any([tasks! = [] for face, tasks in dict_fc.items()]) : for face, tasks in dict_fc.items() :
    for task in tasks : cell, covector = task.vcell = CV[cell]
        if cuttingTest(covector, vcell, V): cell1, cell2 = cellSplitting(face, cell, covector, V, BC, CV)
        print " ", face, cell1, cell2, ", cell, face, cell1, cell2 if cell1 == [] or cell2 == []: print "cell1, cell2
        ==", cell1, cell2 else: adjCells = adjacencyQuery(V, CV)(cell)
        print "cell, adjCells =", cell, adjCells, cell1, cell2
        vcell1 = [] for k in cell1: if vertdict[k] == []: vertdict[k] += [nverts] V += [eval(k)]
        nverts += 1 vcell1 += [vertdict[k]]
        vcell1 = CAT(vcell1) vcell2 = CAT([vertdict[k] for k in cell2])
        V, CV, CVbits, dict_cf, dict_fc, twoCells = splittingControl(face, cell, covector, vcell, vcell1, vcell2, dict_fc, dict_cf,
        twoCells[1]) :
        for adjCell in adjCells: dict_fc[face] += [(adjCell, covector)] dict_cf[adjCell] += [(face, covector)] cellPairs =
        [[vcell1, vcell2]] twoCellIndices += [[twoCells]]
        if DEBUG: showSplitting(V, cellPairs, BC, CV) else: dict_fc[face].remove((cell, covector)) remove the split cell

```

Test for split halting along a boundary facet The cell splitting is operated by the facet's hyperplane $H(f)$, that we call *covector*, and the splitting with it may continues outside f ... !!

This fact may induce some local errors in the decision procedure (attributing either 0 or 1 to each split cell pair). So, when splitting a pair (**cell, face**) — better: (**cell, covector**) — already stored in the data structure, and then computing its adjacent pairs, we should check if the common facet f_{12} between c_1 and c_2 is (or is not) at least partially internal to f .

If this fact is not true, and hence f_{12} is *out*(f) in the induced topology of the $H(f)$ hyperplane, the split process on that pair must be halted: c_1 and c_2 are not stored, and their adjacent cells not split.

```

@D Test for split halting along a boundary facet @""" Test for split halting along a
boundary facet """ def haltingSplitTest(cell, vcell, vcell1, vcell2, boundaryFacet, translVector, tcovector, V):
newFacet = list(set(vcell1.intersection(vcell2))) print " ", vcell1, vcell2, "=", vcell, vcell1, vcell2
print "newFacet, boundaryFacet =", newFacet, boundaryFacet

```

```

translation newFacet = [ eval(vcode(VECTDIFF([V[v], translVector]))) for v in new-
Facet ] boundaryFacet = [ eval(vcode(VECTDIFF([V[v], translVector]))) for v in bound-
aryFacet ] print "newFacet, boundaryFacet =", newFacet, boundaryFacet

```

```

linear transformation: newFacet -> standard (d-1)-simplex transformMat = mat( bound-
aryFacet[1:] + [tcovector[:-1]] ).T.I print "transformMat =", transformMat

```

```

transformation in the subspace  $x_d = 0$  newFacet = AA(COMP([eval, vcode]))((transformMat*
(mat(newFacet).T)).T.tolist()) boundaryFacet = AA(COMP([eval, vcode]))((transformMat*
(mat(boundaryFacet).T)).T.tolist()) print "newFacet, boundaryFacet =", newFacet, boundaryFacet

```

```

projection in  $E^{d-1}$  space and Boolean test newFacet = MKPOL([AA(lambdav : v[:-1])(newFacet), [range
1]), None]) boundaryFacet = MKPOL([AA(lambdav : v[:-1])(boundaryFacet), [range(1, len(boundaryFace
1]), None)]) verts, cells, polys = UKPOL(INTERSECTION([newFacet, boundaryFacet])) print "verts, cells, polys =

```

```

",verts,cells,pols,""ifverts == [] : print(')print"*****cell = ",cells.exit()returnTrueelse :
returnFalse

```

```

cell1 = INTERSECTION([cellHpc,rototranslSubspace]) tolerance=0.0001 use_octree =
Falsecell1 = Plasm.boolop(BOOLE_AND,[cellHpc,rototranslSubspace],tolerance,plasm_config.maxn
UKPOL(cell1)cell1 = AA(vcode)(verts)if@

```

Test about halting the split along a facet @D Test about halting the split along a facet @""" Test about halting the split along a facet """ def haltingSplitTest(face,vcell,adjCell,CV,V,printout=1) facet = list(set(vcell).intersection(CV[adjCell])) points = [V[v] for v in facet] dim = len(points[0]) theMat = Matrix([(dim+1)*[1.] + [p+[1.] for p in points]) covector = [(-1)**(col)*theMat.minor(0,col).determinant() for col in range(dim+1)] if printout: print "face,vcell,CV[adjCell],facet,covector =",face,vcell,CV[adjCell],facet,covector haltingTest = (not cuttingTest(covector,CV[face],V)) if printout: print "haltingTest =",haltingTest print "(set(facet).intersection(CV[adjCell])!=set()) =",(set(facet).intersection(CV[adjCell])!=set()) print "(not cuttingTest(covector,CV[face],V)) =",(not cuttingTest(covector,CV[face],V)) return haltingTest @

4.5 Updating the cells adjacent to the split cell

Once the list of d -cells has been updated with respect to the results of a split operation, it is necessary to consider the possible update of all the cells that are adjacent to the split one. In particular we need to update their lists of vertices, by introducing the new vertices produced by the split, and by updating the dictionaries of tasks, by introducing the new (adjacent) splitting seeds.

Computing the adjacent cells of a given cell To perform this task we make only use of the **CV** list. In a more efficient implementation we should make direct use of the sparse adjacency matrix, to be dynamically updated together with the **CV** list. The computation of the adjacent d -cells of a single d -cell is given here by extracting a column of the $\text{CSR}(M_d M_d^t)$. This can be done by multiplying $\text{CSR}(M_d)$ by its transposed row corresponding to the query d -cell.

```

@D Computing the adjacent cells of a given cell @""" Computing the adjacent cells
of a given cell """ def adjacencyQuery (V,CV): dim = len(V[0]) def adjacencyQuery0 (cell):
nverts = len(CV[cell]) csrCV = csrCreate(CV) csrAdj = matrixProduct(csrCV,csrTranspose(csrCV))
cellAdjacencies = csrAdj.indices[csrAdj.indptr[cell]:csrAdj.indptr[cell+1]] return [acell for
acell in cellAdjacencies if dim != csrAdj[cell,acell] ] nverts] return adjacencyQuery0 @

```

Updating the adjacency matrix At every step of the CDC splitting, generating two output cells **cell1** and **cell2** from the input **cell**, the element of such index in the list **CV** is restored with the **cell1** vertices, and a new (last) element is created in **CV**, to store the **cell2** vertices. Therefore the row of index **cell** of the symmetric adjacency matrix must

be recomputed, being the `cell` column updated consequently. Also, a new last row (and column) must be added to the matrix.

@D Updating the adjacency matrix @""" Updating the adjacency matrix """ pass @

5 Reconstruction of results

5.1 The Boolean algorithm flow

Show the process of CDC splitting @D Show the process of CDC splitting @""" Show the process of CDC splitting """

```
def showSplitting(V,cellPairs,BC,CV):
    VV = AA(LIST)(range(len(V)))
    boundaries = COLOR(RED)(SKEL1(STRUCT(MKPOLS((V,BC)))))
    submodel = COLOR(CYAN)(STRUCT(MKPOLS((V,BC))))
    [] : cells1,cells2 = TRANS(cellPairs)
    out = [COLOR(WHITE)(MKPOL([V,[v + 1 for v in cell] for cell in cells1],None)),
    COLOR(MAGENTA)(MKPOL([V,[v + 1 for v in cell] for cell in cells2],None))]
    VIEW(STRUCT([larModelNumbering(V,[VV,BC,CV],submodel,2)))@
```

Computation of bits of split cells In order to compute, in the simplest and more general way, whether each of the two split d -cells is internal or external to the splitting boundary $d - 1$ -facet, it is necessary to consider the oriented covector ϕ (or one-form) canonically associated to the facet f by the covector representation theorem, i.e. the corresponding oriented hyperplane. In this case, the internal/external attribute of the split cell will be computed by evaluating the pairing $\langle v, \phi \rangle$.

5.2 Final traversal of the CDC

Several cells of the split CDC are characterised as either internal or external to the Boolean arguments A and B according to the splitting process. Such characterisation is stored within the `CVbits` array of pairs of values in $\{-1, 0, 1\}$, where `CVbits[k][h]`, with $k \in \text{range}(\text{len}(C_d))$ and $h \in \text{range}(2)$, has the following meanings:

$$\text{CVbits}[k][h] = \begin{cases} -1, & \text{if position of } c_k \in C_d \text{ is } \textit{unknown} \text{ w.r.t. complex } K_h \\ 0, & \text{if cell } c_k \in C_d \text{ is } \textit{external} \text{ w.r.t. complex } K_h \\ 1, & \text{if cell } c_k \in C_d \text{ is } \textit{internal} \text{ w.r.t. complex } K_h \end{cases}$$

Therefore, a double d -cell visit of CDC must be executed, starting from some d -cell interior to either A or B , and traversing from a cell to its untraversed adjacent cells, but without crossing the complex boundary, until all cells have been visited.

The initial computation of chains of Boolean arguments The initial setting of `CVbits[k][h]` values is done within the splitting process by the `splitCellsCreateVertices` function, and mainly by the `splittingControl` function.

The traversal of Boolean arguments Let us remember that the adjacency matrix between d -cells is computed via SpMSpM multiplication by the double application

`adjacencyQuery(V,CV)(cell),`

where the first application `adjacencyQuery(V,CV)` returns a partial function with bufferization of the adjacency matrix, and the second application to `cell` returns the list of adjacent d -cells sharing with it a $(d - 1)$ -dimensional facet.

Traversing a Boolean argument within the CDC A recursive function `booleanChainTraverse` is given in the script below, where

```
@D Traversing a Boolean argument within the CDC @""" Traversing a Boolean argument within the CDC """
def booleanChainTraverse(h,cell,V,CV,CVbits,value):
  adjCells = adjacencyQuery(V,CV)(cell)
  for adjCell in adjCells:
    if CVbits[adjCell][h] == -1:
      CVbits[adjCell][h] = value
  CVbits = booleanChainTraverse(h,adjCell,V,CV,CVbits,value)
  return CVbits @
```

Boolean fragmentation and classification of CDC @D Boolean fragmentation and classification of CDC @""" Boolean fragmentation and classification of CDC """

```
def booleanChains(arg1,arg2):
  (V1,basis1), (V2,basis2) = arg1,arg2
  model1, model2 = (V1,basis1[-1]), (V2,basis2[-1])
  V,[VV,,CV1,CV2],n12 = covering(model1,model2,2,0)
  CV = sorted(AA(sorted)(Delau defaultdict(list)fork,vinenumerate(V) : vertdict[vcode(v)] += [k]
  BC1 = signedCellularBoundaryCells(V1,basis1)
  BC2 = signedCellularBoundaryCells(V2,basis2)
  submodel1 = mkSignedEdges((V1,BC1))
  submodel2 = mkSignedEdges((V2,BC2))
  VIEW(STRUCT([submode
  BC = sorted([[ vertdict[vcode(V1[v])][0] for v in cell] for cell in BC1] + [ [ vertdict[vcode(V2[v])][0] for v in cell] for cell in BC2])
  BV = list(set(CAT([v for v in BC])))
  VV = AA(LIST)(range(len(V)))
  submodel = SKEL1(STRUCT(MKPOLS((V,CV))))
  VIEW(larModelNumber
  STRUCT([SKEL1(STRUCT(MKPOLS((V,CV))),
  COLOR(RED)(STRUCT(MKPOLS((V,BC))))))
  cells12 = mixedCells(CV,CV1,CV2,n12)
  pivots = mixedCellsOnBoundaries(cells12,BV)
  VBC = invertRelation(V,BC)
  VC = invertRelation(V,CV)
  tasks = splittingTasks(V,pivots,BV,BC,VBC,CV,V
  dict_fc,dict_cf = initTasks(tasks)
  CVbits,cellPairs,twoCellIndices = splitCellsCreateVertices( vertdict,dict_fc,dict_cf, V, BC, CV, VC, len(BC1)
  for k in range(len(CV)):
    print ",CVbits[k],CV[k] =",k,CVbits[k],CV[k]
  for cell in range(len(CV)):
    if CVbits[cell][0] == 1:
      CVbits = booleanChainTraverse(0,cell,V,CV,CVbits,1)
  if CVbits[cell][0] == 0:
    CVbits = booleanChainTraverse(0,cell,V,CV,CVbits,0)
  if CVbits[cell][1] == 1:
    CVbits = booleanChainTraverse(1,cell,V,CV,CVbits,1)
  if CVbits[cell][1] == 0:
    CVbits = booleanChainTraverse(1,cell,V,CV,CVbits,0)
  for k in range(len(CV)):
    print ",CVbits[k],CV[k] =",k,CVbits[k],CV[k]
  chain1,chain2 = TRANS(CVbits)
  print "_cf",dict_cf,print "_fc",dict_fc,""return V,CV,chain1,chain2,CVbits
```

6 Exporting the library

```
@O lib/py/bool.py @""" Module for Boolean ops with LAR """ from matrix import *
@_ Initial import of modules @_ @_ Symbolic utility to represent points as strings @_ @_
Place the vertices of Boolean arguments in a common space @_ @_ Building a covering
of common convex hull @_ @_ Building a partition of common convex hull of vertices @_
@_ Characteristic matrix transposition @_ @_ Look for cells in Delaunay, with vertices in
both operands @_ @_ Look for cells in cells12, with vertices on boundaries @_ @_ Build
intersection tasks @_ @_ Trivial intersection filtering @_ @_ Cell splitting @_ @_ Init face-
cell and cell-face dictionaries @_ @_ Updating the split cell @_ @_ Updating the vertex set
of split cells @_ @_ Managing the splitting dictionaries @_ @_ Test for split halting along a
boundary facet @_ @_ Computing the adjacent cells of a given cell @_ @_ Show the process
of CDC splitting @_ @_ Traversing a Boolean argument within the CDC @_ @_ Boolean
fragmentation and classification of CDC @_ @
```

7 Tests

7.1 2D examples

7.1.1 First examples

Three sets of input 2D data are prepared here, ranging from very simple to a small instance of the hardest kind of dataset, known to produce an output of size $O(n^2)$.

```
@D First set of 2D data: Fork-0 input @""" Definition of Boolean arguments """ V1
= [[3,0],[11,0], [13,10], [10,11], [8,11], [6,11], [4,11], [1,10], [4,3], [6,4], [8,4], [10,3]] FV1 =
[[0,1,8,9,10,11],[1,2,11], [3,10,11], [4,5,9,10], [6,8,9], [0,7,8], [2,3,11], [3,4,10], [5,6,9], [6,7,8]]
EV1 = [[0,1],[0,7],[0,8],[1,2],[1,11],[2,3],[2,11],[3,4],[3,10],[3,11],[4,5],[4,10],[5,6],[5,9],[6,7],[6,8],[6,9],[7,8],[8,9],[9,10]]
VV1 = AA(LIST)(range(len(V1)))
V2 = [[0,3],[14,2], [14,5], [14,7], [14,11], [0,8], [3,7], [3,5]] FV2 = [[0,5,6,7], [0,1,7], [4,5,6],
[2,3,6,7], [1,2,7], [3,4,6]] EV2 = [[0,1],[0,5],[0,7],[1,2],[1,7],[2,3],[2,7],[3,4],[3,6],[4,5],[4,6],[5,6],[6,7]]
VV2 = AA(LIST)(range(len(V2))) @
@D First set of 2D data: Fork-1 input @""" Definition of Boolean arguments """ V1
= [[3,0],[11,0], [13,10], [10,11], [8,11], [6,11], [4,11], [1,10], [4,3], [6,4], [8,4], [10,3]]
FV1 = [[0,1,8,9,10,11],[1,2,11], [3,10,11], [4,5,9,10], [6,8,9], [0,7,8]] EV1 = [[0,1],[0,7],[0,8],[1,2],[1,11],[2,11],[3,10]]
VV1 = AA(LIST)(range(len(V1)))
V2 = [[0,3],[14,2], [14,5], [14,7], [14,11], [0,8], [3,7], [3,5]] FV2 = [[0,5,6,7], [0,1,7], [4,5,6],
[2,3,6,7], [1,2,7], [3,4,6]] EV2 = [[0,1],[0,5],[0,7],[1,2],[1,7],[2,3],[2,7],[3,4],[3,6],[4,5],[4,6],[5,6],[6,7]]
VV2 = AA(LIST)(range(len(V2))) @
```

Input and visualisation of Boolean arguments @D Computation of lower-dimensional cells @""" Computation of edges an input visualisation """ model1 = V1,FV1 model2 =

```
V2,FV2 basis1 = [VV1,EV1,FV1] basis2 = [VV2,EV2,FV2] submodel12 = STRUCT(MKPOLS((V1,EV1))+M
VIEW(larModelNumbering(V1,basis1,submodel12,4)) VIEW(larModelNumbering(V2,basis2,submodel12,4))
@
```

Exporting test file @D Bulk of Boolean task computation @""" Bulk of Boolean task computation """ @i Computation of lower-dimensional cells @i

```
V,CV,chain1,chain2,CVbits = booleanChains((V1,basis1), (V2,basis2)) for k in range(len(CV)):
print ",CVbits[k],CV[k] =",k,CVbits[k],CV[k]
VIEW(EXPLODE(1.2,1.2,1)(MKPOL((V,[cell for cell,c in zip(CV,chain1) if c==1]
)))) VIEW(EXPLODE(1.2,1.2,1)(MKPOL((V,[cell for cell,c in zip(CV,chain2) if c==1]
)))) VIEW(EXPLODE(1.2,1.2,1)(MKPOL((V,[cell for cell,c1,c2 in zip(CV,chain1,chain2)
if c1+c2==2] )))) VIEW(EXPLODE(1.2,1.2,1)(MKPOL((V,[cell for cell,c1,c2 in zip(CV,chain1,chain2)
if c1+c2==1] )))) VIEW(EXPLODE(1.2,1.2,1)(MKPOL((V,[cell for cell,c1,c2 in zip(CV,chain1,chain2)
if c1+c2==1] )))) @
@O test/py/bool/test01.py @import sys """ import modules from larcc/lib """ sys.path.insert(0,
'lib/py/') from bool import * @i First set of 2D data: Fork-0 input @i @i Bulk of Boolean
task computation @i @
```

7.1.2 Two squares

```
@o test/py/bool/test03.py @""" import modules from larcc/lib """ import sys sys.path.insert(0,
'lib/py/') from bool import *
V1 = [[0,0],[10,0],[10,10],[0,10]] FV1 = [range(4)] EV1 = [[0,1],[1,2],[2,3],[3,0]] VV1 =
AA(LIST)(range(len(V1)))
V2 = [[2.5,2.5],[12.5,2.5],[12.5,12.5],[2.5,12.5]] FV2 = [range(4)] EV2 = [[0,1],[1,2],[2,3],[3,0]]
VV2 = AA(LIST)(range(len(V2))) @i Bulk of Boolean task computation @i @
@o test/py/bool/test04.py @""" import modules from larcc/lib """ import sys sys.path.insert(0,
'lib/py/') from bool import *
V1 = [[0,0],[10,0],[10,10],[0,10]] FV1 = [range(4)] EV1 = [[0,1],[1,2],[2,3],[3,0]] VV1 =
AA(LIST)(range(len(V1)))
V2 = [[2.5,2.5],[7.5,2.5],[7.5,7.5],[2.5,7.5]] FV2 = [range(4)] EV2 = [[0,1],[1,2],[2,3],[3,0]]
VV2 = AA(LIST)(range(len(V2))) @i Bulk of Boolean task computation @i @
@o test/py/bool/test05.py @""" import modules from larcc/lib """ import sys sys.path.insert(0,
'lib/py/') from bool import *
V1 = [[2.5,2.5],[7.5,2.5],[7.5,7.5],[2.5,7.5]] FV1 = [range(4)] EV1 = [[0,1],[1,2],[2,3],[3,0]]
VV1 = AA(LIST)(range(len(V1)))
V2 = [[2.5,2.5],[7.5,2.5],[7.5,7.5],[2.5,7.5]] FV2 = [range(4)] EV2 = [[0,1],[1,2],[2,3],[3,0]]
VV2 = AA(LIST)(range(len(V2))) @i Bulk of Boolean task computation @i @
```

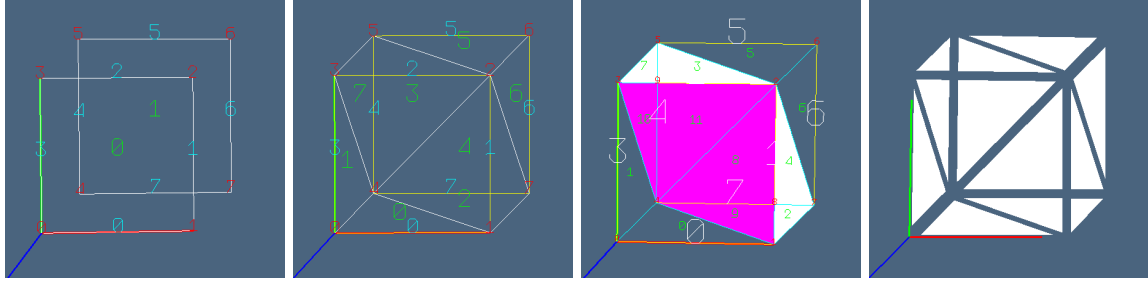



Figure 4: Partitioning of the CDC (Common Delaunay Complex): (a) the two Boolean arguments merged in a single covering; (b) the CDC together with the two (yellow) boundaries; (c) the split CDC cells; (d) the exploded CDC partition.

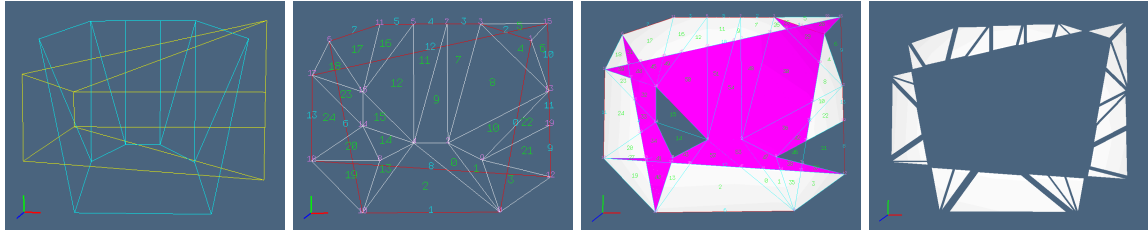


Figure 5: Partitioning of the CDC (Common Delaunay Complex): (a) the two Boolean arguments merged in a single covering; (b) the CDC together with the two (yellow) boundaries; (c) the split CDC cells; (d) the XOR of Boolean arguments.

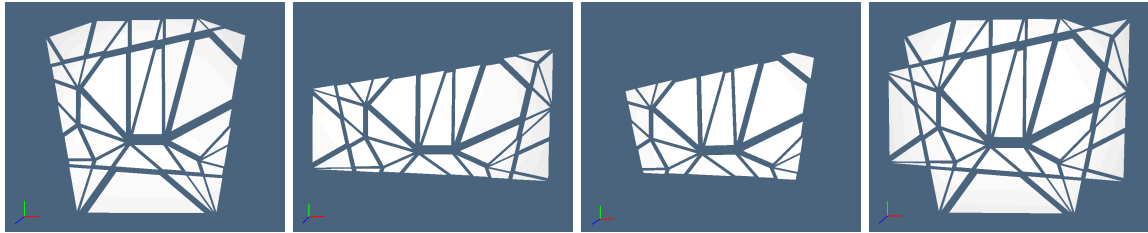


Figure 6: Some chains defined on the CDC (Common Delaunay Complex): (a) the first Boolean argument; (b) the second Boolean argument; (c) the intersection chain; (d) the union chain.

A Appendix: utility functions

```
@D Initial import of modules @from pyplasm import * from scipy import * import sys
""" import modules from larcc/lib """ sys.path.insert(0, 'lib/py/') from lar2psm import *
from simplexn import * from larcc import * from largrid import * from myfont import *
from mapper import * @
```

A.1 Numeric utilities

A small set of utility functions is used to transform a point representation as array of coordinates into a string of fixed format to be used as point key into python dictionaries.

```
@D Symbolic utility to represent points as strings @""" TODO: use package Decimal
(http://docs.python.org/2/library/decimal.html) """ global PRECISION PRECISION =
4
```

```
def prepKey (args): return "[" + ", ".join(args) + "]"
```

```
def fixedPrec(value): out = round(value*10**PRECISION)/10**PRECISION if out
== -0.0: out = 0.0 return str(out)
```

```
def vcode (vect): """ To generate a string representation of a number array. Used to
generate the vertex keys in PointSet dictionary, and other similar operations. """ return
prepKey(AA(fixedPrec)(vect)) @
```