The basic `larcc` module *

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Contents

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1 Basic representations

A few basic representation of topology are used in LARCC. They include some common sparse matrix representations: CSR (Compressed Sparse Row), CSC (Compressed Sparse Column), COO (Coordinate Representation), and BRC (Binary Row Compressed).

1.1 BRC (Binary Row Compressed)

We denote as BRC (Binary Row Compressed) the standard input representation of our LARCC framework. A BRC representation is an array of arrays of integers, with no requirement of equal length for the component arrays. The BRC format is used to represent a (normally sparse) binary matrix. Each component array corresponds to a matrix row, and contains the indices of columns that store a 1 value. No storage is used for 0 values.

BRC format example Let $A = (a_{i,j} \in \{0,1\})$ be a binary matrix. The notation `BRC`(A) is used for the corresponding data structure.

$$A = \begin{pmatrix} 0,1,0,0,0,0,0,1,0,0 \\ 0,0,1,0,0,0,0,0,0,0 \\ 1,0,0,1,0,0,0,0,0,1 \\ 1,0,0,0,0,0,1,0,0,0 \\ 0,0,0,0,0,1,1,1,0,0 \\ 0,0,1,0,1,0,0,0,1,0 \\ 0,0,0,0,0,0,0,0,0,0 \\ 0,1,0,0,0,0,0,1,0,1 \\ 0,0,0,1,0,0,0,0,1,0 \\ 0,1,1,0,1,0,0,0,0,0 \end{pmatrix} \quad \mapsto \quad \texttt{BRC}(A) = \begin{array}{l} \texttt{[[1,7],} \\ \texttt{[2],} \\ \texttt{[0,3,9],} \\ \texttt{[0,6],} \\ \texttt{[5,6,7],} \\ \texttt{[2,4,8],} \\ \texttt{[],} \\ \texttt{[1,7,9],} \\ \texttt{[3,8],} \\ \texttt{[1,2,4]]} \end{array}$$

1.2 Format conversions

From triples to `scipy.sparse` The function `brc2Coo` transforms a `BRC` representation in a list of triples (*row*, *column*, 1) ordered by row.

⟨ Brc to Coo transformation 2 ⟩ ≡

```
def brc2Coo(ListOfListOfInt):
    COOm = [[k,col,1] for k,row in enumerate(ListOfListOfInt)
            for col in row ]
    return COOm
```

◇

Macro referenced in 50b.

Two coordinate compressed sparse matrices `cooFV` and `cooEV` are created below, starting from the `BRC` representation `FV` and `EV` of the incidence of vertices on faces and edges, respectively, for a very simple plane triangulation.

⟨ Test example of Brc to Coo transformation 3a ⟩ ≡

```
print "\n>>> brc2Coo"
V = [[0, 0], [1, 0], [2, 0], [0, 1], [1, 1], [2, 1]]
FV = [[0, 1, 3], [1, 2, 4], [1, 3, 4], [2, 4, 5]]
EV = [[0,1],[0,3],[1,2],[1,3],[1,4],[2,4],[2,5],[3,4],[4,5]]
cooFV = brc2Coo(FV)
cooEV = brc2Coo(EV)
assert cooFV == [[0,0,1],[0,1,1],[0,3,1],[1,1,1],[1,2,1],[1,4,1],[2,1,1],
[2,3,1], [2,4,1],[3,2,1],[3,4,1],[3,5,1]]
assert cooEV == [[0,0,1],[0,1,1],[1,0,1],[1,3,1],[2,1,1],[2,2,1],[3,1,1],
[3,3,1],[4,1,1],[4,4,1],[5,2,1],[5,4,1],[6,2,1],[6,5,1],[7,3,1],[7,4,1],
[8,4,1],[8,5,1]]
◇
```

Macro referenced in 51a.

Conversion to `csr` format Then we give the function `triples2mat` to make the transformation from the sparse matrix, given as a list of triples *row,column,value* (non-zero elements), to the `scipy.sparse` format corresponding to the `shape` parameter, set by default to `"csr"`, that stands for *Compressed Sparse Row*, the normal matrix format of the LARCC framework.

⟨ From list of triples to scipy.sparse 3b ⟩ ≡

```
def triples2mat(triples,shape="csr"):
    n = len(triples)
    data = arange(n)
    ij = arange(2*n).reshape(2,n)
    for k,item in enumerate(triples):
        ij[0][k],ij[1][k],data[k] = item
    return scipy.sparse.coo_matrix((data, ij)).asformat(shape)
◇
```

Macro referenced in 50b.

The conversion from triples to `csr` format is provided below.

⟨ Coo to Csr transformation 3c ⟩ ≡

```
def coo2Csr(COOm):
    CSRm = triples2mat(COOm,"csr")
    return CSRm
◇
```

Macro referenced in 50b.

Two CSR sparse matrices `csrFV` and `csrEV` are generated (by *scipy.sparse*) in the following example:

⟨ Test example of Coo to Csr transformation 3d ⟩ ≡

```
    csrFV = coo2Csr(cooFV)
    csrEV = coo2Csr(cooEV)
    print "\ncsr(FV) =\n", repr(csrFV)
    print "\ncsr(EV) =\n", repr(csrEV)
    ◇
```

Macro referenced in 51a.

The *scipy* printout of the last two lines above is the following:

```
csr(FV) = <4x6 sparse matrix of type '<type 'numpy.int64'>'
          with 12 stored elements in Compressed Sparse Row format>
csr(EV) = <9x6 sparse matrix of type '<type 'numpy.int64'>'
          with 18 stored elements in Compressed Sparse Row format>
```

Conversion from `BRC` to `CSR` format The transformation from BRC to CSR format is implemented slightly differently, according to the fact that the matrix dimension is either unknown (`shape=(0,0)`) or known.

⟨ Brc to Csr transformation 4a ⟩ ≡

```
    def csrCreate(BRCmatrix,lenV=0,shape=(0,0)):
        triples = brc2Coo(BRCmatrix)
        if shape == (0,0):
            CSRmatrix = coo2Csr(triples)
        else:
            CSRmatrix = scipy.sparse.csr_matrix(shape)
            for i,j,v in triples: CSRmatrix[i,j] = v
        return CSRmatrix
    ◇
```

Macro referenced in 50b.

Example The conversion to CSR format of the characteristic matrix *faces-vertices* `FV` is given below for our simple example made by four triangle of a manifold 2D space, graphically shown in Figure 1a. The LAR representation with CSR matrices does not make difference between manifolds and non-manifolds, conversely than most modern solid modelling representation schemes, as shown by removing from `FV` the third triangle, giving the model in Figure 1b.

⟨ Test example of Brc to Csr transformation 4b ⟩ ≡

```
    print "\n>>> brc2Csr"
    V = [[0, 0], [1, 0], [2, 0], [0, 1], [1, 1], [2, 1]]
    FV = [[0, 1, 3], [1, 2, 4], [1, 3, 4], [2, 4, 5]]
    EV = [[0,1],[0,3],[1,2],[1,3],[1,4],[2,4],[2,5],[3,4],[4,5]]
    csrFV = csrCreate(FV)
    csrEV = csrCreate(EV)
    print "\ncsrCreate(FV) =\n", csrFV
```

```
VIEW(STRUCT(MKPOLS((V,FV))))
VIEW(STRUCT(MKPOLS((V,EV))))
```
◇

Macro referenced in 7, 51a.

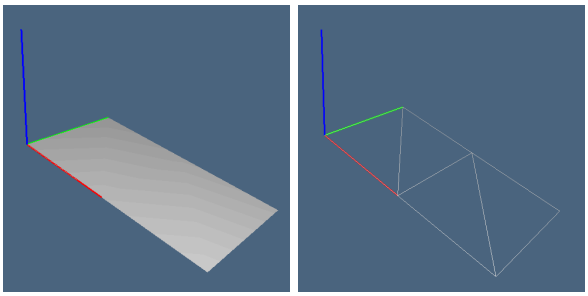

Figure 1: (a) Simplicial 2-complex; (b) its 1-skeleton.

2 Matrix operations

As we know, the LAR representation of topology is based on CSR representation of sparse binary (and integer) matrices. In this section we hence discuss the stack of matrix representations and operations implemented by this module. The current python prototype makes reference to the scipy implementation of sparse matrices. Later implementations in different languages will necessarily make reference to different matrix packages.

2.1 Basic operations

Two utility functions allow to query the number of rows and columns of a CSR matrix, independently from the low-level implementation (that in the following is provided by *scipy.sparse*).

⟨ Query Matrix shape 5a ⟩ ≡

```
def csrGetNumberOfRows(CSRmatrix):
    Int = CSRmatrix.shape[0]
    return Int

def csrGetNumberOfColumns(CSRmatrix):
    Int = CSRmatrix.shape[1]
    return Int
```
◇

Macro referenced in 50b.

⟨ Test examples of Query Matrix shape 5b ⟩ ≡

```
    print "\n>>> csrGetNumberOfRows"
    print "\ncsrGetNumberOfRows(csrFV) =", csrGetNumberOfRows(csrFV)
    print "\ncsrGetNumberOfRows(csrEV) =", csrGetNumberOfRows(csrEV)
    print "\n>>> csrGetNumberOfColumns"
    print "\ncsrGetNumberOfColumns(csrFV) =", csrGetNumberOfColumns(csrFV)
    print "\ncsrGetNumberOfColumns(csrEV) =", csrGetNumberOfColumns(csrEV)
    ◇
```

Macro referenced in 51a.

Sparse to dense matrix transformation The Scipy package provides the useful method `.todense()` in order to transform any sparse matrix format in the corresponding dense format. The function `csr2DenseMatrix` is given here for the sake of generality and portability.

⟨ Sparse to dense matrix transformation 6a ⟩ ≡

```
    def csr2DenseMatrix(CSRm):
        nrows = csrGetNumberOfRows(CSRm)
        ncolumns = csrGetNumberOfColumns(CSRm)
        ScipyMat = zeros((nrows,ncolumns),int)
        C = CSRm.tocoo()
        for triple in zip(C.row,C.col,C.data):
            ScipyMat[triple[0],triple[1]] = triple[2]
        return ScipyMat
    ◇
```

Macro referenced in 50b.

⟨ Test examples of Sparse to dense matrix transformation 6b ⟩ ≡

```
    print "\n>>> csr2DenseMatrix"
    print "\nFV =\n", csr2DenseMatrix(csrFV)
    print "\nEV =\n", csr2DenseMatrix(csrEV)
    ◇
```

Macro referenced in 7, 51a.

Matrix product and transposition The following macro provides the IDE interface for the two main matrix operations required by LARCC, the binary product of compatible matrices and the unary transposition of matrices.

⟨ Matrix product and transposition 6c ⟩ ≡

```
    def matrixProduct(CSRm1,CSRm2):
        CSRm = CSRm1 * CSRm2
        return CSRm

    def csrTranspose(CSRm):
        CSRm = CSRm.T
        return CSRm
    ◇
```

Macro referenced in 50b.

2.2 Characteristic matrices

We define as *characteristic matrices* M_k $(0 \leq k \leq d)$ the binary matrices having as rows the images of the characteristic functions of the k-cells $\alpha_k \subset V$ of a cellular complex with vertices V. Remember that characteristic (or *indicator*) function is

$$\mathbf{1}_A \colon V \to \{0, 1\},$$

which for a given subset A of X, has value 1 at points of A and 0 at points of $V - A$.

Example: from `BRC` to `CSR` to `dense` matrix Let us compute and show in dense form the characteristic matrices of 2- and 1-cells of the simple manifold given in Figure 1. By running the file `test/py/larcc/test08.py` the reader will get the two matrices shown in Example 2

```
"test/py/larcc/test08.py" 7 ≡
    """ Characteristic matrices """
    from larlib import *

    ⟨ Test example of Brc to Csr transformation 4b ⟩
    ⟨ Test examples of Sparse to dense matrix transformation 6b ⟩
    ◇
```

Example 1 (Dense Characteristic matrices)**.** *Let us notice that the two matrices below have the some numbers of columns (indexed by vertices of the cell decomposition). This very fact allows to multiply one matrix for the other transposed, and hence to compute the matrix form of linear operators between the spaces of cells of various dimensions.*

```
FV =
[[1 1 0 1 0 0]
 [0 1 1 0 1 0]
 [0 1 0 1 1 0]
 [0 0 1 0 1 1]]
```

```
EV =
[[1 1 0 0 0 0]
 [1 0 0 1 0 0]
 [0 1 1 0 0 0]
 [0 1 0 1 0 0]
 [0 1 0 0 1 0]
 [0 0 1 0 1 0]
 [0 0 1 0 0 1]
 [0 0 0 1 1 0]
 [0 0 0 0 1 1]]
```

Example 2 (Operators from edges to faces and vice-versa)**.** *As a general rule for operators between two spaces of chains of different dimensions supported by the* same *cellular complex, we use names made by two characters, whose first letter correspond to the target space, and whose second letter to the domain space. Hence* `FE` *must be read as the operator from edges to faces. Of course, since this use correspond to see the first letter as the space generated by rows, and the second letter as the space generated by columns. Notice that the element*

(i, j) *of such matrices stores the number of vertices shared between the (row-)cell* i *and the (column-)cell* j*.*

$$FE = FV\ EV^\top = \begin{matrix}[[2 & 2 & 1 & 2 & 1 & 0 & 0 & 1 & 0] \\ [1 & 0 & 2 & 1 & 2 & 2 & 1 & 1 & 1] \\ [1 & 1 & 1 & 2 & 2 & 1 & 0 & 2 & 1] \\ [0 & 0 & 1 & 0 & 1 & 2 & 2 & 1 & 2]]\end{matrix} \qquad EF = EV\ FV^\top = \begin{matrix}[[2 & 1 & 1 & 0] \\ [2 & 0 & 1 & 0] \\ [1 & 2 & 1 & 1] \\ [2 & 1 & 2 & 0] \\ [1 & 2 & 2 & 1] \\ [0 & 2 & 1 & 2] \\ [0 & 1 & 0 & 2] \\ [1 & 1 & 2 & 1] \\ [0 & 1 & 1 & 2]]\end{matrix}$$

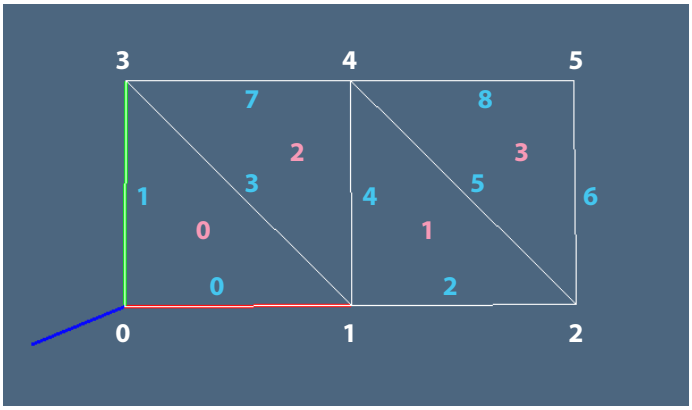

Figure 2: example caption

Matrix elements filtering Some filtering operations on matrix elements are needed in the implementation of various topological operators. Some of such filtering operations are given below.

⟨ Matrix filtering to produce the boundary matrix 8 ⟩ ≡

```
def csrBoundaryFilter(CSRm, facetLengths):
    maxs = [max(CSRm[k].data) for k in range(CSRm.shape[0])]
    inputShape = CSRm.shape
    coo = CSRm.tocoo()
    for k in range(len(coo.data)):
        if coo.data[k]==maxs[coo.row[k]]: coo.data[k] = 1
        else: coo.data[k] = 0
    mtx = coo_matrix((coo.data, (coo.row, coo.col)), shape=inputShape)
    out = mtx.tocsr()
```

```
        return out

    def csrBoundaryFilter1(csrBoundaryBoundaryMat,cells,facets,faces,lenV,FE, CSRm, facetLengths):
        maxs = [max(CSRm[k].data) for k in range(CSRm.shape[0])]
        inputShape = CSRm.shape
        coo = CSRm.tocoo()
        for k in range(len(coo.data)):
            if coo.data[k]==maxs[coo.row[k]]: coo.data[k] = 1
            else: coo.data[k] = 0
        mtx = coo_matrix((coo.data, (coo.row, coo.col)), shape=inputShape)
        out = mtx.tocsr()

        unreliable = [k for k in range(out.shape[0]) if sum(out[k,:].todense()[0]) > 2]
        if unreliable != []:
            for row in unreliable:
                for j in range(len(cells)):
                    if out[row,j] == 1:
                        csrCFE = csrBoundaryBoundaryMat[:,j]
                        cooCFE = csrCFE.tocoo()
                        flawedCells = [cooCFE.row[k] for k,datum in enumerate(cooCFE.data)
                            if datum>2]
                        if all([facet in flawedCells  for facet in FE[row]]):
                            out[row,j]=0
        return out
```

◇

Macro referenced in 50b.

⟨ Test example of Matrix filtering to produce the boundary matrix 9a ⟩ ≡

```
print "\n>>> csrBoundaryFilter"
csrEF = matrixProduct(csrFV, csrTranspose(csrEV)).T
facetLengths = [csrCell.getnnz() for csrCell in csrEV]
CSRm = csrBoundaryFilter(csrEF, facetLengths).T
print "\ncsrMaxFilter(csrFE) =\n", csr2DenseMatrix(CSRm)
```

◇

Macro referenced in 51a.

⟨ Matrix filtering via a generic predicate 9b ⟩ ≡

```
def csrPredFilter(CSRm, pred):
    # can be done in parallel (by rows)
    coo = CSRm.tocoo()
    triples = [[row,col,val] for row,col,val
                in zip(coo.row,coo.col,coo.data) if pred(val)]
    i, j, data = TRANS(triples)
    CSRm = scipy.sparse.coo_matrix((data,(i,j)),CSRm.shape).tocsr()
    return CSRm
```

◇

Macro referenced in 50b.

⟨ Test example of Matrix filtering via a generic predicate 10a ⟩ ≡

```
print "\n>>> csrPredFilter"
CSRm = csrPredFilter(matrixProduct(csrFV, csrTranspose(csrEV)).T, GE(2)).T
print "\nccsrPredFilter(csrFE) =\n", csr2DenseMatrix(CSRm)
```

◇

Macro referenced in 51a.

Correction to boundary operator The more deep issue with LAR (that already appeared at the beginning of LAR experiments, two years ago) is discussed and solved here.

The boundary operator (and the whole LAR approach) works well with convex cells, but MAY give errors (like $\partial\partial \neq 0$) with non-convex cells. At that time, we understood the source of the problem, due to the fact that ALL the vertices of a $(d-1)$-cell EXTERNAL to a NON-CONVEX d-cell may belong to its boundary ... (e.g. BOTH the vertices of a 1-cell external to a non-convex 2-cell)

You might say: convexity is a geometric concept, boundary is topological, so what? Because the input is certainly geometrical, via drawings and/or machine generated `EV,FV` starting from drawings, so the two aspects are strongly interconnected ...

We implement here a general resolution strategy, since it is pretty easy to discover the (d-1)-facets where the problem appears: they are shared by MORE than TWO d-cells ... and this one is a topological ERROR. So, testing $\partial\partial$ on each face, we eliminate the problem *within the boundary operator*, but not within the LAR data structure (to be marked in some way where the problem may appear ... TODO).

My guess is that this source of errors might appear anytime the Boolean input becomes pretty complex, and that it was the greatest source of random errors.

"test/py/larcc/test20.py" 10b ≡

```
""" Correction to boundary operator """
from larlib import *

V,[VV,EV,FV] = larCuboids([2,1],True)
complex = Struct([(V,FV,EV), t(.5,.25), s(.5,.5), (V,FV,EV)])
V,FV,EV = struct2lar(complex)
lines = [[V[v] for v in edge] for edge in EV]
V,FV,EV,polygons = larFromLines(lines)

VV = AA(LIST)(range(len(V)))
submodel = STRUCT(MKPOLS((V,EV)))
VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV],submodel,.5))

csrBoundaryMat = boundary(FV,EV)
print "wrong boundary matrix =",csrBoundaryMat.todense()
```

```
csrBoundaryMat = boundary1(FV,EV,VV)  # <<<<< NOTE !!
print "right boundary matrix =",csrBoundaryMat.todense()
```

⟨ 2-boundary example 11, ... ⟩

```
submodel = viewBoundaryChain((V,FV,EV))([1,1,1,1])
VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV],submodel,.5))
submodel = viewBoundaryChain((V,FV,EV))([0,0,1,1])
VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV],submodel,.5))
```

◇

The printing from example `test/py/larcc/test20.py` is given below. Notice the difference between the fourth lines from the bottom of the two matrices, generated by the function applications `boundary(FV,EV)` and `boundary1(FV,EV,VV)`, respectively.

```
wrong boundary matrix = [
 [0 0 1 0]
 [0 0 1 1]
 [0 1 1 0]
 [0 1 1 0]
 [0 0 1 0]
 [0 0 0 1]
 [1 0 0 1]
 [0 0 0 1]
 [1 0 0 1]
 [0 0 1 0]
 [0 0 0 1]
 [1 1 1 1]
 [1 0 0 1]
 [0 1 1 0]
 [0 0 1 1]]
```

```
right boundary matrix = [
 [0 0 1 0]
 [0 0 1 1]
 [0 1 1 0]
 [0 1 1 0]
 [0 0 1 0]
 [0 0 0 1]
 [1 0 0 1]
 [0 0 0 1]
 [1 0 0 1]
 [0 0 1 0]
 [0 0 0 1]
 [0 0 0 0]
 [1 0 0 1]
 [0 1 1 0]
 [0 0 1 1]]
```

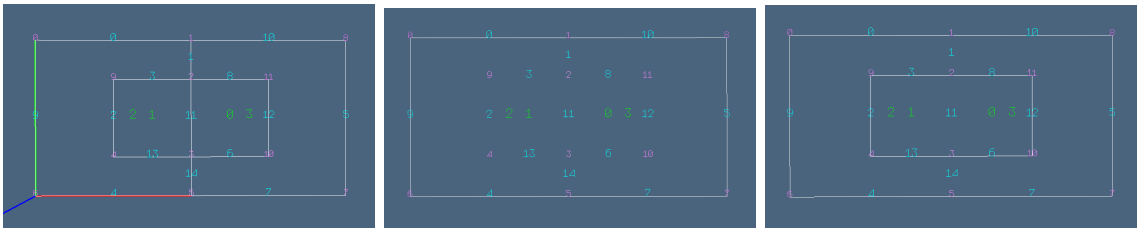

Figure 3: (a) A 2-complex with non-convex cells; (b) boundary of 2-chain [1,1,1,1]; (c) boundary of 2-chain [0,0,1,1].

Whereas the boundary 2-chain is

⟨ 2-boundary example 11 ⟩ ≡

```
""" View boundary chain """
def viewBoundaryChain(larModel):
```

```
        V,FV,EV = larModel
        VV = AA(LIST)(range(len(V)))
        def viewBoundaryChain0 (chain):
            BE = chain2BoundaryChain(boundary1(FV,EV,VV))(chain)
            if chain == [1,1,1,1]: assert BE == [0,4,5,7,9,10]
            if chain == [0,0,1,1]: assert BE == [0,2,3,4,5,6,7,8,9,10,12,13]
            BEV = [EV[e] for e in BE]
            if chain == [1,1,1,1]: assert BEV == [(0,1),(5,6),(7,8),(5,7),(0,6),(1, 8)]
            submodel = STRUCT(MKPOLS((V,BEV)))
            return submodel
        return viewBoundaryChain0
    ◇
```

Macro defined by 11, 12a.
Macro referenced in 10b.

The cellular 2-complex generated by example The printing from example `test/py/larcc/test20.py` is displayed in Figure **??**. The corresponding LAR is the following:

⟨ 2-boundary example 12a ⟩ ≡

```
    V = [[0.0,1.0],[1.0,1.0],[1.0,0.75],[1.0,0.25],[0.5,0.25],[1.0,0.0],
    [0.0,0.0],[2.0,0.0],[2.0,1.0],[0.5,0.75],[1.5,0.25],[1.5,0.75]]

    FV = [[3,2,11,10],[9,2,3,4],[1,2,9,4,3,5,6,0],[1,8,7,5,3,10,11,2]]

    EV = [(0,1),(1,2),(4,9),(2,9),(5,6),(7,8),(3,10),(5,7),(2,11),(0,6),
    (1,8),(2,3),(10,11),(3,4),(3,5)]
    ◇
```

Macro defined by 11, 12a.
Macro referenced in 10b.

2.3 Boundary operator on 3-complex with non-convex cells

Correction to boundary operator

"test/py/larcc/test21.py" 12b ≡

```
    """ Correction to boundary operator """
    from larlib import *

    V = [[0.0,0.0,0.0],[0.0,0.0,1.0],[0.0,1.0,0.0],[0.0,1.0,1.0],[1.0,0.0,0.0],
    [1.0,0.0,1.0],[1.0,1.0,0.0],[1.0,1.0,1.0],[2.0,0.0,0.0],[2.0,0.0,1.0],
    [2.0,1.0,0.0],[2.0,1.0,1.0],[0.5,0.25,0.25],[0.5,0.25,0.75],[0.5,0.75,
    0.25],[0.5,0.75,0.75],[1.0,0.25,0.25],[1.0,0.25,0.75],[1.0,0.75,0.25],
    [1.0,0.75,0.75],[1.5,0.25,0.25],[1.5,0.25,0.75],[1.5,0.75,0.25],[1.5,
    0.75,0.75]]

    CV = [(16,17,18,19,20,21,22,23),(4,5,6,7,8,9,10,11,16,17,18,19,20,21,
```

```
22,23),(12,13,14,15,16,17,18,19),(0,1,2,3,4,5,6,7,12,13,14,15,16,
17,18,19)]

FV = [(0,2,4,6),(12,13,14,15),(4,6,8,10),(0,1,4,5),(16,17,18,19),(4,5,6,
7,16,17,18,19),(17,19,21,23),(16,17,20,21),(0,1,2,3),(18,19,22,23),
(14,15,18,19),(1,3,5,7),(12,13,16,17),(12,14,16,18),(13,15,17,19),
(4,5,8,9),(2,3,6,7),(16,18,20,22),(5,7,9,11),(6,7,10,11),(8,9,10,11),
(20,21,22,23)]

EV = [[0,1],[2,3],[4,5],[6,7],[8,9],[10,11],[0,2],[1,3],[4,6],[5,7],
[8,10],[9,11],[0,4],[1,5],[2,6],[3,7],[4,8],[5,9],[6,10],[7,11],[12,13],
[14,15],[16,17],[18,19],[20,21],[22,23],[12,14],[13,15],[16,18],[17,19],
[20,22],[21,23],[12,16],[13,17],[14,18],[15,19],[16,20],[17,21],[18,22],
[19,23]]

csrBoundaryMat = boundary(CV,FV)
print "wrong boundary matrix =",csrBoundaryMat.todense()
csrBoundaryMat = boundary1(CV,FV,EV)
print "right boundary matrix =",csrBoundaryMat.todense()

VV = AA(LIST)(range(len(V)))
submodel = STRUCT(MKPOLS((V,EV)))
VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV,CV],submodel,.5))
◇
```

Testing correction to boundary operator for general (non-convex) LAR The test example exported in `test/py/larcc/test22.py` is aimed to check the working of LAR on chain complexes supported by cellular decompositions with non-convex but connected cells, possibly of topological genus > 1, i.e. with more than one hole in some face.

`"test/py/larcc/test22.py"` 13a ≡

```
""" Testing correction to boundary operator for general (non-convex) LAR """
from larlib import *

⟨ Input and visualization of a general cellular complex 13b ⟩
⟨ Visualization of the skeletons 15 ⟩
⟨ Computation of corrected boundary operator 16a ⟩
⟨ Visualization of some boundary chains 16b ⟩
◇
```

Input and visualization of a general cellular complex

⟨ Input and visualization of a general cellular complex 13b ⟩ ≡

```
""" Input and visualization of a general cellular complex """

mod1 = larQuote1D([0.2,-0.2,0.2])
```

```
mod2 = larQuote1D([0.5,0.5])
mod3 = larQuote1D([0.5])
mod = larModelProduct([larModelProduct([mod2,mod1]),mod3])

mx = larQuote1D([1,1])
my = larQuote1D([1])
m = larModelProduct([larModelProduct([mx,my]),my])

complex = Struct([m, t(.5,.2,.25), mod])
V,CV0 = struct2lar(complex)
CV = copy(CV0)
CV[1] += CV[0] + CV[4]
CV[3] += CV[2] + CV[5]
VIEW(SKEL_1(STRUCT( MKPOLS((V,CV)))))
◇
```

Macro referenced in 13a.

The LAR of the cellular decomposition shown in Figure **??** is given in Figure 4.

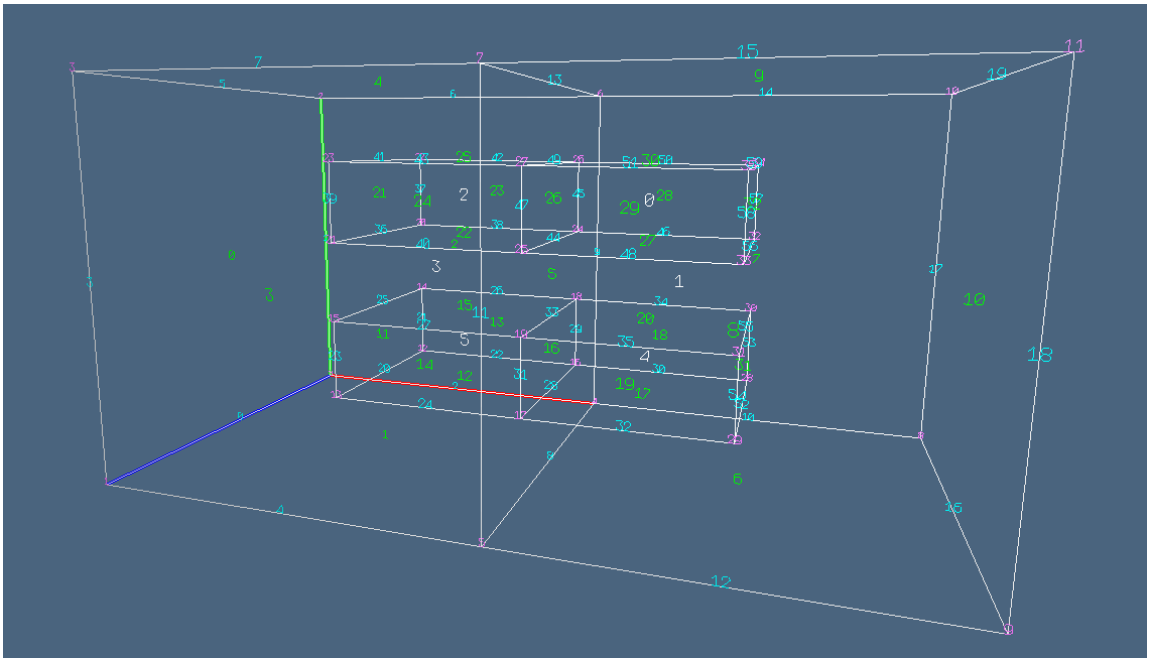

Figure 4: The cellular 3-complex defined below. Cells of different dimension are numbered in different colours.

We have 36 vertices, indexed from 0 to 35, and six 3-cells, numbered from 0 to 5. Notice that the subsets of integers `CV[1]` and `CV[3]` provide the description of the two non-convex cells.

```
V = [[0.0,0.0,0.0],[0.0,0.0,1.0],[0.0,1.0,0.0],[0.0,1.0,1.0], [1.0,0.0,0.0],
[1.0,0.0,1.0],[1.0,1.0,0.0],[1.0,1.0,1.0], [2.0,0.0,0.0],[2.0,0.0,1.0],
[2.0,1.0,0.0],[2.0,1.0,1.0], [0.5,0.2,0.25],[0.5,0.2,0.75],[0.5,0.4,0.25],
[0.5,0.4,0.75], [1.0,0.2,0.25],[1.0,0.2,0.75],[1.0,0.4,0.25],[1.0,0.4,0.75],
[0.5,0.6,0.25],[0.5,0.6,0.75],[0.5,0.8,0.25],[0.5,0.8,0.75], [1.0,0.6,0.25],
[1.0,0.6,0.75],[1.0,0.8,0.25],[1.0,0.8,0.75], [1.5,0.2,0.25],[1.5,0.2,0.75],
[1.5,0.4,0.25],[1.5,0.4,0.75], [1.5,0.6,0.25],[1.5,0.6,0.75],[1.5,0.8,0.25],
[1.5,0.8,0.75]]

CV = [(24,25,26,27,32,33,34,35),(4,5,6,7,8,9,10,11,24,25,26,27,
32,33,34,35,16,17,18,19,28,29,30,31),(20,21,22,23,24,25,26,27),
(0,1,2,3,4,5,6,7,20,21,22,23,24,25,26,27,12,13,14,15,16,17,18,19),
(16,17,18,19,28,29,30,31),(12,13,14,15,16,17,18,19)]
```

Computation and visualization of the skeletons

⟨ Visualization of the skeletons 15 ⟩ ≡

```
"""  Visualization of the skeletons """

def cubeFV(verts):
    [a,b,c,d,  e,f,g,h] = verts
    return [[a,b,c,d],[e,f,g,h],[a,c,e,g],[b,d,f,h],[a,b,e,f],[c,d,g,h]]

FV = COMP([sorted,set,AA(tuple),CAT,AA(cubeFV)])(CV0)
V,EV = larFacets((V,FV),dim=2)
VV = AA(LIST)(range(len(V)))
submodel = STRUCT(MKPOLS((V,EV)))
VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV,CV],submodel,.25))
FV[5] += FV[16] + FV[26]
assert 30==len(boundaryCells(CV0,FV))  # assembly of 3 unrelated 3-complexes
```

◇

Macro referenced in 13a.

```
FV = [(0,1,2,3),(0,1,4,5),(0,2,4,6),(1,3,5,7),(2,3,6,7),
(4,5,6,7,16,17,18,19,24,25,26,27),
(4,5,8,9),(4,6,8,10),(5,7,9,11),(6,7,10,11),(8,9,10,11), (12,13,14,15),
(12,13,16,17),(12,14,16,18),(13,15,17,19), (14,15,18,19),(16,17,18,19),
(16,17,28,29),(16,18,28,30), (17,19,29,31),(18,19,30,31),(20,21,22,23),
(20,21,24,25), (20,22,24,26),(21,23,25,27),(22,23,26,27),(24,25,26,27),
(24,25,32,33),(24,26,32,34),(25,27,33,35),(26,27,34,35), (28,29,30,31),
(32,33,34,35)]
```

Computation of corrected boundary operator Of course, `totalChain = len(CV)*[1]` is the binary coordinate `[1,1,1,1,1,1]` of the cellular chain made by all the six 3-cells in `CV`. Analogously, `BF` is the list of integer indices of boundary 2-faces, corresponding to the coordinate representation given below, i.e. to the binary string of lenght 33, equating the size of the 2-skeleton of the cellular complex.

```
BF = [0, 1, 2, 3, 4, 6, 7, 8, 9, 10]
\texttt{[1,1,1,1,1,0,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0]}
```

Conversely, `BEV` is (a superset of) the 1-skeleton cells of the boundary, according to the image in Figure **??**.

⟨ Computation of corrected boundary operator 16a ⟩ ≡

```
""" Computation of corrected boundary operator """

totalChain = len(CV)*[1]
BF = chain2BoundaryChain(boundary1(CV,FV,EV))(totalChain)
BFV = [FV[f] for f in BF]
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,BFV))))
glass = MATERIAL([1,0,0,0.1,  0,1,0,0.1,  0,0,1,0.1, 0,0,0,0.1, 100])
VIEW(STRUCT(AA(glass)(MKPOLS((V,BFV)))))
VIEW(glass(EXPLODE(1.2,1.2,1.2)(MKPOLS((V,BFV)))))
V,BEV = larFacets((V,BFV),dim=1)
VIEW(EXPLODE(1.2,1.2,1.2)(MKPOLS((V,[e for e in BEV if len(e)==2]))))
◇
```

Macro referenced in 13a.

Visualization of some boundary chains

⟨ Visualization of some boundary chains 16b ⟩ ≡

```
""" Visualization of some boundary chains """

BF = chain2BoundaryChain(boundary1(CV,FV,EV))([1,0,1,1,0,0])
BFV = [FV[f] for f in BF]
V,BEV = larFacets((V,BFV),dim=1)
BEV = [e for e in BEV if len(e)==2]
VIEW(glass(STRUCT(MKPOLS((V,BFV)))))
submodel = STRUCT(MKPOLS((V,BEV)))
VIEW(larModelNumbering(1,1,1)(V,[VV,BEV,BFV],submodel,.25))


obj = Struct([(V,BFV,BEV)])
W,FW,EW = struct2lar(obj)
VIEW(EXPLODE(1.2,1.2,1.2)(MKPOLS((W,EW))))
VIEW(SKEL_1(EXPLODE(1.2,1.2,1.2)(MKTRIANGLES((W,FW,EW)))))

◇
```

Macro referenced in 13a.

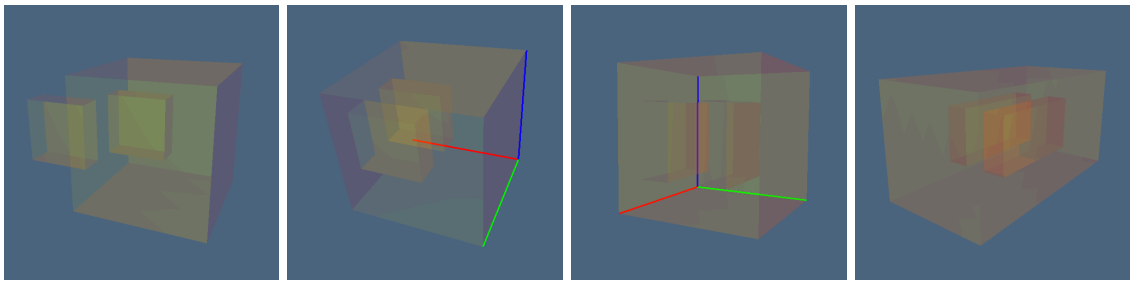

Figure 5: example caption

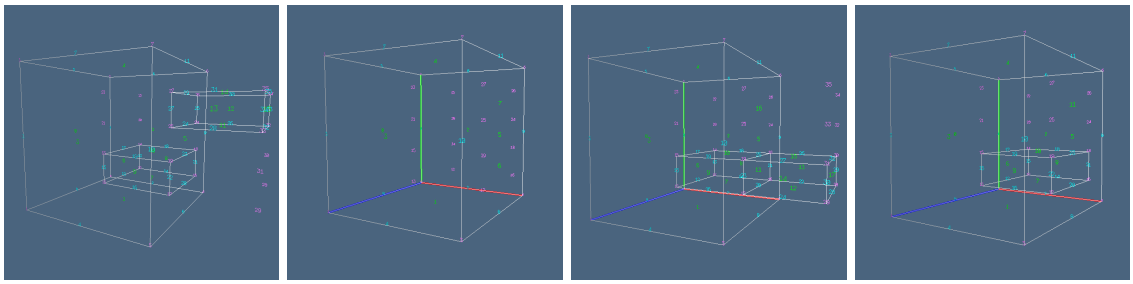

Figure 6: example caption

Relational inversion (characteristic matrix transposition) The operation could be executed by simple matrix transposition of the CSR (Compressed Sparse Row) representation of the sparse characteristic matrix $M_d \equiv$ `CV`. A simple relational inversion using Python lists is given here. The `invertRelation` function is given here, linear in the size of the `CV` list, where the complexity of each cell is constant and small in most cases.

⟨ Characteristic matrix transposition 17 ⟩ ≡

```
""" Characteristic matrix transposition """
def invertRelation(CV):
    def myMax(List):
        if List==[]:  return -1
        else:  return max(List)

    columnNumber = max(AA(myMax)(CV))+1
    VC = [[] for k in range(columnNumber)]
    for k,cell in enumerate(CV):
        for v in cell: VC[v] += [k]
```

```
        return VC
```
◇

Macro referenced in 50b.

2.4 Computation of lower-dimensional skeletons

In most cases, in particular when the cellular complex is made by convex cells, the only cells of maximal dimension must be entered to gain a complete knowledge of the whole complex. Here we show how to compute the $(d-1)$-skeleton of a complex starting from its d-dimensional skeleton.

Extraction of facets of a cell complex The following `larFacets` function returns the LAR model `V,cellFacets` starting from the input `model` parameter. Two optional parameters define the (intrinsic) dimension of the input cells, with default value equal to three, and the eventual presence of a `emptyCellNumber` of empty cells. Their number default to zero when the complex is closed, for example in the case it provides the d-boundary of a $(d+1)$-complex. If empty cells are present, their subset must be located at the end of the `cell` list.

⟨ Extraction of facets of a cell complex 18 ⟩ ≡

```
def setup(model,dim):
    V, cells = model
    csr = csrCreate(cells)
    csrAdjSquareMat = larCellAdjacencies(csr)
    csrAdjSquareMat = csrPredFilter(csrAdjSquareMat, GE(dim)) # ? HOWTODO ?
    return V,cells,csr,csrAdjSquareMat

def larFacets(model, dim=3, emptyCellNumber=0):
    """ Estraction of (d-1)-cellFacets from "model" := (V,d-cells)
        Return (V, (d-1)-cellFacets)
        """
    V,cells,csr,csrAdjSquareMat = setup(model,dim)
    solidCellNumber = len(cells) - emptyCellNumber
    cellFacets = []
    # for each input cell i
    for i in range(len(cells)):
        adjCells = csrAdjSquareMat[i].tocoo()
        cell1 = csr[i].tocoo().col
        pairs = zip(adjCells.col,adjCells.data)
        for j,v in pairs:
            if (i<j) and (i<solidCellNumber):
                cell2 = csr[j].tocoo().col
                cell = list(set(cell1).intersection(cell2))
                cellFacets.append(sorted(cell))
```

```
        # sort and remove duplicates
        cellFacets = sorted(AA(list)(set(AA(tuple)(cellFacets))))
        return V,cellFacets
```
◇

Macro referenced in 50b.

⟨ Computation of cell adjacencies 19a ⟩ ≡
```
def larCellAdjacencies(CSRm):
    CSRm = matrixProduct(CSRm,csrTranspose(CSRm))
    return CSRm
```
◇

Macro referenced in 50b.

Examples Two simple complexes are defined below by providing the pair `V,FV`. In both cases the `EV` relation is computed via the `larFacets` function.

⟨ Test examples of Extraction of facets of a cell complex 19b ⟩ ≡
```
""" A first (simplicial) example """
V = [[0.,0.],[3.,0.],[0.,3.],[3.,3.],[1.,2.],[2.,2.],[1.,1.],[2.,1.]]
FV = [[0,1,3],[1,2,4],[2,4,5],[3,4,6],[4,6,7],[5,7,8], # full
    [1,3,4],[4,5,7], # empty
    [0,1,2],[6,7,8],[0,3,6],[2,5,8]] # exterior
_,EV = larFacets((V,FV),dim=2)
print "\nEV =",EV
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,EV))))

""" Another (cuboidal) example """
FV = [[0,1,6,7],[0,2,4,6],[4,5,6,7],[1,3,5,7],[2,3,4,5],[0,1,2,3]]
_,EV = larFacets((V,FV),dim=2)
print "\nEV =",EV
VV = AA(LIST)(range(len(V)))
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,EV))))
```
◇

Macro referenced in 51a.

Visualization of cell numbers The adjacentcy matrices between 2-cells and 1-cells are printed here. Finally, the complex is displayed by numbering with different colours and sizes (depending on the rank) the complex cells.

⟨ Test examples of Computation of cell adjacencies 19c ⟩ ≡
```
print "\n>>> larCellAdjacencies"
adj_2_cells = larCellAdjacencies(csrCreate(FV))
print "\nadj_2_cells =\n", csr2DenseMatrix(adj_2_cells)
```

```
adj_1_cells = larCellAdjacencies(csrCreate(EV))
print "\nadj_1_cells =\n", csr2DenseMatrix(adj_1_cells)

submodel = mkSignedEdges((V,EV))
VIEW(submodel)
VIEW(larModelNumbering(scalx=1,scaly=1,scalz=1)(V,[VV,EV,FV],submodel,2))
```
◇

Macro referenced in 51a.

3 Topological operations

In this section we provide the matrix representation of operators to compute the more important and useful topological operations on cellular complexes, and/or the indexed relations they return. We start the section by giving a graphical tool used to test the developed software, concerning the graphical writing of the full set of indices of the cells of every dimension in a 3D cuboidal complex.

3.1 Visualization of cellular complexes

It is often necessary to have a visual picture of the generated structures and computations. This section provides some quite versatile visualisation tools of both the cells and/or their integer indices.

Visualization of cell indices As already outlined, the `modelIndexing` function return the *hpc* value assembling both the 1-skeletons of the cells of every dimensions, and the graphical output of their indices, located on the centroid of each cell, and displayed using colors and sizes depending on the *rank* of the cell.

⟨ Visualization of cell indices 20 ⟩ ≡

```
""" Visualization of cell indices """
from larlib import *

def modelIndexing(shape):
    V, bases = larCuboids(shape,True)
    # bases = [[cell for cell in cellComplex if len(cell)==2**k] for k in range(4)]
    color = [ORANGE,CYAN,GREEN,WHITE]
    nums = AA(range)(AA(len)(bases))
    hpcs = []
    for k in range(4):
        hpcs += [SKEL_1(STRUCT(MKPOLS((V,bases[k]))))]
        hpcs += [cellNumbering((V,bases[k]),hpcs[2*k])(nums[k],color[k],0.3+0.2*k)]
    return STRUCT(hpcs)
```
◇

Macro defined by 20, 21a.
Macro referenced in 50b.

⟨ Visualization of cell indices 21a ⟩ ≡

```
""" Numbered visualization of a LAR model """
def larModelNumbering(scalx=1,scaly=1,scalz=1):
    def  larModelNumbering0(V,bases,submodel,numberScaling=1):
        color = [ORANGE,CYAN,GREEN,WHITE]
        nums = AA(range)(AA(len)(bases))
        hpcs = [submodel]
        for k in range(len(bases)):
            hpcs += [cellNumbering((V,bases[k]),submodel)
                        (nums[k],color[k],(0.5+0.1*k)*numberScaling)]
        return STRUCT(hpcs)
        #return EXPLODE(scalx,scaly,scalz)(hpcs)
    return larModelNumbering0
```

◇

Macro defined by 20, 21a.
Macro referenced in 50b.

Drawing of oriented edges The following function return the `hpc` of the drawing with arrows of the oriented 1-cells of a 2D cellular complex. Of course, each edge orientation is from second to first vertex, independently from the vertex indices. Therefore, the edge orientation can be reversed by swapping the vertex indices in the 1-cell definition.

⟨ Drawing of oriented edges 21b ⟩ ≡

```
""" Drawing of oriented edges (2D) """
def mkSignedEdges (model,scalingFactor=1):
    V,EV = model
    assert len(V[0])==2
    hpcs = []
    times = C(SCALARVECTPROD)
    frac = 0.06*scalingFactor
    for e0,e1 in EV:
        v0,v1 = V[e0], V[e1]
        vx,vy = DIFF([ v1, v0 ])
        nx,ny = [-vy, vx]
        v2 = SUM([ v0, times(0.66)([vx,vy]) ])
        v3 = SUM([ v0, times(0.6-frac)([vx,vy]), times(frac)([nx,ny]) ])
        v4 = SUM([ v0, times(0.6-frac)([vx,vy]), times(-frac)([nx,ny]) ])
        verts,cells = [v0,v1,v2,v3,v4],[[1,2],[3,4],[3,5]]
        hpcs += [MKPOL([verts,cells,None])]
    hpc = STRUCT(hpcs)
    return hpc
```

◇

Macro referenced in 50b.

Example of oriented edge drawing An example of drawing of oriented edges is given in `test/py/larcc/test11.py` file, and in Figure 7, showing both the numbering of the cells and the arrows indicating the edge orientation is illustrated in Figure 7, where also the oriented boundary is shown.

"test/py/larcc/test11.py" 22a ≡

```
⟨ Example of oriented edge drawing 22b ⟩
◇
```

⟨ Example of oriented edge drawing 22b ⟩ ≡

```
""" Example of oriented edge drawing """
from larlib import *

V = [[9,0],[13,2],[15,4],[17,8],[14,9],[13,10],[11,11],[9,10],[7,9],[5,9],[3,
8],[0,6],[2,3],[2,1],[5,0],[7,1],[4,2],[12,10],[6,3],[8,3],[3,5],[5,5],[7,6],
[8,5],[10,5],[11,4],[10,2],[13,4],[14,6],[13,7],[11,9],[9,7],[7,7],[4,7],[2,
6],[12,7],[12,5]]

FV = [[0,1,26],[5,6,17],[6,7,17,30],[7,30,31],[7,8,31,32],[24,30,31,35],[3,4,
28],[4,5,17,29,30,35],[4,28,29],[28,29,35,36],[8,9,32,33],[9,10,33],[11,10,
33,34],[11,20,34],[20,33,34],[20,21,32,33],[18,21,22],[21,22,32],[22,23,31,
32],[23,24,31],[11,12,20],[12,16,18,20,21],[18,22,23],[18,19,23],[19,23,24],
[15,19,24,26],[0,15,26],[24,25,26],[24,25,35,36],[2,3,28],[1,2,27,28],[12,13,
16],[13,14,16],[14,15,16,18,19],[1,25,26,27],[25,27,36],[36,27,28]]

VIEW(EXPLODE(1.2,1.2,1)(MKPOLS((V,FV))))
VV = AA(LIST)(range(len(V)))
_,EV = larFacets((V,FV+[range(16)]),dim=2,emptyCellNumber=1)

submodel = mkSignedEdges((V,EV))
VIEW(submodel)
VIEW(larModelNumbering(scalx=1,scaly=1,scalz=1)(V,[VV,EV,FV],submodel,2))

orientedBoundary = signedCellularBoundaryCells(V,[VV,EV,FV])
cells = [EV[e] if sign==1 else REVERSE(EV[e]) for (sign,e) in zip(*orientedBoundary)]
submodel = mkSignedEdges((V,cells))
VIEW(submodel)
◇
```

Macro referenced in 22a, 24a.

Extracting the boundary of whichever chain The boundary of whichever chain, here defined as the list of indices of its cells, then transformed to its coordinate representation (column vector in the given basis), is explicitly computed by matrix product times the matrix of the boundary operator in the given basis, transformed back in its BRC representation, and displayed as LAR model.

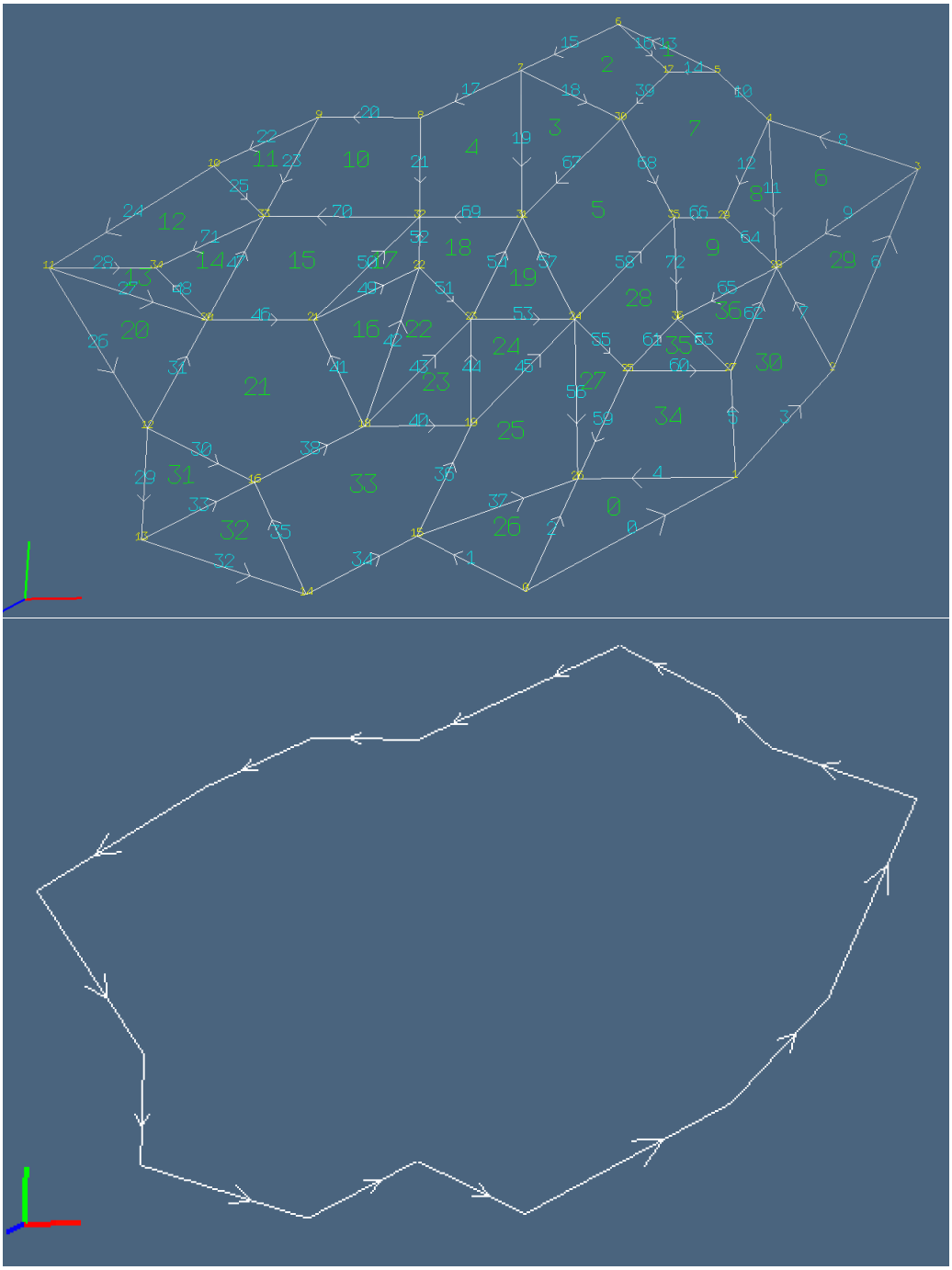

Figure 7: Example of numbered polytopal complex, including edge orientations, and its oriented boundary.

"test/py/larcc/test19.py" 24a ≡

```
""" Example of oriented edge drawing """

⟨ Example of oriented edge drawing 22b ⟩

C2 = csr_matrix((len(FV),1))
for i in [1,2, 12,13,14,15, 22,23, 29,30,31]: C2[i,0] = 1
BD = boundary(FV,EV)
C1 = BD * C2
C_1 = [i for i in range(len(EV)) if ABS(C1[i,0]) == 1 ]
C_2 = [i for i in range(len(FV)) if C2[i,0] == 1 ]

VIEW(EXPLODE(1.2,1.2,1)(MKPOLS((V,[EV[k] for k in C_1] + [FV[k] for k in C_2]))))
◇
```

From 2D chains to boundary chains

⟨ From 2D chains to boundary chains 24b ⟩ ≡

```
""" From 2D chains to boundary chains """
def chain2BoundaryChain(csrBoundaryMat):
    print ">>> chain2BoundaryChain"
    nedges,nfaces = csrBoundaryMat.shape
    def chain2BoundaryChain0(chain):
        row = np.array(range(len(chain)))
        col = np.array([0 for k in range(len(chain))])
        data = np.array(chain)
        csrFaceVect = scipy.sparse.coo_matrix((data, (row, col)), shape=(nfaces,1)).tocsr()
        csrEdgeVect = csrBoundaryMat*csrFaceVect
        boundaryChain = [h for h,val in
            zip(csrEdgeVect.tocoo().row, csrEdgeVect.tocoo().data) if val%2 != 0]
        return boundaryChain
    print "<<< chain2BoundaryChain"
    return chain2BoundaryChain0
◇
```

Macro referenced in 50b.

3.2 Incidence and adjacency operators

Let us start by computing the more interesting subset of the binary relationships between the 4 decompositive and/or boundary entities of 3D cellular models. Therefore, in this case we denote with `C`, `F`, `E`, and `V`, the 3-cells and their faces, edges and vertices, respectively.

The input is the full-fledged LAR representation provided by

$$\texttt{CV} := \texttt{CSR}(M_3) \tag{1}$$
$$\texttt{FV} := \texttt{CSR}(M_2) \tag{2}$$
$$\texttt{EV} := \texttt{CSR}(M_1) \tag{3}$$
$$\texttt{VV} := \texttt{CSR}(M_0) \tag{4}$$

Of course, $\texttt{CSR}(M_0)$ coincides with the identity matrix of dimension $|V|$ and can by excluded by further considerations. Some binary incidence and adjacency relations we are going to compute are:

$$\texttt{CF} := \texttt{CV} \times \texttt{FV}^t = \texttt{CSR}(M_3) \times \texttt{CSR}(M_2)^t \tag{5}$$
$$\texttt{CE} := \texttt{CV} \times \texttt{EV}^t = \texttt{CSR}(M_3) \times \texttt{CSR}(M_1)^t \tag{6}$$
$$\texttt{FE} := \texttt{FV} \times \texttt{EV}^t = \texttt{CSR}(M_2) \times \texttt{CSR}(M_1)^t \tag{7}$$

The other possible operators follow from a similer computational pattern.

The programming pattern for incidence computation A high-level function `larIncidence` useful to compute the LAR representation of the incidence matrix (operator) and the incidence relations is given in the script below.

⟨ Some incidence operators 25a ⟩ ≡

```
""" Some incidence operators """
def larIncidence(cells,facets):
    csrCellFacet = csrCellFaceIncidence(cells,facets)
    cooCellFacet = csrCellFacet.tocoo()
    larCellFacet = [[] for cell in range(len(cells))]
    for i,j,val in zip(cooCellFacet.row,cooCellFacet.col,cooCellFacet.data):
        if val == 1: larCellFacet[i] += [j]
    return larCellFacet
```

⟨ Cell-Face incidence operator 25b ⟩
⟨ Cell-Edge incidence operator 26a ⟩
⟨ Face-Edge incidence operator 26b ⟩
◇

Macro referenced in 50b.

Cell-Face incidence The `csrCellFaceIncidence` and `larCellFace` functions are given below, and exported to the `larcc` module.

⟨ Cell-Face incidence operator 25b ⟩ ≡

```
""" Cell-Face incidence operator """
def csrCellFaceIncidence(CV,FV):
    return boundary(FV,CV)

def larCellFace(CV,FV):
    return larIncidence(CV,FV)
◇
```

Macro referenced in 25a.

Cell-Edge incidence Analogously, the `csrCellEdgeIncidence` and `larCellFace` functions are given in the following script.

⟨ Cell-Edge incidence operator 26a ⟩ ≡

```
""" Cell-Edge incidence operator """
def csrCellEdgeIncidence(CV,EV):
     return boundary(EV,CV)

def larCellEdge(CV,EV):
    return larIncidence(CV,EV)
◇
```

Macro referenced in 25a.

Face-Edge incidence Finally, the `csrCellEdgeIncidence` and `larCellFace` functions are provided below.

⟨ Face-Edge incidence operator 26b ⟩ ≡

```
""" Face-Edge incidence operator """
def csrFaceEdgeIncidence(FV,EV):
    return boundary(EV,FV)

def larFaceEdge(FV,EV):
    return larIncidence(FV,EV)
◇
```

Macro referenced in 25a.

Example The example below concerns a 3D cuboidal grid, by computing a full LAR stack of bases `CV, FV, EV, VV`, showing its fully numbered 3D model, and finally by computing some more useful binary relationships (`CF, CE, FE`), needed for example to compute the signed matrices of boundary operators.

`"test/py/larcc/test10.py"` 26c ≡

```
""" A mesh model and various incidence operators """

from larlib import *

shape = [2,2,2]
V,(VV,EV,FV,CV) = larCuboids(shape,True)
VIEW(modelIndexing(shape))

CF = larCellFace(CV,FV)
CE = larCellFace(CV,EV)
FE = larCellFace(FV,EV)
◇
```

3.2.1 Incidence chain

Let denote with `CF`, `FE`, `EV` the three consecutive incidence relations between k-cells and $(k-1)$-cells $(3 \leq k \leq 0)$ in a 3-complex. In the general multidimensional case, let us call $\texttt{CF}_d$ the generic *binary* incidence operator, between d-cells and $(d-1)$-facets, as:

$$\texttt{CF}_d = M_{d-1}M_d^t,$$

with

$$\texttt{CF}_d := \{a_{ij}\}, \qquad a_{ij} = \begin{cases} 1 & \text{if } M_{d-1}(i)M_d(j) = |f_j| \\ 0 & \text{otherwise} \end{cases}$$

Incidence chain computation The function `incidenceChain`, given below, returns the full stack of `BRC` incidence matrices of a LAR representation for a cellular complex, starting from its list of bases, i.e. from `[VV,EV,FV,CV,...]`. Notice that the function returns the inverse sequence `[EV,FE,CF,...]`, i.e., $\texttt{CF}_k$ $(1 \leq k \leq d)$.

⟨ Incidence chain computation 27a ⟩ ≡

```
""" Incidence chain computation """
def incidenceChain(bases):
    #print "\n len(bases) = ",len(bases),"\n"
    pairsOfBases = zip(bases[1:],bases[:-1])
    relations = [larIncidence(cells,facets)
                    for cells,facets in pairsOfBases]
    return REVERSE(relations)
◇
```

Macro referenced in 50b.

"test/py/larcc/test13.py" 27b ≡

```
""" Example of incidence chain computation """
from larlib import *
```

```
shape = (1,1,2)
print "\n\nFor a better example provide a greater shape!"
V,bases = larCuboids(shape,True)

VV,EV,FV,CV = bases
incidence = incidenceChain([VV,EV,FV,CV])
relations = ["CF","FE","EV"]
for k in range(3):
    print "\n\n incidence", relations[k], "=\n", incidence[k],
print "\n\n"

submodel = SKEL_1(STRUCT(MKPOLS((V,EV))))
VIEW(larModelNumbering(scalx=1,scaly=1,scalz=1)(V,[VV,EV,FV,CV],submodel,1))
◇
```

Example of incidence chain computation When running the `test/py/larcc/test13.py` file one obtains the following printout. Notice that it provides the links between d-cell numerations and the numerations of their faces. See Figure 8 for this purpose.

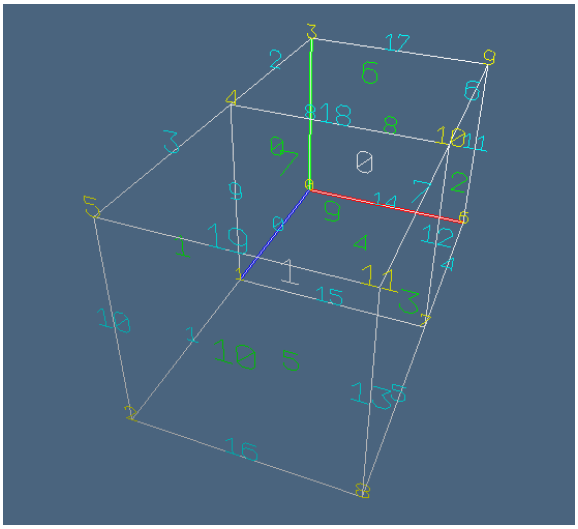

Figure 8: Che stack of incidence relations gives the common links between cell numerations.

⟨ Incidence chain for a 3D cuboidal complex 28 ⟩ ≡

```
incidence CF = [[0,2,4,6,8,9],[1,3,5,7,9,10]]

incidence FE = [[0,2,8,9],[1,3,9,10],[4,6,11,12],[5,7,12,13],[0,4,14,15],
[1,5,15,16],[2,6,17,18],[3,7,18,19],[8,11,14,17],[9,12,15,18],[10,13,16,19]]
```

```
incidence EV = [[0,1],[1,2],[3,4],[4,5],[6,7],[7,8],[9,10],[10,11],[0,3],
[1,4],[2,5],[6,9],[7,10],[8,11],[0,6],[1,7],[2,8],[3,9],[4,10],[5,11]]
```
◇

Macro never referenced.

3.3 Boundary and coboundary operators

When computing the matrices of boundary and coboundary operators it may be useful to distinguish between simplicial complexes and general polytopal complexes, including cuboidal ones. In the first cases all skeletons, and hence the other topological operators, may be computed using only combinatorial methods. In the second case some reference to their geometric embedding must be done, at least to compute the *oriented* boundary and coboundary. Therefore we separate the two cases in the following sections.

Computation of topological relations The function `crossRelation` is used here to compute a topological relation starting from two characteristic matrices `XV` and `YV`, that associate the sets of topological objects X and Y with their vertices, respectively. The technique using sparse binary matrices stored in `CSR` (Compressed Sparse Row) format is used.

⟨ Computation of topological relation 29 ⟩ ≡

```
""" Computation of topological relation """
def crossRelation(lenV,XV,YV,terminal=False):
    if terminal:
        print "\n****\nXV =",XV
        return XV
    else:
        csrXV = csrCreate(XV,lenV)
        csrYV = csrCreate(YV,lenV)
        csrXY = matrixProduct(csrXV, csrYV.T)
        XY = [None for k in range(len(XV))]
        for k,face in enumerate(XV):
            data = csrXY[k].data
            col = csrXY[k].indices
            XY[k] = [col[h] for h,val in enumerate(data) if val==min(len(XV[k]),len(YV[h]))]
            # NOTE: val depends on the relation under consideration ...
        return XY
```
◇

Macro referenced in 50b.

3.3.1 Non-oriented operators

The `boundary` function below takes as parameters the `BRC` representations of d-cells and $(d-1)$-facets, and returns the `CSR` matrix of the boundary operator. Let us notice that such operator uses a mod 2 algebra, since it takes elements within the field $\mathbb{Z}_2 = \{0, 1\}$.

⟨ Test examples of From cells and facets to boundary operator 30a ⟩ ≡

```
V = [[0.0,0.0,0.0],[1.0,0.0,0.0],[0.0,1.0,0.0],[1.0,1.0,0.0],
       [0.0,0.0,1.0],[1.0,0.0,1.0],[0.0,1.0,1.0],[1.0,1.0,1.0]]
CV = [[0,1,2,4],[1,2,4,5],[2,4,5,6],[1,2,3,5],[2,3,5,6],[3,5,6,7]]
FV = [[0,1,2],[0,1,4],[0,2,4],[1,2,3],[1,2,4],[1,2,5],[1,3,5],[1,4,5],[2,3,5],
      [2,3,6],[2,4,5],[2,4,6],[2,5,6],[3,5,6],[3,5,7],[3,6,7],[4,5,6],[5,6,7]]
EV = [[0,1],[0,2],[0,4],[1,2],[1,3],[1,4],[1,5],[2,3],[2,4],[2,5],
      [2,6],[3,5],[3,6],[3,7],[4,5],[4,6],[5,6],[5,7],[6,7]]
VV = AA(LIST)(range(len(V)))

print "\ncoboundary_2 =\n", csr2DenseMatrix(coboundary(CV,FV))
print "\ncoboundary_1 =\n", csr2DenseMatrix(coboundary(FV,EV))
print "\ncoboundary_0 =\n", csr2DenseMatrix(coboundary(EV,VV))
```

◇

Macro referenced in 51a.

In the script below it is necessary to guarantee that both `csrFV` and `csrCV` are created with the same number of column. The initial steps have this purpose.

⟨ From cells and facets to boundary operator 30b ⟩ ≡

```
def boundary(cells,facets):
    lenV = max(max(CAT(AA(list)(cells))),max(CAT(AA(list)(facets))))
    csrCV = csrCreate(cells,lenV)
    csrFV = csrCreate(facets,lenV)
    csrFC = matrixProduct(csrFV, csrTranspose(csrCV))
    facetLengths = [csrCell.getnnz() for csrCell in csrCV]
    return csrBoundaryFilter(csrFC,facetLengths)

def boundary1(CV,FV,EV):
    lenV = max(list(CAT(CV))+CAT(AA(list)(FV)))+1
    csrCV = csrCreate(CV,lenV)
    csrFV = csrCreate(FV,lenV)
    csrFC = matrixProduct(csrFV, csrTranspose(csrCV))
    facetLengths = [csrCell.getnnz() for csrCell in csrCV]
    VV = AA(LIST)(range(lenV))
    csrBoundaryBoundaryMat = boundary(FV,EV)*boundary(CV,FV)
    FE = crossRelation(lenV,CV,FV,EV,True)
    return csrBoundaryFilter1(csrBoundaryBoundaryMat,CV,FV,EV,lenV,FE,csrFC,facetLengths)

def coboundary(cells,facets):
    Boundary = boundary(cells,facets)
    return csrTranspose(Boundary)

def coboundary1(cells,facets):
    Boundary = boundary(cells,facets)
    return csrTranspose(Boundary)
```

◇

Macro referenced in 50b.

⟨ From cells and facets to boundary cells 31a ⟩ ≡

```
def totalChain(cells):
    return csrCreate([[0] for cell in cells])  # ????  zero ??

def boundaryCells(cells,facets):
    csrBoundaryMat = boundary(cells,facets)
    csrChain = totalChain(cells)
    csrBoundaryChain = matrixProduct(csrBoundaryMat, csrChain)
    for k,value in enumerate(csrBoundaryChain.data):
        if value % 2 == 0: csrBoundaryChain.data[k] = 0
    out = [k for k,val in enumerate(csrBoundaryChain.data.tolist()) if val == 1]
    return out
```

◇

Macro referenced in 50b.

⟨ Test examples of From cells and facets to boundary cells 31b ⟩ ≡

```
boundaryCells_2 = boundaryCells(CV,FV)
boundaryCells_1 = boundaryCells([FV[k] for k in boundaryCells_2],EV)

print "\nboundaryCells_2 =\n", boundaryCells_2
print "\nboundaryCells_1 =\n", boundaryCells_1

boundaryModel = (V,[FV[k] for k in boundaryCells_2])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(boundaryModel)))
```

◇

Macro referenced in 51a.

3.3.2 Oriented operators

Two d-cells are said *coherently oriented* when their common $(d-1)$-facet has opposite orientations with respect to the two cells. When the boundary of an orientable solid partitionates its affine hull in two subsets corresponding to the *interior* and the *exterior* of the solid, then the boundary cells can be coherently oriented. This task is performed by the function `signedBoundaryCells` and `signedCellularBoundaryCells` in the following scripts. The sparse matricial structures returned by the functions `signedSimplicialBoundary` and `signedCellularBoundary` take values in the Abelian group $\{-1, 0, 1\}$. We call them *signed* matrices, and call *signed* operators the corresponding boundary and coboundary.

Signed boundary matrix for simplicial complexes The computation of the *signed* boundary matrix for simplicial complexes starts with enumerating the non-zero elements of the mod two (unoriented) boundary matrix. In particular, the `pairs` variable contains all the pairs of incident $((d-1)$-cell, d-cell), corresponding to each 1 elements in the binary

boundary matrix. Of course, their number equates the product of the number of d-cells, times the number of $(d-1)$-facets on the boundary of each d-cell.

For the case of a 3-simplicial complex `CV`, we have $4|$`CV`$|$ `pairs` elements. The actual goal of the function `signedSimplicialBoundary`, in the macro below, is to compute a sign for each of them.

The `pairs` values must be interpreted as (i, j) values in the incidence matrix `FC` (*facets-cells*), and hence as pairs of indices f and c into the characteristic matrices `FV` = `CSR`(M_{d-1}) and `CV` = `CSR`(M_d), respectively.

For each incidence pair `f,c`, the list `vertLists` contains the two lists of vertices associated to `f` and to `c`, called respectively the `face` and the `coface`. For each `face, coface` pair (i.e. for each unit element in the unordered boundary matrix), the `missingVertIndices` list will contain the index of the `coface` vertex not contained in the incident `face`.

Finally, the ± 1 (signed) incidence coefficients are computed and stored in the `faceSigns`, and then located in their actual positions within the `csrSignedBoundaryMat`. The sign of the incidence coefficient associated to the pair (facet,cell), also called (face,coface) in the implementation below, is computed as the sign of $(-1)^k$, where k is the position index of the removed vertex in the facet $\langle v_0, \ldots, v_{k-1}, v_{k+1}, \ldots, v_d \rangle$. of the $\langle v_0, \ldots, v_d \rangle$ cell.

⟨ Signed boundary matrix for simplicial models 32 ⟩ ≡

```
def signedSimplicialBoundary (CV,FV):
    # compute the set of pairs of indices to [boundary face,incident coface]
    coo = boundary(CV,FV).tocoo()
    pairs = [[coo.row[k],coo.col[k]] for k,val in enumerate(coo.data) if val != 0]

    # compute the [face, coface] pair as vertex lists
    vertLists = [[FV[f], CV[c]] for f,c in pairs]

    # compute the local (interior to the coface) indices of missing vertices
    def missingVert(face,coface): return list(set(coface).difference(face))[0]
    missingVertIndices = [c.index(missingVert(f,c)) for f,c in vertLists]

    # signed incidence coefficients
    def checkPermutation(vertLists,missingVertIndices):
        sameOrientation = []
        for (face,coface),index in zip(vertLists,missingVertIndices):
            cell = tuple([vert for k,vert in enumerate(coface) if k!=index])
            if len(cell)==2 and cell==face: sameOrientation += [1]
            else: sameOrientation += [-1]  # TODO: generalize for any "cell"
        return sameOrientation

    sameOrientation = checkPermutation(vertLists,missingVertIndices)
    faceSigns = AA(C(POWER)(-1))(missingVertIndices)
    faceSigns = AA(PROD)(TRANS([faceSigns,sameOrientation]))
```

```
    # signed boundary matrix
    csrSignedBoundaryMat = csr_matrix( (faceSigns, TRANS(pairs)) )
    return csrSignedBoundaryMat
```
◇

Macro referenced in 50b.

Computation of signed boundary simplices The matrix of the signed boundary operator, with elements in $\{-1, 0, 1\}$, is computed in compressed sparse row (CSR) format, and stored in `csrSignedBoundaryMat`. In order to be able to return a list of `signedBoundaryCells` having a coherent orientation, we need to compute the coface of each boundary facet, i.e. the single d-cell having the facet on its boundary, and provide a coherent orientation to such chain of d-cells. The goal is obtained computing the sign of the determinant of the coface matrices, i.e. of square matrices having as rows the vertices of a coface, in normalised homogeneous coordinates.

The chain of boundary facets `boundaryCells`, obtained by multiplying the signed matrix of the boundary operator by the coordinate representation of the total d-chain, is coherently oriented by multiplication times the determinants of the `cofaceMats`.

The `cofaceMats` list is filled with the matrices having per row the position vectors of vertices of a coface, in normalized homogeneous coordinates. The list of signed face indices `orientedBoundaryCells` is returned by the function.

⟨ Orientation of general convex cells 33 ⟩ ≡

```
def swap(mylist): return [mylist[1]]+[mylist[0]]+mylist[2:]

def boundaryCellsCocells(cells,facets):
    csrSignedBoundaryMat = signedSimplicialBoundary(V,cells,facets)
    csrTotalChain = totalChain(cells)
    csrBoundaryChain = matrixProduct(csrSignedBoundaryMat, csrTotalChain)
    cooCells = csrBoundaryChain.tocoo()
    boundaryCells = []
    for k,v in enumerate(cooCells.data):
        if abs(v) == 1:
            boundaryCells += [int(cooCells.row[k] * cooCells.data[k])]
    boundaryCocells = []
    for k,v in enumerate(boundaryCells):
        boundaryCocells += list(csrSignedBoundaryMat[abs(v)].tocoo().col)
    return boundaryCells,boundaryCocells

def signedBoundaryCells(verts,cells,facets):
    boundaryCells,boundaryCocells = boundaryCellsCocells(cells,facets)
    boundaryCofaceMats = [[verts[v]+[1] for v in cells[c]] for c in boundaryCocells]
    boundaryCofaceSigns = AA(SIGN)(AA(np.linalg.det)(boundaryCofaceMats))
    orientedBoundaryCells = list(array(boundaryCells)*array(boundaryCofaceSigns))
```

```
        return orientedBoundaryCells
```
◇

Macro referenced in 50b.

Signed boundary matrix for polytopal complexes

⟨ Signed boundary matrix for polytopal complexes 34a ⟩ ≡

```
    """ Signed boundary matrix for polytopal complexes """
    def signedCellularBoundary(V,bases):
        coo = boundary(bases[-1],bases[-2]).tocoo()
        pairs = [[coo.row[k],coo.col[k]] for k,val in enumerate(coo.data) if val != 0]
        signs = []
        dim = len(bases)-1
        chain = incidenceChain(bases)

        for pair in pairs:        # for each facet/coface pair
            flag = REVERSE(pair) #  [c,f]
            #print "flag 1 =",flag
            for k in range(dim-1):
                cell = flag[-1]
                flag += [chain[k+1][cell][1]]

            verts = [CCOMB([V[v] for v in bases[dim-k][flag[k]]]) for k in range(dim+1)]
            flagMat = [verts[v]+[1] for v in range(dim+1)]
            flagSign = SIGN(np.linalg.det(flagMat))
            signs += [flagSign]

        csrSignedBoundaryMat = csr_matrix( (signs, TRANS(pairs)) )
        # numpy.set_printoptions(threshold=numpy.nan)
        # print csrSignedBoundaryMat.todense()
        return csrSignedBoundaryMat
```
◇

Macro referenced in 50b.

Oriented boundary cells for polytopal complexes

⟨ Signed boundary cells for polytopal complexes 34b ⟩ ≡

```
    """ Signed boundary cells for polytopal complexes """
    from scipy.sparse import *

    def signedCellularBoundaryCells(verts,bases):
        CV = bases[-1]
        boundaryMat = signedCellularBoundary(verts,bases)
        chainCoords = csc_matrix((len(CV), 1))
        for cell in range(len(CV)): chainCoords[cell,0] = 1
```

```
    boundaryCells = list((boundaryMat * chainCoords).tocoo().row)
    orientations = list((boundaryMat * chainCoords).tocoo().data)
    return orientations,boundaryCells
```
◇

Macro referenced in 50b.

3.3.3 Examples

Boundary of a 2D cuboidal grid The `larCuboids` function, when applied to a `shape` parameter and to the optional parameter `full=True`, returns both the intoger vertices `V` of the generated complex, and the list of `bases` of cells of dimension k ($0 \leq k \leq d$), where $d =$ `len(shape)` $- 1$.

"test/py/larcc/test14.py" 35a ≡
```
""" Boundary of a 2D cuboidal grid """
from larlib import *

V,bases = larCuboids([6,6],True)
[VV,EV,FV] = bases
submodel = mkSignedEdges((V,EV))
VIEW(submodel)
VIEW(larModelNumbering(scalx=1,scaly=1,scalz=1)(V,bases,submodel,1))

orientedBoundary = signedCellularBoundaryCells(V,bases)
FV = [EV[e] if sign==1 else REVERSE(EV[e])  for (sign,e) in zip(*orientedBoundary)]
submodel = mkSignedEdges((V,FV))
VIEW(submodel)
VIEW(larModelNumbering(scalx=1,scaly=1,scalz=1)(V,bases,submodel,1))
```
◇

Oriented cuboidal and simplicial cells In the example `test/py/larcc/test15.py` we generate a simplicial and a cuboidal decomposition of the space parallelepiped with `shape` $= [5, 5, 3]$. In both cases the boundary matrix is computed by using the general polytopal approach provided by the `signedCellularBoundaryCells` function, showing in both cases the oriented boundary of the two complexes (Just notice that in the cuboidal version `pyplasm` makes a wrong rendering, to be fixed).

"test/py/larcc/test15.py" 35b ≡
```
""" Oriented cuboidal and simplicial cells (same algorithm) """
from larlib import *

# cuboidal grid
V,bases = larCuboids([5,5,3],True)
[VV,EV,FV,CV] = bases
```

```
    orientedBoundary = signedCellularBoundaryCells(V,AA(AA(REVERSE))([VV,EV,FV,CV]))
    cells = [FV[f] if sign==1 else REVERSE(FV[f])  for (sign,f) in zip(*orientedBoundary)]
    VIEW(EXPLODE(1.25,1.25,1.25)(MKPOLS((V,cells))))

    # simplicial grid
    V,CV = larSimplexGrid1([5,5,3])
    FV = larSimplexFacets(CV)
    EV = larSimplexFacets(FV)
    VV = AA(LIST)(range(len(V)))
    bases = [VV,EV,FV,CV]
    orientedBoundary = signedCellularBoundaryCells(V,bases)
    cells = [FV[f] if sign==1 else REVERSE(FV[f])  for (sign,f) in zip(*orientedBoundary)]
    VIEW(EXPLODE(1.25,1.25,1.25)(MKPOLS((V,cells))))
    ◇
```

"test/py/larcc/test18.py" 36 ≡

```
    """ Oriented cuboidal cells """
    """ Oriented cuboidal cells """
    from larlib import *

    def orientedBoundaryCells(V,(VV,EV,FV,CV)):
        boundaryMat = signedCellularBoundary(V,[VV,EV,FV,CV])
        chainCoords = csc_matrix((len(CV), 1))
        for cell in range(len(CV)): chainCoords[cell,0] = 1
        boundaryCells = list((boundaryMat * chainCoords).tocoo().row)
        orientations = list((boundaryMat * chainCoords).tocoo().data)
        return zip(orientations,boundaryCells)

    def normalVector(V,facet):
        v0,v1,v2 = facet[:3]
        return VECTPROD([ DIFF([V[v1],V[v0]]), DIFF([V[v2],V[v0]]) ])

    # cuboidal grid
    V,bases = larCuboids([5,5,3],True)
    [VV,EV,FV,CV] = bases
    BCpairs = orientedBoundaryCells(V,[VV,EV,FV,CV])
    orientedBoundary = [FV[face] if sign>0 else swap(FV[face]) for (sign,face) in BCpairs]
    normals = [ normalVector(V,facet)  for facet in orientedBoundary ]
    facetCentroids = [CCOMB([V[v] for v in facet]) for facet in orientedBoundary]
    appliedNormals = [[centroid,SUM([centroid,normal])] for (centroid,normal) in zip(facetCentroids
    normalVectors = AA(POLYLINE)(appliedNormals)

    orientedQuads = [[sign,FV[face]] if sign>0 else [sign,swap(FV[face])] for (sign,face) in BCpai
    FVtriangles = CAT([[[v0,v1,v2],[v2,v1,v3]] if sign==1 else [[v0,v1,v2],[v0,v2,v3]]
                for (sign,[v0,v1,v2,v3]) in orientedQuads])

    VIEW(EXPLODE(1.2,1.2,1.2)(MKPOLS((V,FVtriangles))+normalVectors))
```

◇

3.3.4 Boundary orientation of a random (2D) cubical complex

"test/py/larcc/test17.py" 37 ≡

```
"""" Boundary orientation of a random 2D cubical complex """
from larlib import *
from random import random

# test model generation
shape = 20,20
V,FV = larCuboids(shape)
cellSpan = prod(shape)
fraction = 0.5
remove = [int(random()*cellSpan) for k in range(int(cellSpan*fraction)) ]
FV = [FV[k] for k in range(cellSpan) if not (k in remove)]
_,EV = larCuboidsFacets((V,FV))
VV = AA(LIST)(range(len(V)))
orientedBoundary = signedCellularBoundaryCells(V,[VV,EV,FV])
cells = [EV[e] if sign==1 else REVERSE(EV[e]) for (sign,e) in zip(*orientedBoundary)]

# test model visualization
VIEW(STRUCT(MKPOLS((V,FV))))
VIEW(STRUCT(MKPOLS((V,EV))))
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,cells))))
VIEW(STRUCT(MKPOLS((V,cells))))
VIEW(mkSignedEdges((V,cells),2))
◇
```

3.3.5 Boundary orientation of a random (2D) triangulation

Here we provide a 2D example of computation of the oriented boundary of a quite convoluted random cellular complex. The steps performed by the scripts in the following paragraphs are listed below:

1. vertices are generated as random point in the unit circle
2. the Delaunay triangulation of the whole set of points is built.
3. spike-like triangles elimination
4. the 90% of triangles is randomly discarded
5. the input LAR is provided by the remaining triangles
6. the 1-cells are computed, and if $n_i < n_j$ – oriented as $v_i \to v_j$

7. the 2-cells are "coherently oriented" via the sign of their 3x3 determinant using normalised homogeneous coordinates of vertices: ccw if det > 0
8. the signed boundary matrix $[\partial_2]$ is built (with elements in $\{-1, 0, 1\}$)
9. the signed boundary 1-chain (the red one) is computed by $[\partial_2][\mathbf{1}_2]$, where $[\mathbf{1}_2]$ is the coordinate representation of the total 2-chain

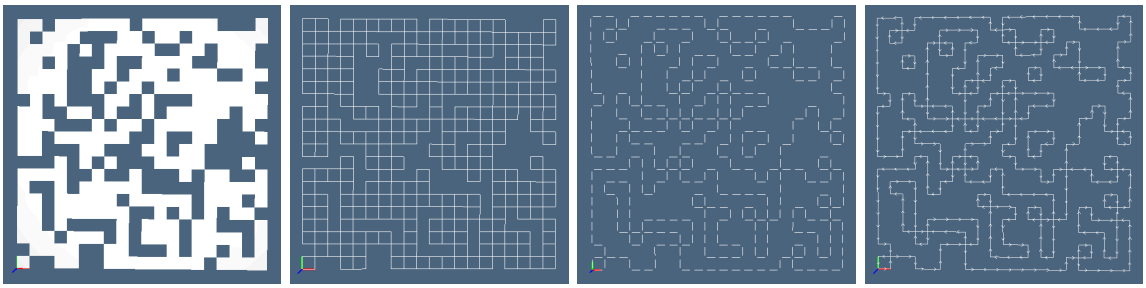

Figure 9: The orientation of the boundary of a random cuboidal 2-complex; (a) 2-cells; (b) 1-cells; (c) exploded boundary 1-chain; (d) oriented boundary 1-chain.

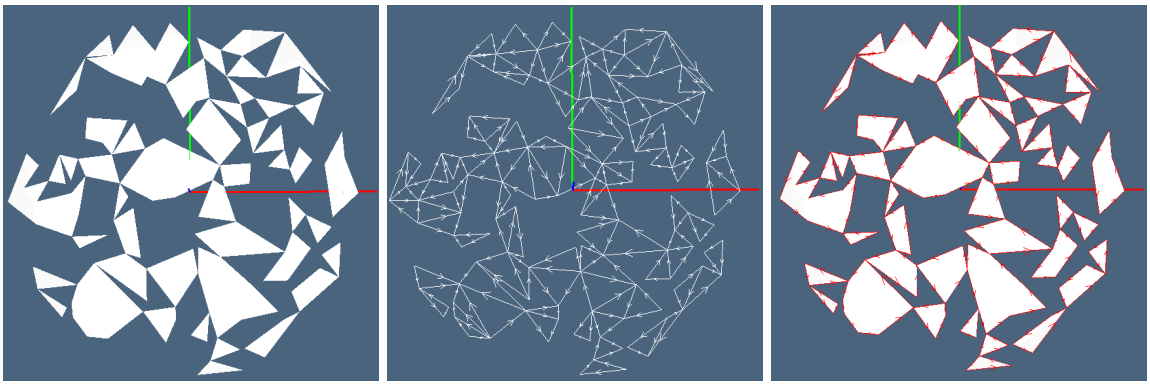

Figure 10: The orientation of the boundary of a random simplicial 2-complex; (a) 2-cells; (b) 1-cells; (c) oriented boundary 1-chain (red).

Top-down implementation

"test/py/larcc/test16.py" 38 ≡

```
""" Boundary orientation of a random 2D triangulation """
from larlib import *
from random import random
from scipy import spatial,linalg
```

⟨ Vertices V generated as random point in the unit circle 39a ⟩
⟨ Delaunay triangulation of the whole set V of points 39b ⟩
⟨ Fraction of triangles randomly discarded 39c ⟩
⟨ Coherently orient the input LAR model (V,FV) 40a ⟩
⟨ Compute the 1-cell and 0-cell bases EV and VV 40b ⟩
⟨ Signed 2-boundary matrix and signed boundary 1-chain 40c ⟩
⟨ Display the boundary 1-chain 40d ⟩
◇

Vertices V generated as random point in the unit circle

⟨ Vertices V generated as random point in the unit circle 39a ⟩ ≡

```
""" Vertices V generated as random point in the unit circle """
verts = []
npoints = 50
for k in range(npoints):
    t = 2*pi*random()
    u = random()+random()
    if u > 1: r = 2-u
    else: r = u
    verts += [[r*cos(t), r*sin(t)]]
VIEW(STRUCT(AA(MK)(verts)))
```

◇

Macro referenced in 38.

Delaunay triangulation of the whole set V of points

⟨ Delaunay triangulation of the whole set V of points 39b ⟩ ≡

```
""" Delaunay triangulation of the whole set V of points """
triangles = spatial.Delaunay(verts)
def area(cell): return linalg.det([verts[v]+[1] for v in cell])/2
cells = [ cell for cell in triangles.vertices.tolist() if area(cell)>PI/(3*npoints)]
V, FV = AA(list)(verts), cells
```

◇

Macro referenced in 38.

Fraction of triangles randomly discarded

⟨ Fraction of triangles randomly discarded 39c ⟩ ≡

```
""" Fraction of triangles randomly discarded """
fraction = 0.25
cellSpan = len(FV)
remove = [int(random()*cellSpan) for k in range(int(cellSpan*fraction)) ]
FV = [FV[k] for k in range(cellSpan) if not k in remove]
```

◇

Macro referenced in 38.

Coherent orientation of input LAR model (V,FV)

⟨ Coherently orient the input LAR model (V,FV) 40a ⟩ ≡

```
""" Coherently orient the input LAR model (V,FV) """
def positiveOrientation(model):
    V,simplices = model
    out = []
    for simplex in simplices:
        theMat = [V[v]+[1] for v in simplex]
        if sign(linalg.det(theMat)) > 0:  out += [simplex]
        else: out += [REVERSE(simplex)]
    return V,out

V,FV = positiveOrientation((V,FV))
```

◇

Macro referenced in 38.

Compute the 1-cell and 0-cell bases EV and VV

⟨ Compute the 1-cell and 0-cell bases EV and VV 40b ⟩ ≡

```
""" Compute the 1-cell and 0-cell bases EV and VV """
EV = larSimplexFacets(FV)
VV = AA(LIST)(range(len(V)))
VIEW(mkSignedEdges((V,EV)))
```

◇

Macro referenced in 38.

Signed boundary matrix $[\partial_2]$ and signed boundary 1-chain

⟨ Signed 2-boundary matrix and signed boundary 1-chain 40c ⟩ ≡

```
""" Signed 2-boundary matrix  and signed boundary 1-chain """
orientedBoundary = signedCellularBoundaryCells(V,[VV,EV,FV])
cells = [EV[e] if sign==1 else REVERSE(EV[e]) for (sign,e) in zip(*orientedBoundary)]
```

◇

Macro referenced in 38.

Display the boundary 1-chain

⟨ Display the boundary 1-chain 40d ⟩ ≡

```
""" Display the boundary 1-chain """
VIEW(STRUCT(MKPOLS((V,FV))))
VIEW(STRUCT(
    MKPOLS((V,FV)) +
    [COLOR(RED)(mkSignedEdges((V,cells)))]  ))
```

◇

Macro referenced in 38.

3.4 Orienting polytopal cells

An orientation can be allocated to a general convex (polytopal) cell by computing the biggest simplex in its interior, and attributing to the cell the orientation of the contained simplex. It is in fact easy to see that the orientation can be propagated via adjacent coherently oriented simplexes, until to cover the whole cell.

The variables in the following script have the meaning specified below: input : "cell" indices of a convex and solid polytopes and "V" vertices; output : biggest "simplex" indices spanning the polytope; `m` : number of cell vertices; `d` : dimension (number of coordinates) of cell vertices; `d+1` : number of simplex vertices; `vcell` : cell vertices; `vsimplex` : simplex vertices; `Id` : identity matrix; `basis` : orthonormal spanning set of vectors e_k; `vector` : position vector of a simplex vertex in translated coordinates; `unUsedIndices` : cell indices not moved to simplex.

⟨ Oriented boundary cells for simplicial models 41 ⟩ ≡

```
def pivotSimplices(V,CV,d=3):
    simplices = []
    for cell in CV:
        vcell = np.array([V[v] for v in cell])
        m, simplex = len(cell), []
        # translate the cell: for each k, vcell[k] -= vcell[0], and simplex[0] := cell[0]
        for k in range(m-1,-1,-1): vcell[k] -= vcell[0]
        # simplex = [0], basis = [], tensor = Id(d+1)
        simplex += [cell[0]]
        basis = []
        tensor = np.array(IDNT(d))
        # look for most distant cell vertex
        dists = [SUM([SQR(x) for x in v])**0.5 for v in vcell]
        maxDistIndex = max(enumerate(dists),key=lambda x: x[1])[0]
        vector = np.array([vcell[maxDistIndex]])
        # normalize vector
        den=(vector**2).sum(axis=-1) **0.5
        basis = [vector/den]
        simplex += [cell[maxDistIndex]]
        unUsedIndices = [h for h in cell if h not in simplex]

        # for k in {2,d+1}:
        for k in range(2,d+1):
            # update the orthonormal tensor
            e = basis[-1]
            tensor = tensor - np.dot(e.T, e)
            # compute the index h of a best vector
            # look for most distant cell vertex
            dists = [SUM([SQR(x) for x in np.dot(tensor,v)])**0.5
            if h in unUsedIndices else 0.0
```

```
                for (h,v) in zip(cell,vcell)]
                # insert the best vector index h in output simplex
                maxDistIndex = max(enumerate(dists),key=lambda x: x[1])[0]
                vector = np.array([vcell[maxDistIndex]])
                # normalize vector
                den=(vector**2).sum(axis=-1) **0.5
                basis += [vector/den]
                simplex += [cell[maxDistIndex]]
                unUsedIndices = [h for h in cell if h not in simplex]
            simplices += [simplex]
        return simplices

    def simplexOrientations(V,simplices):
        vcells = [[V[v]+[1.0] for v in simplex] for simplex in simplices]
        return [SIGN(np.linalg.det(vcell)) for vcell in vcells]
    ◇
```

Macro referenced in 50b.

Affine transformations of points Some primitive maps of points to points are given in the following, including translation, rotation and scaling of array of points via direct transformation of their coordinates. Second-order functions are used in order to employ their curried version to transform geometric assemblies.

⟨ Affine transformations of d-points 42 ⟩ ≡

```
    def larTranslate (tvect):
        def larTranslate0 (points):
            return [VECTSUM([p,tvect]) for p in points]
        return larTranslate0

    def larRotate (angle):        # 2-dimensional !! TODO: n-dim
        def larRotate0 (points):
            a = angle
            return [[x*COS(a)-y*SIN(a), x*SIN(a)+y*COS(a)] for x,y in points]
        return larRotate0

    def larScale (svect):
        def larScale0 (points):
            print "\n points =",points
            print "\n svect =",svect
            return [AA(PROD)(TRANS([p,svect])) for p in points]
        return larScale0
    ◇
```

Macro referenced in 50b.

4 Piecewise-linear mapping of topological spaces

A very simple but foundational software subsystem is developed in this section, by giving a general mechanism to produce curved maps of topological spaces, via the simplicial decomposition of a chart, i.e. of a planar embedding of the fundamental polygon of a d-dimensional manifold, and the definition of coordinate functions to be applied to its vertices (0-cells of the decomposition) to generate an embedding of the manifold.

4.1 Domain decomposition

A simplicial map is a map between simplicial complexes with the property that the images of the vertices of a simplex always span a simplex. Simplicial maps are thus determined by their effects on vertices, and provide a piecewise-linear approximation of their underlying polyhedra.

Since double simmeries are always present in the curved primitives generated in the module, an alternative cellular decomposition with cuboidal cells is provided. The default choice is "cuboid".

Standard and scaled decomposition of unit domain The `larDomain` of given `shape` is decomposed by `larSimplexGrid1` as an hypercube of dimension $d \equiv$ `len(shape)`, where the `shape` tuple provides the number or row, columns, pages, etc. of the decomposition.

⟨ Generate a simplicial decomposition ot the $[0,1]^d$ domain 43a ⟩ ≡

```
"""" cellular decomposition of the unit d-cube """"
def larDomain(shape, cell='cuboid'):
    if cell=='simplex': V,CV = larSimplexGrid1(shape)
    elif cell=='cuboid': V,CV = larCuboids(shape)
    V = larScale( [1./d for d in shape])(V)
    return [V,CV]
```

◇

Macro referenced in 50b.

A scaled simplicial decomposition is provided by the second-order `larIntervals` function, with `len(shape)` and `len(size)` parameters, where the d-dimensionale vector `len(size)` is assumed as the scaling vector to be applied to the point $\mathbf{1} \in \mathbb{E}^d$.

⟨ Scaled simplicial decomposition ot the $[0,1]^d$ domain 43b ⟩ ≡

```
def larIntervals(shape, cell='cuboid'):
    def larIntervals0(size):
        V,CV = larDomain(shape,cell)
        V = larScale( size)(V)
        return [V,CV]
    return larIntervals0
```

◇

Macro referenced in 50b.

4.2 Mapping domain vertices

The second-order textttlarMap function is the LAR implementation of the PLaSM primitive `MAP`. It is applied to the array `coordFuncs` of coordinate functions and to the simplicially decomposed `domain`, returning an embedded and/or curved `domain` instance.

⟨ Primitive mapping function 44a ⟩ ≡

```
def larMap(coordFuncs):
    if isinstance(coordFuncs, list): coordFuncs = CONS(coordFuncs)
    def larMap0(domain,dim=2):
        V,CV = domain
        V = AA(coordFuncs)(V)  # plasm CONStruction
        return [V,CV]
        # checkModel([V,CV])  TODO
    return larMap0
```

◇

Macro referenced in 50b.

4.3 Identify close or coincident points

The function `checkModel`, applied to a `model` parameter, i.e. to a (vertices, cells) pair, returns the model after identification of vertices with coincident or very close position vectors. The `checkModel` function works as follows: first a dictionary `vertDict` is created, with key a suitably approximated position converted into a string by the `vcode` converter (given in the Appendix), and with value the list of vertex indices with the same (approximated) position. Then, an `invertedindex` array is created, associating each original vertex index with the new index produced by enumerating the (distinct) keys of the dictionary. Finally, a new list `CV` of cells is created, by substituting the new vertex indices for the old ones.

⟨ Create a dictionary with key the point location 44b ⟩ ≡

```
from collections import defaultdict
def checkModel(model,dim=2):
    V,CV = model; n = len(V)
    vertDict = defaultdict(list)
    for k,v in enumerate(V): vertDict[vcode(v)].append(k)
    points,verts = TRANS(vertDict.items())
    invertedindex = [None]*n
    V = []
    for k,value in enumerate(verts):
        V.append(eval(points[k]))
        for i in value:
            invertedindex[i]=k
    CV = [[invertedindex[v] for v in cell] for cell in CV]
    # filter out degenerate cells
    CV = [list(set(cell)) for cell in CV if len(set(cell))>=dim+1]
```

```
        return [V, CV]
```
◇

Macro referenced in 50b.

2-cell with high topological genus

"test/py/larcc/test23.py" 45a ≡
```
    """ 2-cell with high topological genus """
    from larlib import *

    ⟨ Output of 2-cell with high topological genus 0. 45b ⟩
    ⟨ Output of 2-cell with high topological genus 1. 45c ⟩
    ⟨ Output of 2-cell with high topological genus 2. 45d ⟩
```
◇

⟨ Output of 2-cell with high topological genus 0. 45b ⟩ ≡
```
    """ 2-cell with high topological genus 0. """
    side = QUOTE(5*[1,-1])
    holes = PROD([side,side])
    V,FV,_ = UKPOL(holes)
    FV = [[v-1 for v in f] for f in FV]
    EV = CAT([[[v,f[(k+1)%4]] for k,v in enumerate(f+[f[0]][:-1])] for f in FV])
    VIEW(STRUCT(MKPOLS((V,EV))))

    (W,_) = larBox((-1,-1),(10,10))
    (_,(_,EW,FW)) = larCuboids((1,1),True)
    complex = Struct([(W,FW,EW),(V,FV,EV)])
    V,FV,EV = struct2lar(complex)
```
◇

Macro referenced in 45a, 46.

⟨ Output of 2-cell with high topological genus 1. 45c ⟩ ≡
```
    """ 2-cell with high topological genus 1. """
    FV = [sorted(CAT(FV))]
    # EV = sorted(AA(sorted)(EV))  # p2t bug if uncommented: CHECK
    VIEW(STRUCT(MKPOLS((V,EV))))

    VV = AA(LIST)(range(len(V)))
    submodel = STRUCT(MKPOLS((V,EV)))
    VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV],submodel,1.5))
```
◇

Macro referenced in 45a.

⟨ Output of 2-cell with high topological genus 2. 45d ⟩ ≡

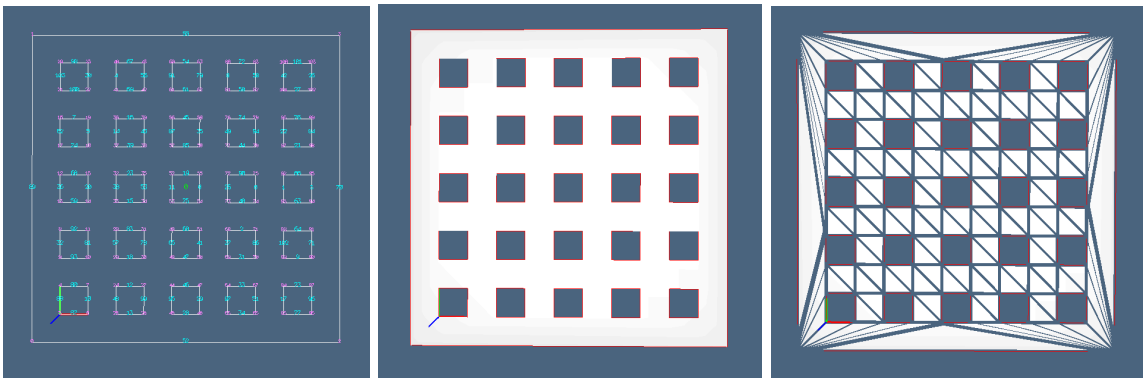

Figure 11: LAR of a 2-complex: (a) numbering of complex 0-, 1- and 2-cells (just one, numbered 0); (b) solid display of the complex, with boundary 1-cells (all 1-cells) colored in red; (c) triangulation of the interior, made for display purpose.

```
""" 2-cell with high topological genus 2. """

# LAR data structures
csrBoundaryMat = boundary(FV,EV)
boundaryChain = chain2BoundaryChain(csrBoundaryMat)([1])
triangleSet = larTriangulation( (V,EV) )

# PyPLaSM data structures
hpcChain = AA(JOIN)(AA(AA(MK))(CAT(triangleSet)))
hpcChainBoundary = AA(COLOR(RED))(MKPOLS((V,[EV[e] for e in boundaryChain])))

VIEW(STRUCT( hpcChain + hpcChainBoundary ))
VIEW(EXPLODE(1.2,1.2,1.2)( hpcChain + hpcChainBoundary ))
◇
```

Macro referenced in 45a.

Explicit LAR of 2-cell with high topological genus The explicit definition of the LAR of the 2-complex shown in Figura 12 is given below. The reader should notice that the LAR contains the 2-faces description `EV` of a single 2-cell—of cardinality $O(V)$, and that the bulk of this representation is the array of edge indices `EV`, given here in lexicographic order.

"test/py/larcc/test24.py" 46 ≡

```
""" Explicit LAR of 2-cell with high topological genus """
from larlib import *
```

⟨ Output of 2-cell with high topological genus 0. 45b ⟩

```
    FV = [CAT(FV)] + sorted(AA(list)(FV))[1:]
    # EV = sorted(AA(sorted)(EV))  # p2t bug if uncommented: CHECK
    model = V,FV,EV

    VV = AA(LIST)(range(len(V)))
    submodel = STRUCT(MKPOLS((V,EV)))
    VIEW(larModelNumbering(1,1,1)(V,[VV,EV,FV],submodel,1.5))

    # LAR data structures
    chain = [1]+[0]*(len(FV)-1)
    outModel,triangleSet = larComplexChain(model)(chain)

    viewLarComplexChain(model)([0]+[1]*(len(FV)-1))
    viewLarComplexChain(model)([1]+[0]*(len(FV)-1))
    viewLarComplexChain(model)([1]+[0]*5 + [1]*(len(FV)-6))
    viewLarComplexChain(model)([1]*(len(FV)))
    ◇
```

"test/py/larcc/test25.py" 47 ≡

```
    """ 2-cell with high topological genus """
    from larlib import *

    V = [[-1.0,-1.0],[-1.0,10.0],[10.0,-1.0],[10.0,10.0],[0.0,1.0],[0.0,0.0],[1.0,0.0],
    [1.0,1.0],[0.0,3.0],[0.0,2.0],[1.0,2.0],[1.0,3.0],[0.0,5.0],[0.0,4.0],[1.0,4.0],
    [1.0,5.0],[0.0,7.0],[0.0,6.0],[1.0,6.0],[1.0,7.0],[0.0,9.0],[0.0,8.0],[1.0,8.0],
    [1.0,9.0],[2.0,1.0],[2.0,0.0],[3.0,0.0],[3.0,1.0],[2.0,3.0],[2.0,2.0],[3.0,2.0],
    [3.0,3.0],[2.0,5.0],[2.0,4.0],[3.0,4.0],[3.0,5.0],[2.0,7.0],[2.0,6.0],[3.0,6.0],
    [3.0,7.0],[2.0,9.0],[2.0,8.0],[3.0,8.0],[3.0,9.0],[4.0,1.0],[4.0,0.0],[5.0,0.0],
    [5.0,1.0],[4.0,3.0],[4.0,2.0],[5.0,2.0],[5.0,3.0],[4.0,5.0],[4.0,4.0],[5.0,4.0],
    [5.0,5.0],[4.0,7.0],[4.0,6.0],[5.0,6.0],[5.0,7.0],[4.0,9.0],[4.0,8.0],[5.0,8.0],
    [5.0,9.0],[6.0,1.0],[6.0,0.0],[7.0,0.0],[7.0,1.0],[6.0,3.0],[6.0,2.0],[7.0,2.0],
    [7.0,3.0],[6.0,5.0],[6.0,4.0],[7.0,4.0],[7.0,5.0],[6.0,7.0],[6.0,6.0],[7.0,6.0],
    [7.0,7.0],[6.0,9.0],[6.0,8.0],[7.0,8.0],[7.0,9.0],[8.0,1.0],[8.0,0.0],[9.0,0.0],
    [9.0,1.0],[8.0,3.0],[8.0,2.0],[9.0,2.0],[9.0,3.0],[8.0,5.0],[8.0,4.0],[9.0,4.0],
    [9.0,5.0],[8.0,7.0],[8.0,6.0],[9.0,6.0],[9.0,7.0],[8.0,9.0],[8.0,8.0],[9.0,8.0],
    [9.0,9.0]]

    FV = [[0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,
    28,29,30, 31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,
    54,55,56,57,58,59,60, 61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,
    80,81,82,83,84,85,86,87,88,89,90, 91,92,93,94,95,96,97,98,99,100,101,102,103],[4,
    5,6,7],[8,9,10,11],[12,13,14,15],[16,17,18, 19],[20,21,22,23],[24,25,26,27],[28,
    29,30,31],[32,33,34,35],[36,37,38,39],[40,41,42,43],[ 44,45,46,47],[48,49,50,51],
    [52,53,54,55],[56,57,58,59],[60,61,62,63],[64,65,66,67],[68,69, 70,71],[72,73,74,
    75],[76,77,78,79],[80,81,82,83],[84,85,86,87],[88,89,90,91],[92,93,94,95],[96,97,
    98,99],[100,101,102,103]]
```

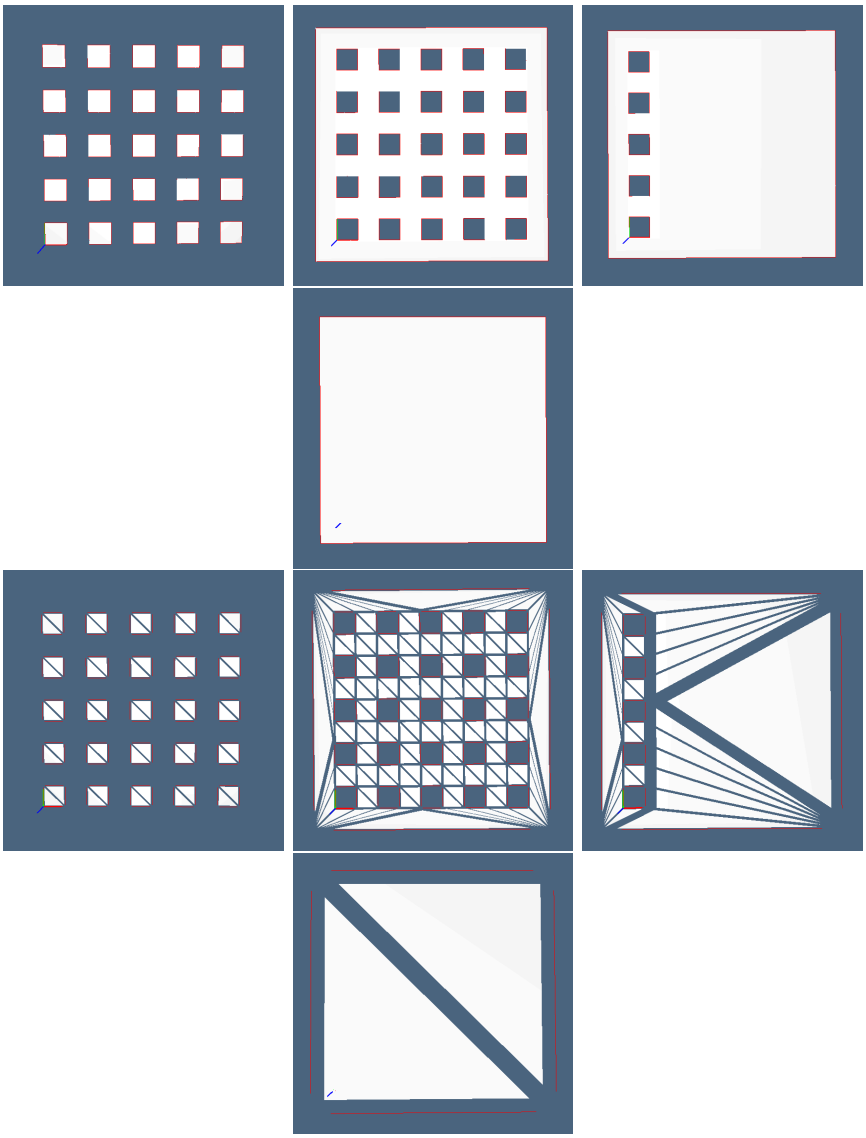

Figure 12: LAR of a 2-complex. Upper row: interior (white) and boundary (red) of different 2-chains; Lower row: triangulations of the chains. Warning: all extracted from LAR of a complex with the same boundary operator ... :o)

```
EV = [(54,55),(92,93),(68,71),(94,95),(40,41),(18,19),(74,75),(16,19),(80,81),(89,
90),(6,7),(52,53),(24,27),(25,26),(36,37),(33,34),(36,39),(84,85),(29,30),(52,55),
(14,15),(97,98),(96,97),(32,35),(17,18),(72,73),(102,103),(101,102),(45,46),(46,47),
(22,23),(69,70),(8,9),(64,67),(65,66),(58,59),(12,13),(68,69),(32,33),(37,38),(73,
74),(50,51),(100,101),(38,39),(77,78),(56,59),(44,47),(49,50),(24,25),(76,77),(81,
82),(66,67),(0,2),(34,35),(60,63),(1,3),(42,43),(28,29),(82,83),(13,14),(48,51),
(61,62),(16,17),(93,94),(88,91),(48,49),(92,95),(40,43),(12,15),(41,42),(2,3),(90,
91),(80,83),(84,87),(76,79),(53,54),(96,99),(85,86),(30,31),(62,63),(4,7),(10,11),
(5,6),(28,31),(98,99),(57,58),(70,71),(56,57),(4,5),(0,1),(72,75),(60,61),(8,11),
(9,10),(78,79),(44,45),(86,87),(64,65),(20,23),(26,27),(21,22),(100,103),(88,89),
(20,21)]

chain1 = [0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1]
chain2 = [1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0]
chain3 = [1,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1]
chain4 = [1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1]

model = V,FV,EV
viewLarComplexChain(model)(chain1)
viewLarComplexChain(model)(chain2)
viewLarComplexChain(model)(chain3)
viewLarComplexChain(model)(chain4)
◇
```

5 Exporting the library

5.1 MIT licence

⟨ The MIT Licence 49 ⟩ ≡

```
"""
The MIT License
===============

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    SOFTWARE OR THE USE OR OTHER DEALINGS IN THE SOFTWARE.
    """
    ◇
```

Macro referenced in 50b.

5.2 Importing of modules or packages

⟨ Importing of modules or packages 50a ⟩ ≡

```
    from larlib import *

    import collections
    import numpy as np
    from scipy import zeros,arange,mat,amin,amax,array
    from scipy.sparse import vstack,hstack,csr_matrix,coo_matrix,lil_matrix,triu
    ◇
```

Macro referenced in 50b.

5.3 Writing the library file

"larlib/larlib/larcc.py" 50b ≡

```
    # -*- coding: utf-8 -*-
    """ Basic LARCC library """
```

⟨ The MIT Licence 49 ⟩
⟨ Importing of modules or packages 50a ⟩
⟨ Affine transformations of d-points 42 ⟩
⟨ From list of triples to scipy.sparse 3b ⟩
⟨ Brc to Coo transformation 2 ⟩
⟨ Coo to Csr transformation 3c ⟩
⟨ Brc to Csr transformation 4a ⟩
⟨ Query Matrix shape 5a ⟩
⟨ Sparse to dense matrix transformation 6a ⟩
⟨ Matrix product and transposition 6c ⟩
⟨ Matrix filtering to produce the boundary matrix 8 ⟩
⟨ Matrix filtering via a generic predicate 9b ⟩
⟨ Characteristic matrix transposition 17 ⟩
⟨ From cells and facets to boundary operator 30b ⟩
⟨ From cells and facets to boundary cells 31a ⟩
⟨ Computation of topological relation 29 ⟩
⟨ Signed boundary matrix for simplicial models 32 ⟩

⟨ Orientation of general convex cells 33 ⟩
⟨ Computation of cell adjacencies 19a ⟩
⟨ Extraction of facets of a cell complex 18 ⟩
⟨ Some incidence operators 25a ⟩
⟨ Visualization of cell indices 20, ... ⟩
⟨ Numbered visualization of a LAR model ? ⟩
⟨ Drawing of oriented edges 21b ⟩
⟨ Incidence chain computation 27a ⟩
⟨ Signed boundary matrix for polytopal complexes 34a ⟩
⟨ Signed boundary cells for polytopal complexes 34b ⟩
⟨ Oriented boundary cells for simplicial models 41 ⟩
⟨ Generate a simplicial decomposition ot the $[0,1]^d$ domain 43a ⟩
⟨ Scaled simplicial decomposition ot the $[0,1]^d$ domain 43b ⟩
⟨ Create a dictionary with key the point location 44b ⟩
⟨ Primitive mapping function 44a ⟩
⟨ From 2D chains to boundary chains 24b ⟩

```
if __name__ == "__main__":
    ⟨ Test examples 51a ⟩
```

◇

6 Unit tests

⟨ Test examples 51a ⟩ ≡

⟨ Test example of Brc to Coo transformation 3a ⟩
⟨ Test example of Coo to Csr transformation 3d ⟩
⟨ Test example of Brc to Csr transformation 4b ⟩
⟨ Test examples of Query Matrix shape 5b ⟩
⟨ Test examples of Sparse to dense matrix transformation 6b ⟩
⟨ Test example of Matrix filtering to produce the boundary matrix 9a ⟩
⟨ Test example of Matrix filtering via a generic predicate 10a ⟩
⟨ Test examples of From cells and facets to boundary operator 30a ⟩
⟨ Test examples of From cells and facets to boundary cells 31b ⟩
⟨ Test examples of Computation of cell adjacencies 19c ⟩
⟨ Test examples of Extraction of facets of a cell complex 19b ⟩
◇

Macro referenced in 50b.

Comparing oriented and unoriented boundary

"test/py/larcc/test09.py" 51b ≡

```
""" comparing oriented boundary and unoriented boundary extraction on a simple example """
```

```
import sys; sys.path.insert(0, 'lib/py/')
from largrid import *
from larcc import *

V,CV = larSimplexGrid1([1,1,1])
FV = larSimplexFacets(CV)

orientedBoundary = signedBoundaryCells(V,CV,FV)
orientedBoundaryFV = [FV[-k] if k<0 else swap(FV[k]) for k in orientedBoundary]
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,orientedBoundaryFV))))

BF = boundaryCells(CV,FV)
boundaryCellsFV = [FV[k] for k in BF]
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,boundaryCellsFV))))
◇
```

"test/py/larcc/test12.py" 52a ≡

```
""" comparing edge orientation and oriented boundary extraction """
import sys; sys.path.insert(0, 'lib/py/')
from largrid import *
from larcc import *

V,FV = larSimplexGrid1([5,5])
EV = larSimplexFacets(FV)
VIEW(mkSignedEdges((V,EV)))

orientedBoundary = signedBoundaryCells(V,FV,EV)
orientedBoundaryEV = [EV[-k] if k<0 else swap(EV[k]) for k in orientedBoundary]
VIEW(mkSignedEdges((V,orientedBoundaryEV)))
◇
```

A Appendix: Tutorials

A.1 Model generation, skeleton and boundary extraction

"test/py/larcc/test01.py" 52b ≡

```
""" Model generation, skeleton and boundary extraction """
from larlib import *
⟨ input of 2D topology and geometry data 53a ⟩
⟨ characteristic matrices 53b ⟩
⟨ incidence matrix 53c ⟩
⟨ boundary and coboundary operators 53d ⟩
⟨ product of cell complexes 53e ⟩
⟨ 2-skeleton extraction 54a ⟩
⟨ 1-skeleton extraction 54b ⟩
⟨ 0-coboundary computation 54c ⟩
```

⟨ 1-coboundary computation 55a ⟩
⟨ 2-coboundary computation 55b ⟩
⟨ boundary chain visualisation 55c ⟩
◇

⟨ input of 2D topology and geometry data 53a ⟩ ≡

```
# input of geometry and topology
V2 = [[4,10],[8,10],[14,10],[8,7],[14,7],[4,4],[8,4],[14,4]]
EV = [[0,1],[1,2],[3,4],[5,6],[6,7],[0,5],[1,3],[2,4],[3,6],[4,7]]
FV = [[0,1,3,5,6],[1,2,3,4],[3,4,6,7]]
```
◇

Macro referenced in 52b.

⟨ characteristic matrices 53b ⟩ ≡

```
# characteristic matrices
csrFV = csrCreate(FV)
csrEV = csrCreate(EV)
print "\nFV =\n", csr2DenseMatrix(csrFV)
print "\nEV =\n", csr2DenseMatrix(csrEV)
```
◇

Macro referenced in 52b.

⟨ incidence matrix 53c ⟩ ≡

```
# product
csrEF = matrixProduct(csrEV, csrTranspose(csrFV))
print "\nEF =\n", csr2DenseMatrix(csrEF)
```
◇

Macro referenced in 52b.

⟨ boundary and coboundary operators 53d ⟩ ≡

```
# boundary and coboundary operators
facetLengths = [csrCell.getnnz() for csrCell in csrEV]
boundary = csrBoundaryFilter(csrEF,facetLengths)
coboundary_1 = csrTranspose(boundary)
print "\ncoboundary_1 =\n", csr2DenseMatrix(coboundary_1)
```
◇

Macro referenced in 52b.

⟨ product of cell complexes 53e ⟩ ≡

```
# product operator
mod_2D = (V2,FV)
V1,topol_0 = [[0.],[1.],[2.]], [[0],[1],[2]]
topol_1 = [[0,1],[1,2]]
mod_0D = (V1,topol_0)
```

```
mod_1D = (V1,topol_1)
V3,CV = larModelProduct([mod_2D,mod_1D])
mod_3D = (V3,CV)
VIEW(EXPLODE(1.2,1.2,1.2)(MKPOLS(mod_3D)))
print "\nk_3 =", len(CV), "\n"
```
◇

Macro referenced in 52b.

⟨ 2-skeleton extraction 54a ⟩ ≡
```
# 2-skeleton of the 3D product complex
mod_2D_1 = (V2,EV)
mod_3D_h2 = larModelProduct([mod_2D,mod_0D])
mod_3D_v2 = larModelProduct([mod_2D_1,mod_1D])
_,FV_h = mod_3D_h2
_,FV_v = mod_3D_v2
FV3 = FV_h + FV_v
SK2 = (V3,FV3)
VIEW(EXPLODE(1.2,1.2,1.2)(MKPOLS(SK2)))
print "\nk_2 =", len(FV3), "\n"
```
◇

Macro referenced in 52b.

⟨ 1-skeleton extraction 54b ⟩ ≡
```
# 1-skeleton of the 3D product complex
mod_2D_0 = (V2,AA(LIST)(range(len(V2))))
mod_3D_h1 = larModelProduct([mod_2D_1,mod_0D])
mod_3D_v1 = larModelProduct([mod_2D_0,mod_1D])
_,EV_h = mod_3D_h1
_,EV_v = mod_3D_v1
EV3 = EV_h + EV_v
SK1 = (V3,EV3)
VIEW(EXPLODE(1.2,1.2,1.2)(MKPOLS(SK1)))
print "\nk_1 =", len(EV3), "\n"
```
◇

Macro referenced in 52b.

⟨ 0-coboundary computation 54c ⟩ ≡
```
# boundary and coboundary operators
np.set_printoptions(threshold=sys.maxint)
csrFV3 = csrCreate(FV3)
csrEV3 = csrCreate(EV3)
csrVE3 = csrTranspose(csrEV3)
facetLengths = [csrCell.getnnz() for csrCell in csrEV3]
boundary = csrBoundaryFilter(csrVE3,facetLengths)
coboundary_0 = csrTranspose(boundary)
print "\ncoboundary_0 =\n", csr2DenseMatrix(coboundary_0)
```
◇

Macro referenced in 52b.

⟨ 1-coboundary computation 55a ⟩ ≡

```
csrEF3 = matrixProduct(csrEV3, csrTranspose(csrFV3))
facetLengths = [csrCell.getnnz() for csrCell in csrFV3]
boundary = csrBoundaryFilter(csrEF3,facetLengths)
coboundary_1 = csrTranspose(boundary)
print "\ncoboundary_1.T =\n", csr2DenseMatrix(coboundary_1.T)
```

◇

Macro referenced in 52b.

⟨ 2-coboundary computation 55b ⟩ ≡

```
csrCV = csrCreate(CV)
csrFC3 = matrixProduct(csrFV3, csrTranspose(csrCV))
facetLengths = [csrCell.getnnz() for csrCell in csrCV]
boundary = csrBoundaryFilter(csrFC3,facetLengths)
coboundary_2 = csrTranspose(boundary)
print "\ncoboundary_2 =\n", csr2DenseMatrix(coboundary_2)
```

◇

Macro referenced in 52b.

⟨ boundary chain visualisation 55c ⟩ ≡

```
# boundary chain visualisation
boundaryCells_2 = boundaryCells(CV,FV3)
boundary = (V3,[FV3[k] for k in boundaryCells_2])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(boundary)))
```

◇

Macro referenced in 52b.

A.2 Boundary of 3D simplicial grid

"test/py/larcc/test02.py" 55d ≡

```
""" Boundary of 3D simplicial grid """
from larlib import *

⟨ boundary of 3D simplicial grid 55e ⟩
```

◇

⟨ boundary of 3D simplicial grid 55e ⟩ ≡

```
V,CV = larSimplexGrid1([10,10,3])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,CV))))
SK2 = (V,larSimplexFacets(CV))
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(SK2)))
_,FV = SK2
```

```
SK1 = (V,larSimplexFacets(FV))
_,EV = SK1
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(SK1)))

boundaryCells_2 = boundaryCells(CV,FV)
boundary = (V,[FV[k] for k in boundaryCells_2])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(boundary)))
print "\nboundaryCells_2 =\n", boundaryCells_2

boundaryCells_2 = signedBoundaryCells(V,CV,FV)
boundaryFV = [FV[-k] if k<0 else swap(FV[k]) for k in boundaryCells_2]

VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,boundaryFV))))
print "\nboundaryCells_2 =\n", boundaryFV
◇
```

Macro referenced in 55d.

A.3 Oriented boundary of a random simplicial complex

"test/py/larcc/test03.py" 56a ≡

```
""" Oriented boundary of a random simplicial complex """
from larlib import *

⟨ Importing external modules 56b ⟩
⟨ Generating and viewing a random 3D simplicial complex 56c ⟩
⟨ Computing and viewing its non-oriented boundary 57a ⟩
⟨ Computing and viewing its oriented boundary 57b ⟩
◇
```

⟨ Importing external modules 56b ⟩ ≡

```
""" Importing external modules """
from scipy.spatial import Delaunay
import numpy as np
◇
```

Macro referenced in 56a.

⟨ Generating and viewing a random 3D simplicial complex 56c ⟩ ≡

```
verts = np.random.rand(10000, 3) # 1000 points in 3-d
verts = [AA(lambda x: 2*x)(VECTDIFF([vert,[0.5,0.5,0.5]])) for vert in verts]
verts = [vert for vert in verts if VECTNORM(vert) < 1.0]
tetra = Delaunay(verts)
cells = [cell for cell in tetra.vertices.tolist()
         if  ((verts[cell[0]][2]<0) and (verts[cell[1]][2]<0)
                and (verts[cell[2]][2]<0) and (verts[cell[3]][2]<0) ) ]
V, CV = verts, cells
VIEW(MKPOL([V,AA(AA(lambda k:k+1))(CV),[]]))
```

◇

Macro referenced in 56a.

⟨ Computing and viewing its non-oriented boundary 57a ⟩ ≡

```
FV = larSimplexFacets(CV)
VIEW(MKPOL([V,AA(AA(lambda k:k+1))(FV),[]]))
boundaryCells_2 = boundaryCells(CV,FV)
print "\nboundaryCells_2 =\n", boundaryCells_2
bndry = (V,[FV[k] for k in boundaryCells_2])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(bndry)))
```

◇

Macro referenced in 56a.

⟨ Computing and viewing its oriented boundary 57b ⟩ ≡

```
boundaryCells_2 = signedBoundaryCells(V,CV,FV)
print "\nboundaryCells_2 =\n", boundaryCells_2
boundaryFV = [FV[-k] if k<0 else swap(FV[k]) for k in boundaryCells_2]
boundaryModel = (V,boundaryFV)
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(boundaryModel)))
```

◇

Macro referenced in 56a.

A.4 Oriented boundary of a simplicial grid

"test/py/larcc/test04.py" 57c ≡

⟨ Generate and view a 3D simplicial grid 57d ⟩
⟨ Computing and viewing the 2-skeleton of simplicial grid 57e ⟩
⟨ Computing and viewing the oriented boundary of simplicial grid 58a ⟩
◇

⟨ Generate and view a 3D simplicial grid 57d ⟩ ≡

```
""" Generate and view a 3D simplicial grid """
from larlib import *

V,CV = larSimplexGrid1([4,4,4])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,CV))))
```

◇

Macro referenced in 57c.

⟨ Computing and viewing the 2-skeleton of simplicial grid 57e ⟩ ≡

```
FV = larSimplexFacets(CV)
EV = larSimplexFacets(FV)
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,FV))))
```

◇

Macro referenced in 57c.

⟨ Computing and viewing the oriented boundary of simplicial grid 58a ⟩ ≡

```
csrSignedBoundaryMat = signedSimplicialBoundary (V,CV,FV)
boundaryCells_2 = signedBoundaryCells(V,CV,FV)
boundaryFV = [FV[-k] if k<0 else swap(FV[k]) for k in boundaryCells_2]
boundary = (V,boundaryFV)
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(boundary)))
◇
```

Macro referenced in 57c.

A.5 Skeletons and oriented boundary of a simplicial complex

"test/py/larcc/test05.py" 58b ≡

```
""" Skeletons and oriented boundary of a simplicial complex """
from larlib import *

⟨ Skeletons computation and visualisation ? ⟩
⟨ Oriented boundary matrix visualization 58d ⟩
⟨ Computation of oriented boundary cells 58e ⟩
◇
```

⟨ Skeletons computation and vilualisation 58c ⟩ ≡

```
""" Skeletons computation and vilualisation """
V,FV = larSimplexGrid1([3,3])
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,FV))))
EV = larSimplexFacets(FV)
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,EV))))
VV = larSimplexFacets(EV)
VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS((V,VV))))
◇
```

Macro never referenced.

⟨ Oriented boundary matrix visualization 58d ⟩ ≡

```
""" Oriented boundary matrix visualization """
np.set_printoptions(threshold='nan')
csrSignedBoundaryMat = signedSimplicialBoundary (V,FV,EV)
Z = csr2DenseMatrix(csrSignedBoundaryMat)
print "\ncsrSignedBoundaryMat =\n", Z
import matplotlib.pyplot
from pylab import *
matshow(Z)
show()
◇
```

Macro referenced in 58b.

⟨ Computation of oriented boundary cells 58e ⟩ ≡

```
    """  Computation of oriented boundary cells """
    boundaryCells_1 = signedBoundaryCells(V,FV,EV)
    print "\nboundaryCells_1 =\n", boundaryCells_1
    boundaryEV = [EV[-k] if k<0 else swap(EV[k]) for k in boundaryCells_1]
    bndry = (V,boundaryEV)
    VIEW(EXPLODE(1.5,1.5,1.5)(MKPOLS(bndry)))
    ◇
```

Macro referenced in 58b.

A.6 Boundary of random 2D simplicial complex

"test/py/larcc/test06.py" 59a ≡

```
    """ Boundary of random 2D simplicial complex """
    from larlib import *
    from scipy.spatial import Delaunay

    ⟨ Test for quasi-equilateral triangles 59b ⟩
    ⟨ Generation and selection of random triangles 60a ⟩
    ⟨ Boundary computation and visualisation 60b ⟩
    ◇
```

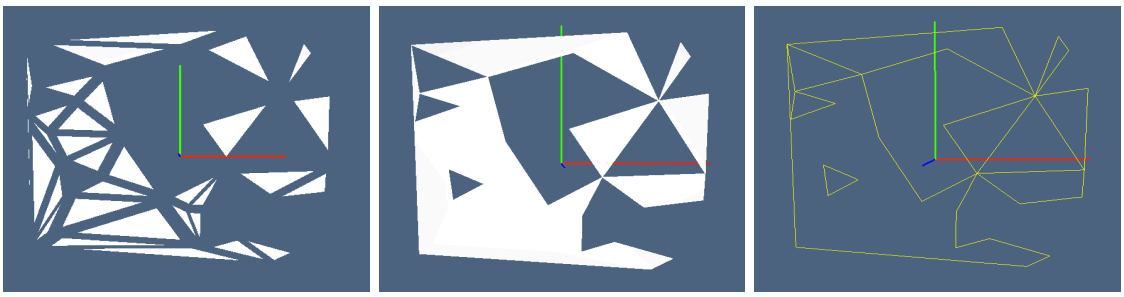

Figure 13: example caption

⟨ Test for quasi-equilateral triangles 59b ⟩ ≡

```
    """ Test for quasi-equilateral triangles """
    def quasiEquilateral(tria):
        a = VECTNORM(VECTDIFF(tria[0:2]))
        b = VECTNORM(VECTDIFF(tria[1:3]))
        c = VECTNORM(VECTDIFF([tria[0],tria[2]]))
        m = max(a,b,c)
        if m/a < 1.7 and m/b < 1.7 and m/c < 1.7: return True
        else: return False
    ◇
```

Macro referenced in 59a.

⟨ Generation and selection of random triangles 60a ⟩ ≡

```
""" Generation and selection of random triangles """
verts = np.random.rand(50,2)
verts = (verts - [0.5,0.5]) * 2
triangles = Delaunay(verts)
cells = [ cell for cell in triangles.vertices.tolist()
         if (not quasiEquilateral([verts[k] for k in cell])) ]
V, FV = AA(list)(verts), cells
EV = larSimplexFacets(FV)
pols2D = MKPOLS((V,FV))
VIEW(EXPLODE(1.5,1.5,1.5)(pols2D))
◇
```

Macro referenced in 59a.

⟨ Boundary computation and visualisation 60b ⟩ ≡

```
""" Boundary computation and visualisation """
orientedBoundary = signedBoundaryCells(V,FV,EV)
submodel = mkSignedEdges((V,orientedBoundary))
VIEW(submodel)
◇
```

Macro referenced in 59a.

⟨ Decompose a permutation into cycles 60c ⟩ ≡

```
""" Decompose a permutation into cycles """
def permutationOrbits(List):
    d = dict((i,int(x)) for i,x in enumerate(List))
    out = []
    while d:
        x = list(d)[0]
        orbit = []
        while x in d:
            orbit += [x],
            x = d.pop(x)
        out += [CAT(orbit)+orbit[0]]
    return out

if __name__ == "__main__":
    print [2, 3, 4, 5, 6, 7, 0, 1]
    print permutationOrbits([2, 3, 4, 5, 6, 7, 0, 1])
    print [3,9,8,4,10,7,2,11,6,0,1,5]
    print permutationOrbits([3,9,8,4,10,7,2,11,6,0,1,5])
◇
```

Macro never referenced.

A.7 Assemblies of simplices and hypercubes

"test/py/larcc/test07.py" 61a ≡

```
""" Assemblies of simplices and hypercubes """
from larlib import *

⟨ Definition of 1-dimensional LAR models 61b ⟩
⟨ Assembly generation of squares and triangles 61c ⟩
⟨ Assembly generation of cubes and tetrahedra 61d ⟩
◇
```

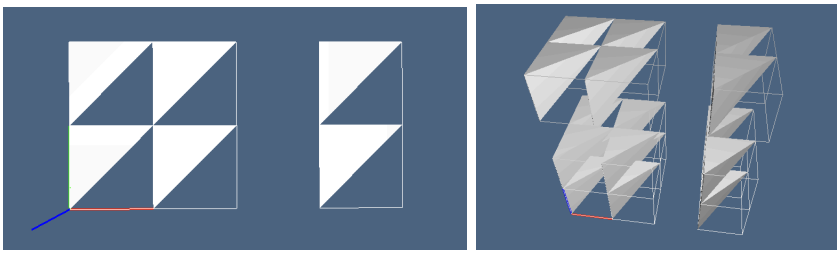

Figure 14: (a) Assemblies of squares and triangles; (b) assembly of cubes and tetrahedra.

⟨ Definition of 1-dimensional LAR models 61b ⟩ ≡

```
""" Definition of 1-dimensional LAR models  """
geom_0,topol_0 = [[0.],[1.],[2.],[3.],[4.]],[[0,1],[1,2],[3,4]]
geom_1,topol_1 = [[0.],[1.],[2.]], [[0,1],[1,2]]
mod_0 = (geom_0,topol_0)
mod_1 = (geom_1,topol_1)
◇
```

Macro referenced in 61a.

⟨ Assembly generation of squares and triangles 61c ⟩ ≡

```
""" Assembly generation of squares and triangles """
squares = larModelProduct([mod_0,mod_1])
V,FV = squares
simplices = pivotSimplices(V,FV,d=2)
VIEW(STRUCT([ MKPOL([V,AA(AA(C(SUM)(1)))(simplices),[]]),
              SKEL_1(STRUCT(MKPOLS((V,FV)))) ]))
◇
```

Macro referenced in 61a.

⟨ Assembly generation of cubes and tetrahedra 61d ⟩ ≡

```
""" Assembly generation  of cubes and tetrahedra """
cubes = larModelProduct([squares,mod_0])
V,CV = cubes
simplices = pivotSimplices(V,CV,d=3)
VIEW(STRUCT([ MKPOL([V,AA(AA(C(SUM)(1)))(simplices),[]]),
              SKEL_1(STRUCT(MKPOLS((V,CV)))) ]))
◇
```

Macro referenced in 61a.

References

[CL13] CVD-Lab, *Linear algebraic representation*, Tech. Report 13-00, Roma Tre University, October 2013.