

# ImagesToLARModel, a tool for creation of three-dimensional models from a stack of images

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## **Abstract**

Here we will present a software for creating a three-dimensional model from a stack of images. This can be useful because of the simplicity of these type of representations. In particular a scope of use can be offered by medicine, where there is an enormous number of images but with very complex two-dimensional representations.

This work will use the LAR representation ([[CL13](#)]) with the Julia language, because of its simplicity, showing how it can be used for quickly process image data.

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# 1 Introduction

This work has the aim to transform a two-dimensional representation of a model (based on a stack of images) into a three-dimensional representation based on the LAR schema. In particular, it will produce a single obj model which can be viewed with standard graphics softwares.

In the past were developed other softwares using same principles (see [PDFJ15]). However, they were optimized for speed and cannot be able to accept huge amounts of data. With the rise of the big data era, we now have more and more data available for research purposes, so softwares must be able to deal with them. A typical hardware environment is based on a cluster of computers where computation can be distributed among a lot of different processes. However, as stated by *Amdahl's law*, the speedup of a program using multiple processors is limited by the time needed for the sequential fraction of the program. So use of parallel techniques for dealing with big data is not important for time performance gain but for memory space gain. In fact, our biggest problem is lack of memory, due to model sizes. As a consequence, every parts of this software is written with the clear objective of minimizing memory usage at the cost of losing something in terms of time performance. So, for example, images will be converted in blocks determined by a grid size (see section 5) among different processes and different machines of the cluster



Figure 1: Amdahl's law

## 1.1 Why Julia

Ricordare che precedenti versioni erano in python

Semplicità

Efficienza

Capacità di realizzare programmi paralleli con poco sforzo

## 2 Software structure

### 2.1 Julia packages

This software will be distributed as a Julia Package. For the actual release (Julia 0.4) a package is a simple git project with the structure showed in figure 2



Figure 2: Julia module structure

Source code must be in folder `src`, while in `test` folder there are module tests with a `runtests.jl` for executing them and with a `REQUIRE` file for specifying tests dependencies. For listing dependencies for the entire project, there is another `REQUIRE` file in main folder. As an example in figure 3 there is the `REQUIRE` file for `ImagesToLARMModel.jl`.

After creating this structure for a project it can be pushed on a git repository and installed on Julia systems. The usual installation procedure use this syntax:

```
Pkg.add("Package-name")
```

This will check for that package in METADATA.jl repository on github where there are all official Julia package. However it is also possible to install an unofficial package (on a public git repository) using this syntax:



```
julia 0.3
JSON
Logging
PyCall
Images
Colors
Clustering
```

Figure 3: REQUIRE contents for `ImagesToLARModel.jl`

```
Pkg.clone("git://repository-address.git")
```

This will install the package on your system with all the dependencies listed in REQUIRE file.

## 2.2 Architecture of ImagesToLARModel

In previous section we have seen how to create a Julia package for distribute our application. Now we focus on the structure of our application. In `src` folder we can find the following modules:

**ImagesToLARModel.jl**: main module for the software, it takes input parameters and start images conversion

**ImagesConversion.jl**: it is called by `ImagesToLARModel.jl` module and controls the entire conversion process calling all other modules

**GenerateBorderMatrix.jl**: it generates the boundary operator for grid specified in input, saving it in a JSON file

**PngStack2Array3dJulia.jl**: it is responsible of images loading and conversion into computable data

**Lar2Julia.jl**: it contains a small subset of LAR functions written in Julia language

**LARUtils.jl**: it contains utility functions for manipulation of LAR models

**Smoother.jl**: it contains function for smoothing of LAR models

**Model2Obj.jl**: it contains function that manipulates obj files

In figure 9 there is a simple schema of dependencies between modules.

Next sections of this document will explain in details all these modules showing also the code involved in conversion

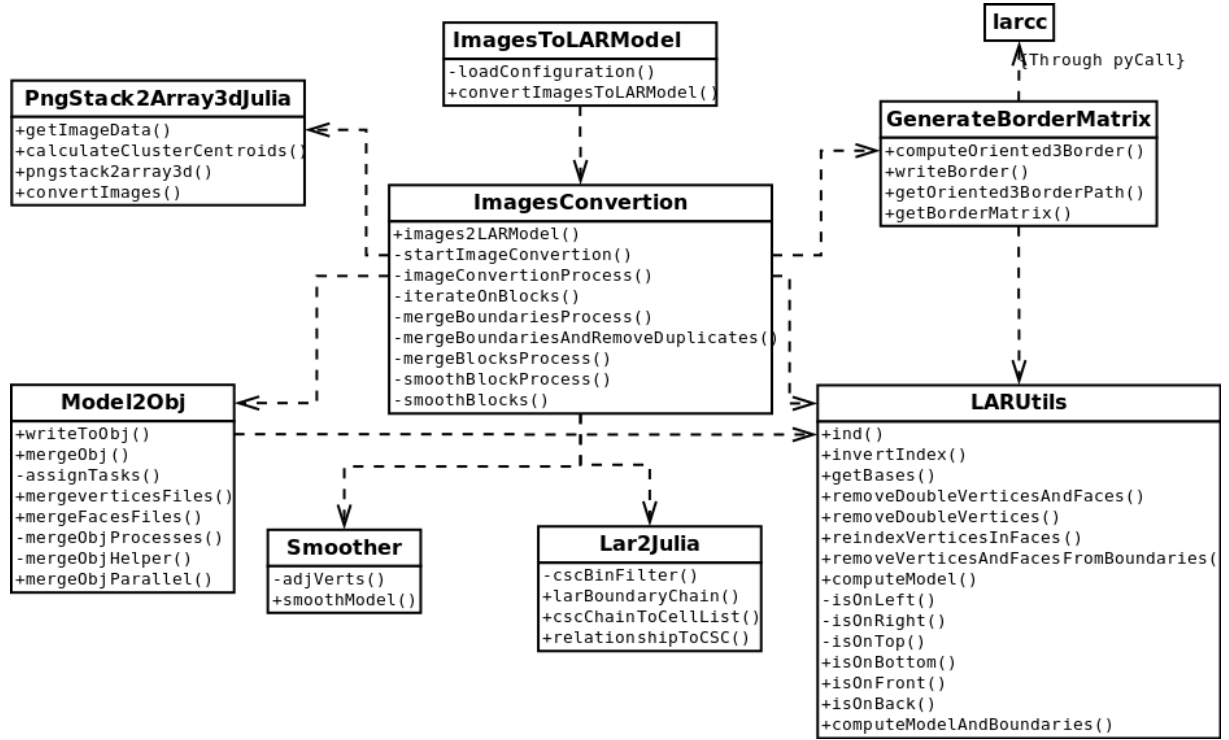


Figure 4: Schema of module dependencies of ImagesToLARModel

### 3 ImagesToLARModel

This is the main module for the application; it takes the input data and start conversion calling `ImagesConversion.jl`.

#### 3.1 Calling modules

As we have already said, this first module has the responsibility of starting the conversion calling all other modules in the package. In Julia calling modules requires that they are in a path specified by `LOAD_PATH` array. So at the beginning of this module we need to add this line:

```

< update load path 6 > ≡
    push!(LOAD_PATH, Pkg.dir("ImagesToLARModel/src"))
    ◇

```

Fragment referenced in 98.

`Pkg.dir()` function gives us the path of the Julia installation, so `Pkg.dir("ImagesToLARModel/src")` returns “ $\langle \textit{Julia} - \textit{path} \rangle / \textit{ImagesToLARModel/src}$ ”

After this line we can now import all modules defined here and export public functions:

```
 $\langle \textit{modules import ImagesToLARModel 7a} \rangle \equiv$   
    import JSON  
    import ImagesConversion  
    import PngStack2Array3dJulia  
  
    using Logging  
  
    export convertImagesToLARModel, prepareData  
  
     $\diamond$ 
```

Fragment referenced in 98.

## 3.2 Input loading for data preparation

Data preparation (see Section 3.4 takes several parameters:

- `inputDirectory`: The path of the directory containing the stack of images
- `outputDirectory`: The path of the directory with the output images
- `crop`: Parameter for images resizing (they can be extended or cropped)
- `noise_shape`: Intensity of the denoising filter for images (0 if you want to disable it)
- `threshold`: set a threshold for raw data. Pixels under that threshold will be set to black, otherwise they will be set to white. If threshold is not specified, segmentation will be done using a clustering algorithm
- `threshold3d`: set a threshold for the three-dimensional filter (see Section 4.2.3)
- `zDim`: set the stack dimension for the three-dimensional filter (see Section 4.2.3)

Because of their number it has been realized a function for simply loading them from a JSON configuration file; this is the code:

```
 $\langle \textit{load JSON configuration for data preparation 7b} \rangle \equiv$ 
```



```

function loadConfigurationPrepareData(configurationFile)
    """
    load parameters from JSON file for data preparation

    configurationFile: Path of the configuration file
    """

    configuration = JSON.parse(configurationFile)

    crop = Void
    try
        crop = configuration["crop"]
    catch
    end

    noise_shape = 0
    try
        noise_shape = configuration["noise_shape"]
    catch
    end

    threshold = Void
    try
        threshold = configuration["threshold"]
    catch
    end

    threshold3d = 0
    try
        threshold3d = configuration["threshold3d"]
    catch
    end

    zDim = 0
    try
        zDim = configuration["zDim"]
    catch
    end

    return configuration["inputDirectory"], configuration["outputDirectory"],
        crop, noise_shape, threshold, threshold3d, zDim

end
◇

```

Fragment referenced in 98.

A valid JSON file has the following structure:

```
{
  "inputDirectory": "Path of the input directory",
  "outputDirectory": "Path of the output directory",
  "crop": Parameter for images resizing (they can be extended or cropped)
  "noise_shape": A number which indicates the intensity of the denoising
filter (0 if you want to disable denoising)
  "threshold": set a threshold for raw data. Pixels under that threshold
will be set to black, otherwise they will be set to white
  "threshold3d": A number indicating the chosen threshold for the
three-dimensional filter (0 if you want to disable this filter)
  "zDim": A number indicating the number of images computed
at once from the three-dimensional filter (0 if you want to take the entire stack) }
```

For example, we can write:

```
{
  "inputDirectory": "/home/juser/IMAGES/",
  "outputDirectory": "/home/juser/OUTPUT/",
  "crop": [[1,800],[1,600],[1,50]],
  "noise_shape": 0,
  "threshold": 13,
  "threshold3d": 100,
  "zDim": 0
}
```

*crop*, *noise\_shape*, *threshold*, *threshold3d* and *zDim* are optional parameters

### 3.3 Input loading for images conversion

Images conversion takes several parameters:

- *inputDirectory*: The path of the directory containing the stack of images
- *outputDirectory*: The path of the directory containing the output

- nx, ny, nz: Sizes of the grid chosen for image segmentation (see section 5)
- DEBUG\_LEVEL: Debug level for Julia logger
- parallelMerge (experimental): Choose between sequential or parallel merge of files (see section 10)

Because of their number it has been realized a function for simply loading them from a JSON configuration file; this is the code:

```

⟨load JSON configuration 10⟩ ≡
function loadConfiguration(configurationFile)
    """
    load parameters from JSON file

    configurationFile: Path of the configuration file
    """

    configuration = JSON.parse(configurationFile)

    DEBUG_LEVELS = [DEBUG, INFO, WARNING, ERROR, CRITICAL]

    parallelMerge = false
    try
        if configuration["parallelMerge"] == "true"
            parallelMerge = true
        else
            parallelMerge = false
        end
    catch
    end

    return configuration["inputDirectory"], configuration["outputDirectory"],
        configuration["nx"], configuration["ny"], configuration["nz"],
        DEBUG_LEVELS[configuration["DEBUG_LEVEL"]],
        parallelMerge

end
◇

```

Fragment referenced in 98.

A valid JSON file has the following structure:

```
{
  "inputDirectory": "Path of the input directory",
  "outputDirectory": "Path of the output directory",
  "nx": x grid size,
  "ny": y grid size,
  "nz": border z,
  "DEBUG_LEVEL": julia Logging level (can be a number from 1 to 5)
  "parallelMerge": "true" or "false"
}
```

For example, we can write:

```
{
  "inputDirectory": "/home/juser/IMAGES/",
  "outputDirectory": "/home/juser/OUTPUT/",
  "nx": 2,
  "ny": 2,
  "nz": 2,
  "DEBUG_LEVEL": 2
}
```

As we can see, in a valid JSON configuration file `DEBUG_LEVEL` can be a number from 1 to 5. Instead, when we explicitly define parameters, `DEBUG_LEVEL` can only be one of the following Julia constants:

- `DEBUG`
- `INFO`
- `WARNING`
- `ERROR`
- `CRITICAL`

*parallelMerge* is an optional parameter

### 3.4 Data preparation

$\langle \text{data preparation from JSON file 11} \rangle \equiv$

```

function prepareData(configurationFile)
    """
    Prepare the input data converting all files into png
    format with the desired resizing and denoising

    configurationFile: Path of the configuration file
    """
    inputPath, outputPath, crop,
        noise_shape, threshold,
        threshold3d, zDim = loadConfigurationPrepareData(open(configurationFile))

    prepareData(inputPath, outputPath, crop, noise_shape,
        threshold, threshold3d, zDim)

end
◇

```

Fragment referenced in 98.

$\langle \text{manual data preparation 12} \rangle \equiv$

```

function prepareData(inputPath, outputPath,
    crop = Void, noise_shape = 0, threshold = Void,
    threshold3d = 0, zDim = 0)
    """
    Prepare the input data converting all files into png
    format with the desired resizing and denoising

    inputPath: Directory containing the stack of images
    outputPath: Directory which will contain the output
    crop: Parameter for images resizing (they can be
        extended or cropped)
    noise_shape: The shape for image denoising
    threshold: Threshold for the raw data. All pixels under it
        will be set to black, otherwise they will be set to white
    threshold3d: A number indicating the chosen threshold for
        three-dimensional filter (0 if you want to disable this filter)
    zDim: A number indicating the number of images computed at once from the
        three-dimensional filter (0 if you want to take the entire stack)
    """
    # Create output directory
    try
        mkpath(outputPath)
    catch
    end
end

```

```

        PngStack2Array3dJulia.convertImages(inputPath, outputPath, crop, noise_shape,
                                             threshold, threshold3d, zDim)
    end
    ◇

```

Fragment referenced in 98.

### 3.5 Starting conversion

As we have already said, this module has the only responsibility to collect data input and starts other modules. These are the functions that start the process and the only exposed to the application users:

```

⟨ Start conversion from JSON file 13a ⟩ ≡
function convertImagesToLARModel(configurationFile)
    """
    Start conversion of a stack of images into a 3D model
    loading parameters from a JSON configuration file

    configurationFile: Path of the configuration file
    """
    inputDirectory, outputDirectory, nx, ny, nz,
        DEBUG_LEVEL, parallelMerge = loadConfiguration(open(configurationFile))
    convertImagesToLARModel(inputDirectory, outputDirectory,
                            nx, ny, nz, DEBUG_LEVEL, parallelMerge)
end
    ◇

```

Fragment referenced in 98.

```

⟨ Start manual conversion 13b ⟩ ≡
function convertImagesToLARModel(inputDirectory, outputDirectory,
                                nx, ny, nz, DEBUG_LEVEL = INFO,
                                parallelMerge = false)
    """
    Start conversion of a stack of images into a 3D model

    inputDirectory: Directory containing the stack of images
    outputDirectory: Directory containing the output
    nx, ny, nz: Border dimensions

```

```

DEBUG_LEVEL: Debug level for Julia logger. It can be one of the following:
- DEBUG
- INFO
- WARNING
- ERROR
- CRITICAL
parallelMerge: Choose if you want to use the algorithm
for parallel merging (experimental)
"""
# Create output directory
try
    mkpath(outputDirectory)
catch
end

Logging.configure(level=DEBUG_LEVEL)
ImagesConversion.images2LARModel(nx, ny, nz,
    inputDirectory, outputDirectory, parallelMerge)
end
◇

```

Fragment referenced in 98.

## 4 PngStack2Array3dJulia

This module has the responsibility of convert a png image into an array of values that will be passed to other modules

### 4.1 Module imports

These are modules needed for this part of the package and the public functions exported

```

⟨ modules import PngStack2Array3dJulia 14 ⟩ ≡
    using Images # For loading png images
    using Colors # For grayscale images
    using PyCall
    using Clustering
    using Logging
    @pyimport scipy.ndimage as ndimage

    export pngstack2array3d, getImageData, convertImages
◇

```

Fragment referenced in 101b.

We need `Images`, `Clustering` and `Colors` packages for manipulating png images and `PyCall` for using Python functions for noise removal from images. As a consequence, we need a python environment with `scipy` to be able to run the package

## 4.2 Convert input to png

First thing to do in our program is getting our input folder and convert the stack of images into png format with only two values. This process lets us to avoid managing an enormous variety of formats during computation, simplifying code used for transformation.

Conversion needs the following parameters:

- `inputPath`: path of the folder containing the original images
- `outputPath`: path where we will save png images
- `crop`: parameters for images resizing (they can be extended or cropped)
- `threshold`: set a threshold for raw data. Pixels under that threshold will be set to black, otherwise they will be set to white. If the threshold is not set, the image will be converted using a clustering algorithm
- `threshold3d`: Set a threshold for the three-dimensional filter (see Section 4.2.3)
- `zDim`: Set the stack dimension for the three-dimensional filter (see Section 4.2.3)

Now we can examine single parts of conversion process. We need to open the single image doing the following operations:

1. Open images using `Images` library (which relies on `ImageMagick`) and save them in greyscale png format
2. Resize the images according to the `crop` parameter
3. Apply a denoising filter for the image
4. Set the threshold for the image or start the clustering algorithm

This is the code used for every step.

```
⟨ Greyscale conversion 15 ⟩ ≡
    rgb_img = convert(Image{ColorTypes.RGB}, img)
    gray_img = convert(Image{ColorTypes.Gray}, rgb_img) ◇
```



Fragment referenced in 18.

As we can see, we first need to convert image to RGB and then reconverting to greyscale. Without the RGB conversion these rows will return a stackoverflow error due to the presence of alpha channel

```
⟨ Image resizing 16a ⟩ ≡  
  if(crop!= Void)  
    # Resize images on x-axis and y-axis  
    gray_img = resizeImage(gray_img, crop)  
  end ◇
```

Fragment referenced in 18.

The code for image resizing will be better explained in Section 4.2.1.

Now we have to reduce noise on the image. The best choice consists in using a *median filter* from package `scipy.ndimage`, because it preserves better the edges of the image:

```
⟨ Reduce noise 16b ⟩ ≡  
  imArray = raw(gray_img)  
  # Denoising  
  if noise_shape_detect != 0  
    imArray = ndimage.median_filter(imArray, noise_shape_detect)  
  end ◇
```

Fragment referenced in 18.

The `Images.jl` `raw` function used here, get all pixel values saving them in an Array, which we have called *imArray*. In Figure 5 we can see how the array will be like for a sample greyscale image.

Finally we can set a threshold for image data. The idea is to get a value from the user and set to white all pixel over the threshold and set to black the remaining ones.

```
⟨ Image thresholding 16c ⟩ ≡  
  if(threshold != Void)  
    imArray = map(x-> if x > threshold return 0xff else return 0x00 end, imArray)  
  else  
    imArray = clusterImage(imArray)  
  end  
  gray_img = grayim(imArray) ◇
```

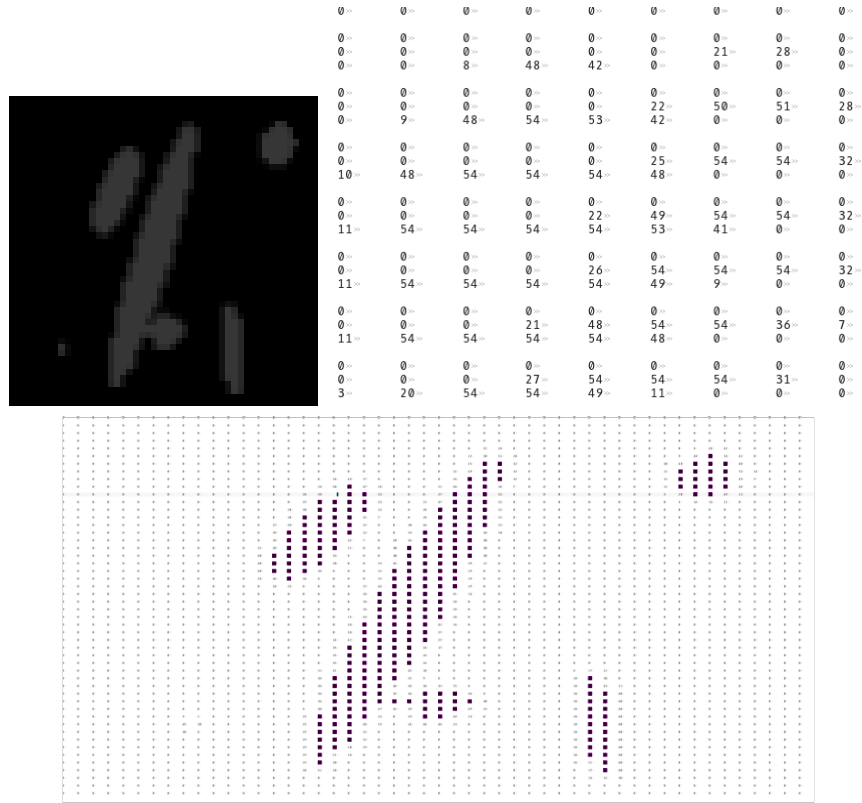


Figure 5: Reading raw data from image. (a) Original greyscale image (b) A view of raw data array (c) The entire raw data array with main color highlighted

Fragment referenced in 18.

The code used for image clustering will be explained in Section 4.2.2.

After these operations we can write the single image on disk. However, the stack computed at the moment, could have non-relevant pixels for our model (especially if there is a lot of noise in images). So to speed-up next computation and produce a final result with better quality we can introduce a *three-dimensional filter* for choosing only the useful pixels for the model. In Section 4.2.3 we will see the details of the implementation of this filter.

$\langle 3D \text{ filtering } 17 \rangle \equiv$

```

# Filtering out non-relevant parts of the model
if(threshold3d != 0)
    imageFilter3D(outputPath, threshold3d, zDim)
end ◇

```

Fragment referenced in 18.

This is the code for the entire function:

```

⟨ Convert to png 18 ⟩ ≡
function convertImages(inputPath, outputPath,
                      crop = Void, noise_shape_detect = 0, threshold = Void,
                      threshold3d = 0, zDim = 0)
    """
    Get all images contained in inputPath directory
    saving them in outputPath directory in png format.
    Images will be resized according with the crop parameter
    and if folder contains an odd number of images another one will be
    added

    inputPath: Directory containing input images
    outputPath: Temporary directory containing png images
    crop: Parameter for images resizing (they can be
          extended or cropped)
    noise_shape_detect: Shape for the denoising filter
    threshold: Threshold for the raw data. All pixel under it
              will be set to black, otherwise they will be set to white
    """

    imageFiles = readdir(inputPath)

    ⟨ Resize images on z-axis 21 ⟩

    for imageFile in imageFiles
        img = imread(string(inputPath, imageFile))
        ⟨ Greyscale conversion 15 ⟩
        ⟨ Image resizing 16a ⟩

        ⟨ Reduce noise 16b ⟩
        ⟨ Image thresholding 16c ⟩

        outputFilename = string(outputPath, imageFile[1:rsearch(imageFile, ".")[1]], "png")
        imwrite(gray_img, outputFilename)
    end
end

```

```

    end
     $\langle 3D \text{ filtering } 17 \rangle$ 
end
 $\diamond$ 

```

Fragment referenced in 101b.

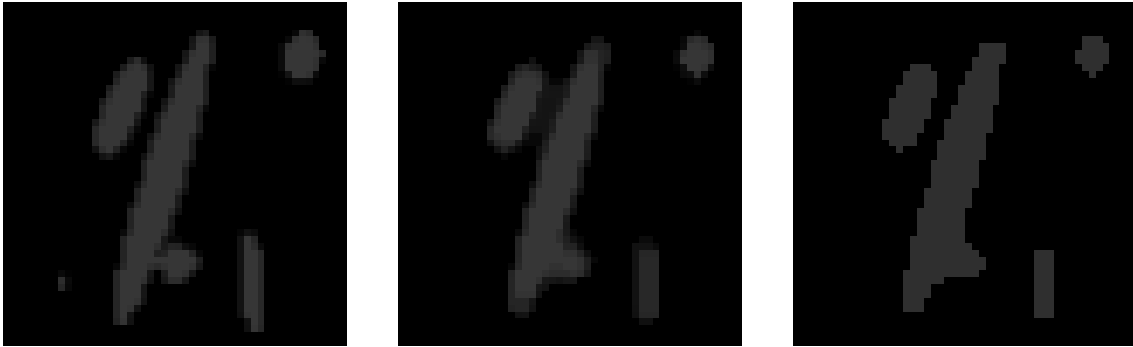


Figure 6: Image transformation. (a) Original greyscale image (b) Denoised image (c) Two-colors image

#### 4.2.1 Image resizing

Now we will see in detail how to resize images on x and y axis. The most important parameter is *crop*, which is a list of numbers that contains the desired dimensions for the stack of images.

Given the list  $[[xcropStart, xcropEnd], [ycropStart, ycropEnd], [zcropStart, zcropEnd]]$  we can have different cases based on the list values, as we can see in Figure 7.

So with the same parameter we can both resize or extend images. In particular, when we have to extend them, we have to get the raw data and concatenate a zeroed array to it. On the other hand, for image cropping we can use the `subim` function from the `Images` package.

```

 $\langle image \text{ resizing } 19 \rangle \equiv$ 
function resizeImage(image, crop)
    """
    Utility function for images resize

    image: the input image
    crop: a list containing the crop parameters

```

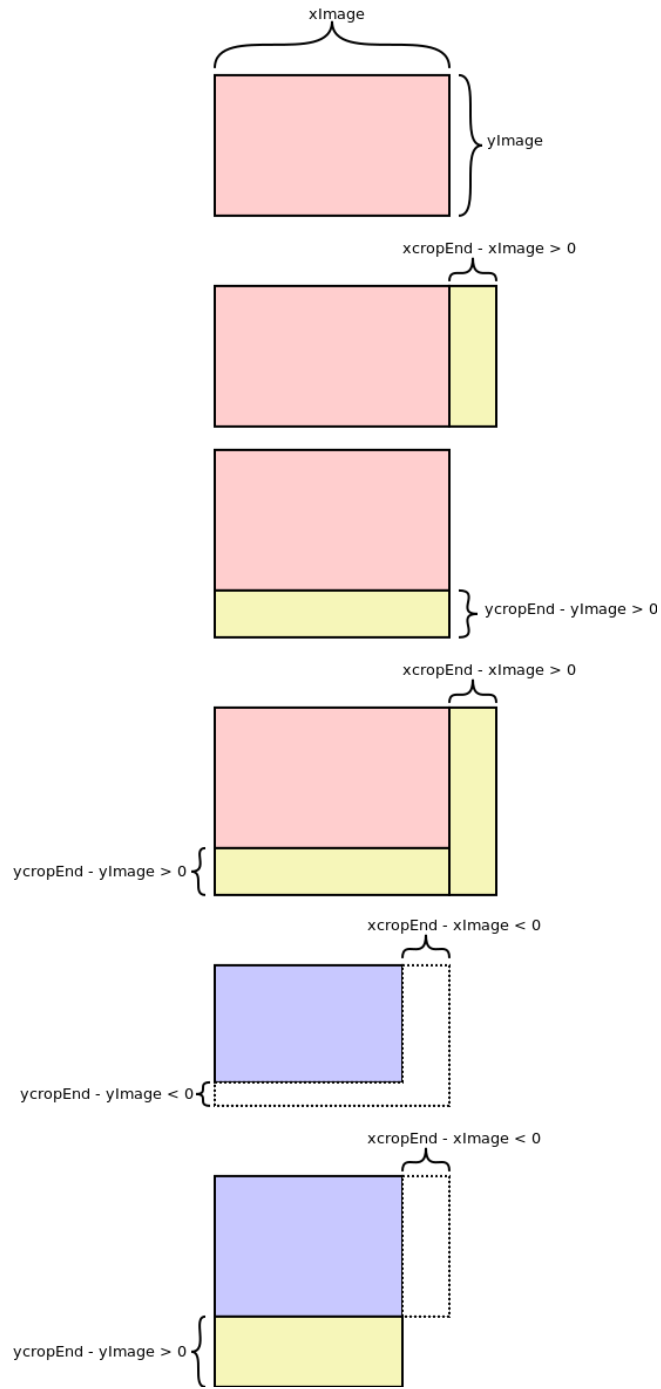


Figure 7: Some interesting resize cases. (a) The original image (b) Extension on the x dimension (c) Extension on the y dimension (d) Extension on both dimensions (e) Crop of both x and y (f) Crop of x and extension of y

```

        for the three dimensions

returns the resized image
"""
dim = size(image)
if(crop[1][2] > dim[1])
    # Extending the images on the x axis
    imArray = raw(image)
    zeroArray = zeros(UInt8, dim[2])
    for i in (1 : (crop[1][2] - dim[1]))
        imArray = vcat(imArray, transpose(zeroArray))
    end
    image = grayim(imArray)
end

if(crop[2][2] > dim[2])
    # Extending the images on the y axis
    imArray = raw(image)
    zeroArray = zeros(UInt8, size(image)[1])
    for i in (1: (crop[2][2] - dim[2]))
        imArray = hcat(imArray, zeroArray)
    end
    image = grayim(imArray)
end
return subim(image, crop[1][1]:crop[1][2], crop[2][1]:crop[2][2])
end ◊

```

Fragment referenced in 101b.

However our stack of images have three dimensions, where the z-axis is represented by the number of images. So the third list for the crop parameters resize the stack removing or adding other images.

```

⟨ Resize images on z-axis 21 ⟩ ≡
#Resizing on the z axis
if(crop!= Void)
    numberOfImages = length(imageFiles)
    if(crop[3][2] > numberOfImages)
        imageWidth = crop[1][2] - crop[1][1] + 1
        imageHeight = crop[2][2] - crop[2][1] + 1
        for i in 1 : crop[3][2] - numberOfImages
            imArray = zeros(UInt8, imageWidth, imageHeight)
            img = grayim(imArray)
            outputFilename = string(outputPath, "/", imageFiles[end][1:rsearch(imageFiles[end], ".")

```

```

                                "_added-", i , ".png")
        imwrite(img, outputFilename)
    end
end
imageFiles = imageFiles[crop[3][1]:min(numberOfImages, crop[3][2])]
end ◇

```

Fragment referenced in 18.

#### 4.2.2 Image clustering

When the user does not set a threshold for data segmentation, the software uses a k-means clustering algorithm for determining the values for binary images. First thing to do is to change raw data so it can be passed to the clustering function of the `Clustering.jl` package. After clustering completion, data is set to `0x00` or `0xff` depending on the algorithm assignments.

```

⟨ image clustering 22 ⟩ ≡
function clusterImage(imArray)
    """
    Get a binary representation of an image returning
    a two-color image using clustering

    imArray: array containing pixel values

    return the imArray with only two different values
    """

    imageWidth = size(imArray)[1]
    imageHeight = size(imArray)[2]

    # Formatting data for clustering
    image3d = Array{Array{UInt8,2},0}()
    push!(image3d, imArray)
    pixels = reshape(image3d[1], (imageWidth * imageHeight), 1)

    # Computing assignments from the raw data
    kmeansResults = kmeans(convert{Float64}(transpose(pixels)), 2)

    qnt = kmeansResults.assignments
    centers = kmeansResults.centers

    if(centers[1] == centers[2])

```

```

    if centers[1] < 30 # I assume that a full image can have light gray pixels
      qnt = fill(0x00, size(qnt))
    else
      qnt = fill(0xff, size(qnt))
    end
  else
    minIndex = findmin(centers)[2]
    qnt = map(x-> if x == minIndex return 0x00 else return 0xff end, qnt)
  end

  return reshape(qnt, imageWidth, imageHeight)
end ◊

```

Fragment referenced in 101b.

We can see that sometimes the `Clustering.jl` library returns the same values for both centroid centers. This could happen when the images is completely empty or it has only colored pixels. So, we need to check this cases and fill the assignments array `qnt` with the right values based on a fixed threshold.

### 4.2.3 three-dimensional model filter

Now we can see the implementation of a filter for removal of noise from our models. It is different from filters used in common image processing because it effectively removes only groups of linked pixels whose dimensions are under a given threshold. So this filter is able to consider the three-dimensional model described in our images to delete the non-relevant pixels. The main idea behind this filter is very simple. We assume that big groups of pixels which are directly linked are interesting for the final model; so we just need to navigate pixels (as they were nodes in a graph) that are adjacent and filter out only groups under the threshold at the end of the visit. We first need a simple function for a DFS of a graph:

```

⟨ DFS function 23 ⟩ ≡
function visitFromNode(node, adjacentRel, visited)
  """
  Visit a graph starting from a node using a DFS

  node: the starting node
  adjacentRel: a list where in position i there are all
              adjacent nodes to i
  visited: the visited nodes
  """
  toVisit = Array{Int, 0}

```



```

visitedNodes = Array(Int, 0)
push!(toVisit, node)
while (length(toVisit) != 0)
    n = pop!(toVisit)
    if !in(n, visited)
        push!(visited, n)
        push!(visitedNodes, n)
        adj_list = adjacentRel[n]
        for adj in adj_list
            push!(toVisit, adj)
        end
    end
end
return visitedNodes
end ◊

```

Fragment referenced in 29.

This is a function valid for every type of graph. What can change from an application to another is the *adjacency condition*. In this case we can see that our function uses the `adjacentRel` parameter, which is a list where for every position  $i$  there are all nodes that are adjacent to  $i$ . The relationship of adjacency used in this case is trivial. In fact we assume that:

*Given a pixel with coordinates  $(xPixel, yPixel, zPixel)$  we consider only the following adjacent pixels:*

- $z \in [zPixel - 1, zPixel + 1]$
- $coordinates = \{(xPixel - 1, yPixel, z), (xPixel + 1, yPixel, z), (xPixel, yPixel - 1, z), (xPixel, yPixel + 1, z)\}$

This is the function that implements the algorithm we have seen above

```

⟨ find adjacent pixels 24 ⟩ ≡
function getAdjacentPixels(imageArray)
    """
    Find all adjacent pixels in the stack of images

    imageArray: the array containing the images

    Returns a list containing list of adjacent pixels
    """

```

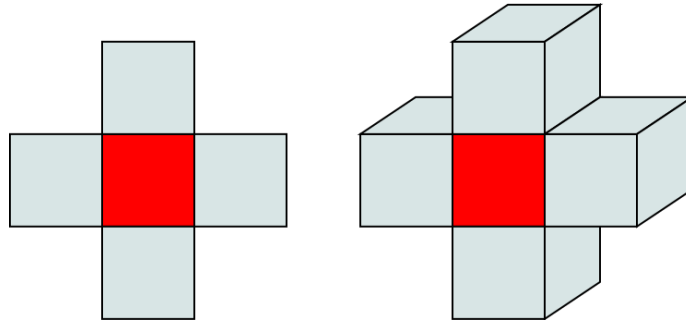


Figure 8: Adjacency relationship for pixels. (a) A 2D view of the relationship. (b) A 3D view of the relationship (where the z-axis is determined by previous and next pictures in the array stack)

```

nx = size(imageArray[1])[1]
ny = size(imageArray[1])[2]

PP = Array(Array{Int}, nx * ny * length(imageArray))
for(pixel in 1: (nx * ny * length(imageArray)))
    PP[pixel] = Array{Int, 0}
    xPixel, yPixel, zPixel = pixelCoords(pixel, nx, ny)
    if(imageArray[zPixel][xPixel, yPixel] != 0x00)
        # Querying adjacent pixels
        for z in max(1, zPixel - 1) : min(zPixel + 1, length(imageArray))
            for y in max(1, yPixel - 1) : min(yPixel + 1, ny)
                for x in max(1, xPixel - 1) : min(xPixel + 1, nx)
                    if(x == xPixel || y == yPixel)
                        index = pixelIndex(x, y, z, nx, ny)
                        if(index != pixel && imageArray[z][x, y] != 0x00)
                            push!(PP[pixel], index)
                        end
                    end
                end
            end
        end
    end
end
return PP
end ◇

```

Fragment referenced in 29.

How we can see, we also need to transform pixel coordinates into an index and vice versa. So we defined the following utility functions:

```

< pixel coordinates to index 26a > ≡
function pixelIndex(x, y, z, nx, ny)
    """
    Given the coordinates of a pixel
    of the image matrix return the index
    of the linearized matrix
    """
    return x + nx * (y - 1) + nx * ny * (z - 1)
end ◇

```

Fragment referenced in 29.

```

< pixel index to coordinates 26b > ≡
function pixelCoords(ind, nx, ny)
    """
    Given the index of a pixel
    returns the coordinates of the pixel
    """

    xCoord = (ind - 1) % nx + 1
    yCoord = convert(Int, trunc((ind - 1) % (nx * ny) / nx)) + 1
    zCoord = convert(Int, trunc((ind - 1) / (nx * ny))) + 1

    return xCoord, yCoord, zCoord
end ◇

```

Fragment referenced in 29.

Now we can examine the main function for this filter. First of all, to reduce the quantity of memory involved in the process we must divide the number of images computed at once by a single process using a parameter called **zDim**. After block division we can start the function that will be executed on every process on the images of the previous, current and next blocks (saving only images for the current one). This is the code:

```

< 3D model filtering main function 26c > ≡

```

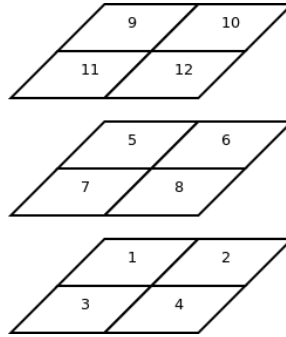


Figure 9: Enumerating schema used for pixel indexing.

```
function imageFilter3D(imageDirectory, threshold, zDim = 0)
  """
  Implementation of a filter for a stack of images
  It traverses a stack of images loading zDim images
  at once finding the adjacent pixels. If the number of
  adjacent pixels is less than a threshold, the pixels
  will be deleted

  imageDirectory: The directory containg the images
  threshold: the minimum number of adjacent pixels for the result
  zDim: the number of images to load at once
  """
  imageFiles = readdir(imageDirectory)
  imageFiles = map((s) -> string(imageDirectory, s), imageFiles)

  if zDim == 0
    zDim = length(imageFiles)
  end

  numberOfBlocks = convert(Int, trunc(length(imageFiles)/zDim))

  if length(imageFiles) % zDim != 0
    numberOfBlocks += 1
  end

  tasks = Array(RemoteRef, 0)
  for zBlock in 1: numberOfBlocks
    endBlock = min(zBlock * zDim, length(imageFiles))
    startBlock = (zBlock - 1) * zDim + 1
    startPrevBlock = max(startBlock - zDim, 1)
    endNextBlock = min(endBlock + zDim, length(imageFiles))
```

```

    blockFiles = imageFiles[startPrevBlock : endNextBlock]

    startBlockInd = startBlock - startPrevBlock + 1
    endBlockInd = startBlockInd + endBlock - startBlock

    task = @spawn filter3DProcessFunction(blockFiles, startBlockInd, endBlockInd, threshold)
    push!(tasks, task)

end
# Waiting for task completion
for task in tasks
    wait(task)
end
end ◇

```

Fragment referenced in 29.

Finally we can see the function executed in every process for images filtering. We just need to iterate on all pixels of the stack of images that are full and that have not been visited yet and start the DFS visit obtaining the list of visited pixels. If its length is less than the **threshold** parameter we set all those pixels to zero. After all pixels have been visited we can write the resulting images on disk

*⟨ process function for 3D filter 28 ⟩* ≡

```

function filter3DProcessFunction(blockFiles, startBlock, endBlock, threshold)
    """
    Process function for the 3D filter.
    It takes a single block and processes all files
    on a single process

    blockFiles: The array of files of previous, current and next blocks
    startBlock: Index of the first file of the current block
    endBlock: Index of the last file of the current block
    threshold: The threshold for data filtering
    """
    zDim = length(blockFiles)
    imageArray = Array{Array{UInt8,2}, zDim}
    for i in 1: zDim
        img = imread(blockFiles[i])
        imageArray[i] = raw(img)
    end
end

```

```

# Now I can start navigation of the graph determined
# by these images
visited = Array{Int, 0}
nx = size(imageArray[1])[1]
ny = size(imageArray[1])[2]
PP = getAdjacentPixels(imageArray)
for i in 1:(zDim * nx * ny)
    xPixel, yPixel, zPixel = pixelCoords(i, nx, ny)
    if imageArray[zPixel][xPixel, yPixel] != 0x00 && !in(i, visited)
        visitedPixels = visitFromNode(i, PP, visited)
        if length(visitedPixels) < threshold
            for pixel in visitedPixels
                x, y, z = pixelCoords(pixel, nx, ny)
                imageArray[z][x, y] = 0x00
            end
        end
    end
end

# Now I can write the results on file
for i in startBlock: endBlock
    imwrite(grayim(imageArray[i]), blockFiles[i])
end
end ◇

```

Fragment referenced in 29.

$\langle 3d \text{ model filtering } 29 \rangle \equiv$   
 $\langle DFS \text{ function } 23 \rangle$   
 $\langle pixel \text{ coordinates to index } 26a \rangle$   
 $\langle pixel \text{ index to coordinates } 26b \rangle$   
 $\langle find \text{ adjacent pixels } 24 \rangle$   
 $\langle process \text{ function for } 3D \text{ filter } 28 \rangle$   
 $\langle 3D \text{ model filtering main function } 26c \rangle \diamond$

Fragment referenced in 101b.

### 4.3 Getting data from a png

Now we need to load information data from png images. In particular we are interested in getting width and height of an image. As stated in [W3C] document, a standard PNG file contains a *signature* followed by a sequence of *chunks* (each one with a specific type).

The signature always contains the following values:

137 80 78 71 13 10 26 10

This signature indicates that the remainder of the datastream contains a single PNG image, consisting of a series of chunks beginning with an IHDR chunk and ending with an IEND chunk. Every chunk is preceded by four bytes indicating its length.

As we are interested in width and height we need to parse the IHDR chunk. It is the first chunk in PNG datastream and its type field contains the decimal values:

73 72 68 82

The header also contains:

Width	4 bytes
Height	4 bytes
Bit depth	1 bytes
Color type	1 byte
Compression method	1 byte
Filter method	1 byte
Interlace method	1 byte

So for reading width and height we need first 24 bytes; the first eight contain the signature, then we have four bytes for length, four bytes for the type field and eight bytes for information we are interested in. This is the code:

```
< Get image data 30 > ≡  
function getImageData(imageFile)  
    ""  
    Get width and height from a png image  
    ""  
  
    input = open(imageFile, "r")  
    data = readbytes(input, 24)  
  
    if (convert(Array{Int},data[1:8]) != reshape([137 80 78 71 13 10 26 10],8))  
        error("This is not a valid png image")  
    end
```

```

w = data[17:20]
h = data[21:24]

width = reinterpret(Int32, reverse(w))[1]
height = reinterpret(Int32, reverse(h))[1]

close(input)

return width, height
end
◇

```

Fragment referenced in 101b.

#### 4.4 Transform pixels into three-dimensional array

Now we can study the most important part of this module, where images are converted into data usable by other modules for the creation of the three-dimensional model. The basic concept consists in transforming every single pixel in an integer value representing color, obtaining a matrix containing only two values representing background and foreground of the image.

Now we will follow the code. This function uses three parameters:

- path: Path of the images directory
- minSlice: First image to read
- maxSlice: Last image to read

For every image we want to transform in the interval  $[\text{minSlice}, \text{maxSlice})$  we have to read it from disk and save pixel informations into a multidimensional Array.

This is the complete code:

```

⟨ Pixel transformation 31 ⟩ ≡
function pngstack2array3d(path, minSlice, maxSlice)
    """
    Import a stack of PNG images into a 3d array

    path: path of images directory
    minSlice and maxSlice: number of first and last slice
    """

```



```

# image3d contains all images values
image3d = Array{Array{UInt8,2}, 0}

debug("maxSlice = ", maxSlice, " minSlice = ", minSlice)
files = readdir(path)

for slice in minSlice : (maxSlice - 1)
    debug("slice = ", slice)
    imageFilename = string(path, files[slice + 1])
    debug("image name: ", imageFilename)
    img = imread(imageFilename) # Open png image with Julia Package
    imArray = raw(img) # Putting pixel values into RAW 3d array
    debug("imArray size: ", size(imArray))

    # Inserting page on another list
    push!(image3d, imArray)

end
return image3d
end
◇

```

Fragment referenced in 101b.

## 5 ImagesConversion

Now we will study the most important module for this package: `ImagesConversion`. It has the responsibility of doing the entire conversion process delegating tasks to the other modules.

### 5.1 General algorithm

Now we will examine, in a general way, the algorithm used for conversion from a two-dimensional to a three-dimensional representation of our biomedical models.

We have already seen in section 4 how to get information from a png image, obtaining arrays with only two values; one for the **background** color and one for **foreground** color. This is only the first step of the complete conversion process.

Now we focus only on a single image of the stack. Our two-dimensional representation, consists of pixels of two different colors (where only the one associated with foreground is significant); so we can obtain a three-dimensional representation simply replacing every foreground pixel with a small cube. Focusing on the entire stack of images, the full

three-dimensional representation can be obtained simply overlapping all the image representations

This algorithm is very simple, however we does not considered problems concerning lack of memory. In fact, we could have images so big that we cannot build these models entirely in memory; moreover they would require a lot of CPU time for computation. A good solution to these problems consists in taking our representation based on images and divide according to a **grid**.

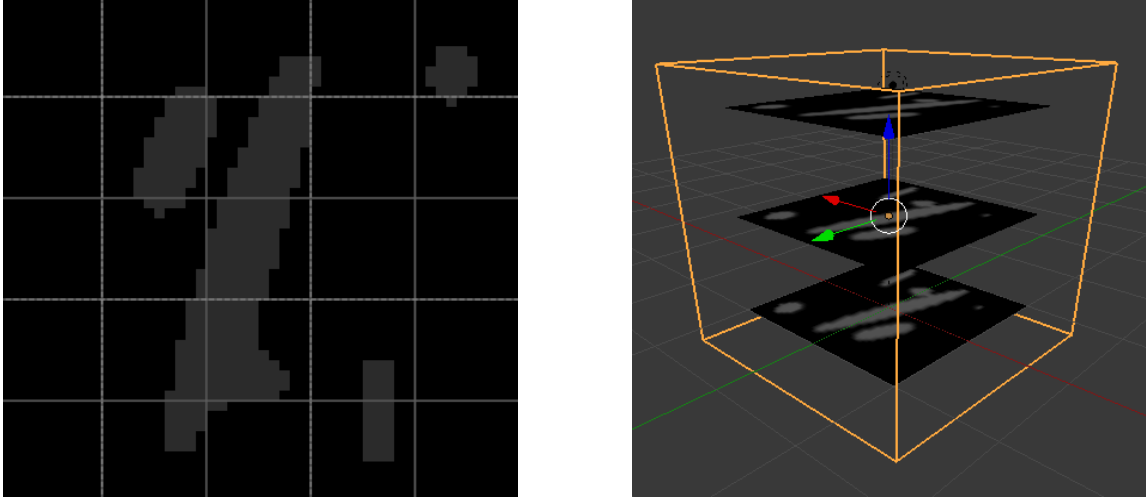


Figure 10: The grid used for parallel computation (a) 2D grid on a single image (b) 3D grid for the stack of images

So, instead of converting the entire model with a unique process, we can subdivide the input among a lot of processes, where every process will execute the conversion process on a small number of **blocks** according to the grid subdivision.

Summing up we can define the following terms, which will be used in next parts of this documentation:

- **Grid:** It is the subdivision of the entire stack of images, with sizes defined by the user.
- **Block:** It is a single cell of the grid
- **xBlock:** It is the x-coordinate of a block
- **yBlock:** It is the y-coordinate of a block

- **zBlock:** It is the z-coordinate of a block

$xBlock$  and  $yBlock$  are defined on a single image, while  $zBlock$  is defined on different images; in the code it will often be replaced by terms **StartImage** and **EndImage**, which indicate the first image and the last image of that block respectively.

In next subsections we will examine the conversion algorithm in detail, showing what happens for every block of the grid.

## 5.2 Module imports

These are modules needed for this part of the package and the public functions exported.

```
< modules import ImagesConversion 34a > ≡
    import GenerateBorderMatrix
    import PngStack2Array3dJulia
    import Lar2Julia
    import Model2Obj
    import LARUtils
    import Smoother

    using Logging

    export images2LARModel
    ◇
```

Fragment referenced in 99a.

## 5.3 Data preparation

As a first thing, we will see how to prepare our data for conversion process. Firstly we need to compute the LAR boundary operator for finding boundaries of our cells (for the generation see section 6) getting width and height from our images.

Later we can start conversion with all these parameters calling **startImageConversion** function, which will be explained in next subsection.

```
< main function for ImagesConversion 34b > ≡
    function images2LARModel(nx, ny, nz,
                            inputDirectory, outputDirectory,
                            parallelMerge)
        """
        Convert a stack of images into a 3d model
```

```

"""

info("Starting model creation")

# Get sizes of the stack of images
fileList = readdir(inputDirectory)
imageWidth, imageHeight = PngStack2Array3dJulia.getImageData(
    string(inputDirectory, fileList[1]))
imageDepth = length(fileList)

# Computing border matrix
info("Computing border matrix")
try
    mkdir(string(outputDirectory, "BORDERS"))
catch
end
borderFilename = GenerateBorderMatrix.getOriented3BorderPath(
    string(outputDirectory, "BORDERS"), nx, ny, nz)

# Starting images conversion and border computation
startImageConversion(inputDirectory, outputDirectory, borderFilename,
    imageHeight, imageWidth, imageDepth,
    nx, ny, nz,
    parallelMerge)

end
◇

```

Fragment referenced in 99a.

## 5.4 Conversion pipeline

Now we can see how conversion of images works. In section 5.1 we have seen how to execute the single conversion of a pixel into a voxel using our grid for parallel computation. However, with that algorithm, we obtain models with internal boundaries between blocks and with squared edge. So we need to create a **conversion pipeline** which will progressively refine our models. In Figure 11 there are the steps used for our conversion



Figure 11: Images conversion pipeline

Every single step of the pipeline, is executed in parallel for every block of the grid; so we need a general purpose function for blocks iteration which will take as a parameter a function that will execute it. So we can define the `iterateOnBlocks` function which takes the following parameters:

- **inputDirectory:** Directory which contains input files for the process function
- **imageHeight, imageWidth, imageDepth:** Sizes of the stack of images
- **imageDx, imageDy, imageDz:** Sizes of the grid
- **processFunction:** Function that contains instructions for execution of a single step of the pipeline for every block

This function will iterate on all blocks of the image grid executing the process function, which will be different for every pipeline step. This is the code used:

*(parallel block iteration 36)*  $\equiv$

```
function iterateOnBlocks(inputDirectory,
                        imageHeight, imageWidth, imageDepth,
                        imageDx, imageDy, imageDz,
                        processFunction)
    """
    Simple function that iterates on blocks for executing
    a task described by a processFunction

    inputDirectory: Directory which contains input files for the process function
    imageHeight, imageWidth, imageDepth: Images sizes
    imageDx, imageDy, imageDz: Sizes of cells grid
    processFunction: Function that will be executed on a separate task
    """

    beginImageStack = 0
    endImage = beginImageStack

    tasks = Array(RemoteRef, 0)
    for zBlock in 0:(imageDepth / imageDz - 1)
        startImage = endImage
        endImage = startImage + imageDz
        for xBlock in 0:(imageWidth / imageDx - 1)
            for yBlock in 0:(imageHeight / imageDy - 1)
                task = @spawn processFunction(inputDirectory,
                                              xBlock, yBlock,
                                              startImage, endImage,
                                              imageDx, imageDy,
                                              imageWidth, imageHeight)
```

```

        push!(tasks, task)
    end
end
end

# Waiting for tasks
for task in tasks
    wait(task)
end
end ◇

```

Fragment referenced in 99a.

First of all we need to iterate on the grid finding the `zBlock` coordinate; we saw earlier that the `imageDz` parameter must be a divisor of the image depth, so we will have exactly  $imageDepth/imageDz$  blocks on the `z` coordinate. Moreover, at every `zBlock` correspond a `startImage` and an `endImage` where  $endImage - startImage = imageDz$ .

Now we can iterate on the `xBlock` and `yBlock`, parallelizing the conversion process spawning a new process for every block. Finally, we have to wait for tasks completion.

Now we can see the entire pipeline for images conversion.

First of all we need to compute the centroids from the best image using module `PngStack2Array3dJulia` and get the previously computed border matrix in csc sparse array format

```

⟨get border matrix 37⟩ ≡
    try
        mkdir(string(outputDirectory, "BORDERS"))
    catch
    end
    debug("Opening border file: border_", imageDx, "-", imageDy, "-", imageDz, ".json")
    boundaryMat = GenerateBorderMatrix.getBorderMatrix(
        string(outputDirectory, "BORDERS/", "border_",
            imageDx, "-", imageDy, "-", imageDz, ".json"))
    ◇

```

Fragment referenced in 38b.

Now we can start the pipeline:

```

⟨ pipeline conversion 38a ⟩ ≡
    # Starting pipeline conversion
    info("Starting images conversion")
    ⟨ pixels to voxels conversion step 44a ⟩

    info("Merging boundaries")
    ⟨ boundaries merge step 47a ⟩

    info("Merging blocks")
    ⟨ block merge step 48 ⟩

    info("Smoothing models")
    ⟨ smoothing step 52 ⟩

    info("Merging obj models")
    ⟨ final file merge 53a ⟩
end ◇

```

Fragment referenced in 38b.

As we can see, last pipeline step does not require iteration on all grid blocks. This is the code for the function that starts the pipeline, with the parts explained earlier:

```

⟨ start conversion of images 38b ⟩ ≡

function startImageConversion(sliceDirectory, outputDirectory, borderFilename,
                             imageHeight, imageWidth, imageDepth,
                             imageDx, imageDy, imageDz,
                             parallelMerge)
    """
    Support function for converting a stack of images into a model

    sliceDirectory: directory containing the image stack
    """

    ⟨ get border matrix 37 ⟩
    ⟨ pipeline conversion 38a ⟩
end
◇

```

Fragment referenced in 99a.

### 5.4.1 Images conversion step

Now we will focus on the first step of our pipeline conversion: *images conversion*. First thing to do is read an image calling the `PngStack2Array3dJulia`.

```
⟨ image read 39a ⟩ ≡  
    theImage = PngStack2Array3dJulia.pngstack2array3d(sliceDirectory,  
                                                       startImage, endImage)  
    ◇
```

Fragment referenced in 42.

Now we can start iterating on other blocks of the grid:

```
⟨ block iteration 39b ⟩ ≡  
    for xBlock in 0:(imageWidth / imageDx - 1)  
        for yBlock in 0:(imageHeight / imageDy - 1)  
  
            xStart = xBlock * imageDx  
            yStart = yBlock * imageDy  
            zStart = startImage  
  
            xEnd = xStart + imageDx  
            yEnd = yStart + imageDy  
  
            imageDz = length(theImage)  
  
            debug("*****")  
            debug(string("xStart = ", xStart, " xEnd = ", xEnd))  
            debug(string("yStart = ", yStart, " yEnd = ", yEnd))  
            debug("theImage dimensions: ", size(theImage)[1], " ",  
                  size(theImage[1])[1], " ", size(theImage[1])[2]) ◇
```

Fragment referenced in 42.

Here *xStart* and *yStart* are the absolute coordinates of the model and are calculated from the block coordinates. Now we can get the current slice for the entire image (with size (*imageDx*, *imageDy*, *imageDz*)), check values for every single pixel into it and, if it represents a foreground point, put it into an array called `chain3D`. This structure contains indexes of the linearized array created from the matrix. In Figure 12 there is a sample conversion from the matrix to the array



$$\begin{pmatrix} 0^0 & 0^2 \\ 0^1 & 0^3 \end{pmatrix} \begin{pmatrix} 46^4 & 0^6 \\ 46^5 & 46^7 \end{pmatrix} \rightarrow 0^0 \ 0^1 \ 0^2 \ 0^3 \ 46^4 \ 46^5 \ 0^6 \ 46^7$$

$$\begin{pmatrix} 0^0 & 0^2 \\ 0^1 & 0^3 \end{pmatrix} \begin{pmatrix} 0^4 & 46^6 \\ 46^5 & 46^7 \end{pmatrix} \rightarrow 0^0 \ 0^1 \ 0^2 \ 0^3 \ 0^4 \ 46^5 \ 46^6 \ 46^7$$

Figure 12: Transformation of a matrix resulting from a 2x2x2 grid into a linearized array (with cells indexes) (a) First example (b) Second example

As we can see from that figure, from a 2x2x2 grid we can obtain eight values for the single block (or **cell**), where the indexes for the foreground pixels represent indexes of non-empty cells in a 2x2x2 cuboidal geometry. This is the code for getting foreground pixels:

```

⟨ get image slice 40 ⟩ ≡
    chains3D = Array{Int, 0}
    for z in 1 : imageDz
        for y in 1 : imageDy
            for x in 1 : imageDx
                if(theImage[z][x + xStart, y + yStart] == 0xff)
                    index = x - 1 + (y - 1) * imageDx + (z - 1) * (imageDx * imageDy)
                    push!(chains3D, index)
                end
            end
        end
    end
end ◇

```

Fragment referenced in 42.

Now that we have full cells for the geometry, we can convert them into a *LAR model*. In particular, we are interested in cell boundaries for every block (as we want to obtain only the boundaries for the final model) so we can call function `larBoundaryChain` from `Lar2Julia` module (which will be explained in section 7). In Figure 13 there are some examples of models extracted from a single  $2 \times 2 \times 2$  block.

After model computation, next step is getting vertices and faces from model cells writing results to file. However, as we have already said, we are only interested in boundaries of the final model while now we have only boundaries of a single block. Consequently, we have to separate boundaries from the inner faces of the block on different files (boundaries separation will be explained in section 8). As we can see later, we will merge boundaries together deleting common faces on both block borders, obtaining a model without internal faces. These are pieces of code for getting the inner block model with the boundaries and for file writing:

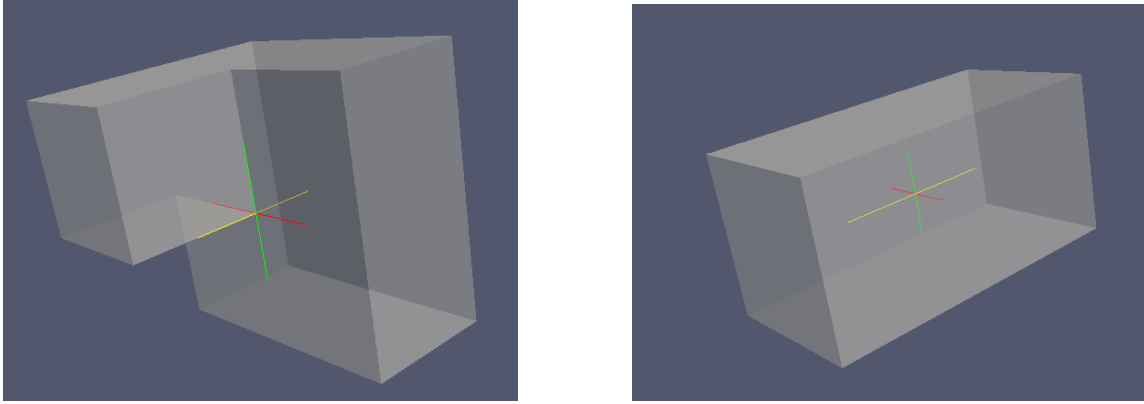


Figure 13: Sample models of 2x2x2 blocks

```

⟨get inner model and boundaries 41a⟩ ≡
    models = LARUtils.computeModelAndBoundaries(imageDx, imageDy, imageDz,
                                                xStart, yStart, zStart, objectBoundaryChain)

    V, FV = models[1][1] # inside model
    V_left, FV_left = models[2][1]
    V_right, FV_right = models[3][1] # right boundary
    V_top, FV_top = models[4][1] # top boundary
    V_bottom, FV_bottom = models[5][1] # bottom boundary
    V_front, FV_front = models[6][1] # front boundary
    V_back, FV_back = models[7][1] # back boundary
    ◇

```

Fragment referenced in 42.

```

⟨write block models to file 41b⟩ ≡
    # Writing all models on disk
    model_outputFilename = string(outputDirectory, "MODELS/model_output_", xBlock,
                                   "-", yBlock, "_", startImage, "_", endImage)
    Model2Obj.writeToObj(V, FV, model_outputFilename)

    left_outputFilename = string(outputDirectory, "MODELS/left_output_", xBlock,
                                   "-", yBlock, "_", startImage, "_", endImage)
    Model2Obj.writeToObj(V_left, FV_left, left_outputFilename)

    right_outputFilename = string(outputDirectory, "MODELS/right_output_", xBlock,
                                   "-", yBlock, "_", startImage, "_", endImage)
    Model2Obj.writeToObj(V_right, FV_right, right_outputFilename)

```

```

top_outputFilename = string(outputDirectory, "MODELS/top_output_", xBlock,
                             "-", yBlock, "_", startImage, "_", endImage)
Model2Obj.writeToObj(V_top, FV_top, top_outputFilename)

bottom_outputFilename = string(outputDirectory, "MODELS/bottom_output_", xBlock,
                                "-", yBlock, "_", startImage, "_", endImage)
Model2Obj.writeToObj(V_bottom, FV_bottom, bottom_outputFilename)

front_outputFilename = string(outputDirectory, "MODELS/front_output_", xBlock,
                                "-", yBlock, "_", startImage, "_", endImage)
Model2Obj.writeToObj(V_front, FV_front, front_outputFilename)

back_outputFilename = string(outputDirectory, "MODELS/back_output_", xBlock,
                               "-", yBlock, "_", startImage, "_", endImage)
Model2Obj.writeToObj(V_back, FV_back, back_outputFilename) ◇

```

Fragment referenced in 42.

This is the `processFunction` for this pipeline step

```

⟨ image conversion process 42 ⟩ ≡
    function imageConversionProcess(sliceDirectory,
                                    startImage, endImage,
                                    imageDx, imageDy,
                                    imageWidth, imageHeight,
                                    outputDirectory,
                                    boundaryMat)
    """
    Support function for converting a stack of image on a single
    independent process
    """

    ⟨ image read 39a ⟩

    ⟨ block iteration 39b ⟩

        ⟨ get image slice 40 ⟩

        if(length(chains3D) != 0)
            # Computing boundary chain
            debug("chains3d = ", chains3D)
            debug("Computing boundary chain")
            objectBoundaryChain = Lar2Julia.larBoundaryChain(boundaryMat, chains3D)

```

```

        debug("Converting models into obj")
        try
            mkdir(string(outputDirectory, "MODELS"))
        catch
        end
        < get inner model and boundaries 41a >

        < write block models to file 41b >
    else
        debug("Model is empty")
    end
end
end
end
end ◇

```

Fragment referenced in 99a.

This is the code for starting this pipeline step:

```

< pixelsToVoxels function 43 > ≡
function pixelsToVoxels(sliceDirectory,
                        imageHeight, imageWidth, imageDepth,
                        imageDx, imageDy, imageDz,
                        outputDirectory,
                        boundaryMat)

    """
    Function for conversion of pixels into voxels. It is different
    from iterateOnBlocks because it needs a different distribution
    of tasks between processes
    """

    beginImageStack = 0
    endImage = beginImageStack

    tasks = Array{RemoteRef, 0}
    for zBlock in 0:(imageDepth / imageDz - 1)
        startImage = endImage
        endImage = startImage + imageDz
        task = @spawn imageConversionProcess(sliceDirectory,
                                              startImage, endImage,
                                              imageDx, imageDy,
                                              imageWidth, imageHeight,
                                              outputDirectory,
                                              boundaryMat)

        push!(tasks, task)
    end
end

```

```

end

# Waiting for tasks
for task in tasks
    wait(task)
end
end ◇

```

Fragment referenced in 99a.

```

⟨ pixels to voxels conversion step 44a ⟩ ≡
    @time pixelsToVoxels(sliceDirectory,
                        imageHeight, imageWidth, imageDepth,
                        imageDx, imageDy, imageDz,
                        outputDirectory,
                        boundaryMat) ◇

```

Fragment referenced in 38a.

How we can see, for this step we do not use the `iterateOnBlocks` function, in fact pixel to voxel conversion is more efficient if we parallelize tasks assigning to each process an entire z-Block.

#### 5.4.2 Boundaries merge step

Next step of our pipeline consists in *boundaries merge*. In fact, we have already seen that for every non-empty cell we create files for the inner parts and for the boundaries of the block. So if we want a final model without boundaries between internal blocks, we need to merge them removing duplicated faces on both sides (see Section 8.6 for a better explanation of this step). The following is the `processFunction`:

```

⟨ boundary merge process function 44b ⟩ ≡
    function mergeBoundariesProcess(modelDirectory,
                                    xBlock, yBlock,
                                    startImage, endImage,
                                    imageDx, imageDy,
                                    imageWidth, imageHeight)

        """
        Helper function for mergeBoundaries.
        It is executed on different processes
    """
    end

```

```

modelDirectory: Directory containing model files
startImage: Block start image
endImage: Block end image
imageDx, imageDy: x and y sizes of the grid
imageWidth, imageHeight: Width and Height of the image
"""

# Merging right Boundary
firstPath = string(modelDirectory, "/right_output_", xBlock, "-", yBlock,
                    "_", startImage, "_", endImage)
secondPath = string(modelDirectory, "/left_output_", xBlock, "-", yBlock + 1,
                    "_", startImage, "_", endImage)
mergeBoundariesAndRemoveDuplicates(firstPath, secondPath)

# Merging top boundary
firstPath = string(modelDirectory, "/top_output_", xBlock, "-", yBlock,
                    "_", startImage, "_", endImage)
secondPath = string(modelDirectory, "/bottom_output_", xBlock, "-", yBlock,
                    "_", endImage, "_", endImage + (endImage - startImage))
mergeBoundariesAndRemoveDuplicates(firstPath, secondPath)

# Merging front boundary
firstPath = string(modelDirectory, "/front_output_", xBlock, "-", yBlock,
                    "_", startImage, "_", endImage)
secondPath = string(modelDirectory, "/back_output_", xBlock + 1, "-", yBlock,
                    "_", startImage, "_", endImage)
mergeBoundariesAndRemoveDuplicates(firstPath, secondPath)
end ◇

```

Fragment referenced in 99a.

For every block we do the following merges:

- right boundary with the left boundary of the next block on the right
- top boundary with the bottom boundary of the next block on the top
- front boundary with the back boundary of the next block on the front

all merges are executed by the function `mergeBoundariesAndRemoveDuplicates` which does the work calling the `Model2Obj` and `LARUtils` libraries for loading and cleaning of the boundaries models.

$\langle \textit{merge boundaries utility function 45} \rangle \equiv$



This is the code used to start this pipeline step:

```
⟨ boundaries merge step 47a ⟩ ≡
    @time iterateOnBlocks(string(outputDirectory, "MODELS"),
                          imageHeight, imageWidth, imageDepth,
                          imageDx, imageDy, imageDz,
                          mergeBoundariesProcess) ◇
```

Fragment referenced in 38a.

### 5.4.3 Block merge step

At this step of the computation, we have files with the inner parts of a single block model and the remaining boundaries. Now we need to merge the blocks removing double vertices and faces, so we can save space and prepare our model to the *smoothing step*. This is the code of the `processFunction`:

```
⟨ Block merge process function 47b ⟩ ≡
    function mergeBlocksProcess(modelDirectory,
                                xBlock, yBlock,
                                startImage, endImage,
                                imageDx, imageDy,
                                imageWidth, imageHeight)

    """
    Helper function for mergeBlocks.
    It is executed on different processes

    modelDirectory: Directory containing model files
    startImage: Block start image
    endImage: Block end image
    imageDx, imageDy: x and y sizes of the grid
    imageWidth, imageHeight: Width and Height of the image
    """

    blockCoordsV = string(xBlock, "-", yBlock, "_", startImage,
                          "_", endImage, "_vtx.stl")
    blockCoordsFV = string(xBlock, "-", yBlock, "_", startImage,
                          "_", endImage, "_faces.stl")

    arrayV = [string(modelDirectory, "/left_output_", blockCoordsV),
              string(modelDirectory, "/right_output_", blockCoordsV),
              string(modelDirectory, "/top_output_", blockCoordsV),
              string(modelDirectory, "/bottom_output_", blockCoordsV),
              string(modelDirectory, "/front_output_", blockCoordsV),
```



```

        string(modelDirectory, "/back_output_", blockCoordsV),
        string(modelDirectory, "/model_output_", blockCoordsV)]

arrayFV = [string(modelDirectory, "/left_output_", blockCoordsFV),
           string(modelDirectory, "/right_output_", blockCoordsFV),
           string(modelDirectory, "/top_output_", blockCoordsFV),
           string(modelDirectory, "/bottom_output_", blockCoordsFV),
           string(modelDirectory, "/front_output_", blockCoordsFV),
           string(modelDirectory, "/back_output_", blockCoordsFV),
           string(modelDirectory, "/model_output_", blockCoordsFV)]

V, FV = Model2Obj.getModelsFromFiles(arrayV, arrayFV)
V, FV = LARUtils.removeDoubleVerticesAndFaces(V, FV, 0)
for i in 1:length(arrayV)
    if(isfile(arrayV[i]))
        rm(arrayV[i])
        rm(arrayFV[i])
    end
end

Model2Obj.writeToObj(V, FV, string(modelDirectory, "/model_output_",
                                   xBlock, "-", yBlock, "-", startImage, "-", endImage))

end ◇

```

Fragment referenced in 99a.

For a better explanation of the `LARUtils` function that remove duplicated vertices, you can see Section [8.4](#)

This is the code for block merge starting

```

⟨ block merge step 48 ⟩ ≡
    @time iterateOnBlocks(string(outputDirectory, "MODELS"),
                          imageHeight, imageWidth, imageDepth,
                          imageDx, imageDy, imageDz,
                          mergeBlocksProcess) ◇

```

Fragment referenced in 38a.

#### 5.4.4 Smoothing step

Now we have obtained models without internal boundaries between blocks and without double vertices and faces in a single block. However this partial model has squared edges, so we need to smooth them. The `processFunction` for this step, is the following:

*⟨ Smooth block process function 49 ⟩* ≡

```
function smoothBlocksProcess(modelDirectory,
                             xBlock, yBlock,
                             startImage, endImage,
                             imageDx, imageDy,
                             imageWidth, imageHeight)

  """
  Smoothes a block in a single process

  modelDirectory: Path of the directory containing all blocks
                  that will be smoothed
  startImage, endImage: start and end image for this block
  imageDx, imageDy: sizes of the grid
  imageWidth, imageHeight: sizes of the images
  """

  # Loading the current block model
  blockFileV = string(modelDirectory, "/model_output_", xBlock, "-", yBlock,
                      "_", startImage, "_", endImage, "_vtx.stl")
  blockFileFV = string(modelDirectory, "/model_output_", xBlock, "-", yBlock,
                      "_", startImage, "_", endImage, "_faces.stl")

  if isfile(blockFileV)
    # Loading only model of the current block
    blockModelV, blockModelFV = Model2Obj.getModelsFromFiles([blockFileV], [blockFileFV])
    blockModelV, blockModelFV = LARUtils.removeDoubleVerticesAndFaces(blockModelV,
                                                                    blockModelFV, 0)

    # Loading a unique model from this block and its adjacents
    modelsFiles = Array(String, 0)
    for x in xBlock - 1:xBlock + 1
      for y in yBlock - 1:yBlock + 1
        for z in range(startImage - (endImage - startImage), (endImage - startImage), 3)
          push!(modelsFiles, string(modelDirectory, "/model_output_",
                                   x, "-", y, "_", z, "_", z + (endImage - startImage)))
        end
      end
    end

    modelsFilesV = map((s) -> string(s, "_vtx.stl"), modelsFiles)
    modelsFilesFV = map((s) -> string(s, "_faces.stl"), modelsFiles)

    modelV, modelFV = Model2Obj.getModelsFromFiles(modelsFilesV, modelsFilesFV)
    modelV, modelFV = LARUtils.removeDoubleVerticesAndFaces(modelV, modelFV, 0)

    # Now I have to save indices of vertices of the current block model
```

```

blockVerticesIndices = Array(Int, 0)
for i in 1:length(blockModelV)
  for j in 1:length(modelV)
    if blockModelV[i] == modelV[j]
      push!(blockVerticesIndices, j)
    end
  end
end

# Now I can apply smoothing on this model
V_sm, FV_sm = Smoother.smoothModel(modelV, modelFV)

# Now I have to get only block vertices and save them on the new model
V_final = Array{Array{Float64}, 0}
for i in blockVerticesIndices
  push!(V_final, V_sm[i])
end
outputFilename = string(modelDirectory, "/smoothed_output_", xBlock, "-",
                        yBlock, "_", startImage, "_", endImage)
Model2Obj.writeToObj(V_final, blockModelFV, outputFilename)
end
end ◇

```

Fragment referenced in 99a.

An explanation of the smoothing algorithm used there, can be found in Section 9.2. What we need to remember here, is the importance of having the adjacent vertices for every vertex of our block. In fact, according to the chosen smoothing algorithm, every vertex is replaced with a new one with coordinates computed from the mean positions of its adjacent. However, loading of the entire model into memory cannot be done because of its sizes; so we created a simple algorithm which loads only near blocks to the current one. In fact, for every block we want to smooth, we load the twenty six adjacent blocks on all directions and the chosen one. We create a unique model with it (removing double vertices and faces) and then smoothing it with the algorithm in **Smoother** module. Finally we save only smoothed vertices for the chosen block and continue with the other blocks. In Figure 15 there is a graphical explanation for the algorithm.

Moreover, this **processFunction** can only execute a single iteration of the smoothing algorithm, so we need a function that can be able to execute more times the algorithm:

```

⟨ execute smoothing function 50 ⟩ ≡
function smoothBlocks(modelDirectory,
                      imageHeight, imageWidth, imageDepth,

```

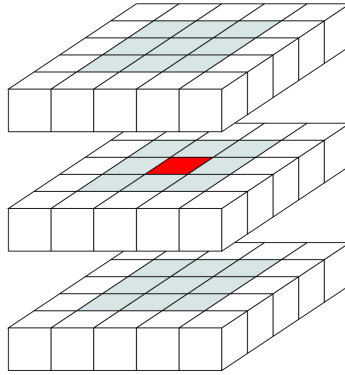


Figure 15: Smoothing of a single block. The red block at the center of the figure is the current one, while the other twenty six colored ones are the blocks that will be part of the model which will be smoothed for this iteration

```

                                imageDx, imageDy, imageDz)
"""
Smooths all blocks of the
model
"""

iterations = 1
for i in 1:iterations
    info("Iteration ", i)

    iterateOnBlocks(modelDirectory,
                    imageHeight, imageWidth, imageDepth,
                    imageDx, imageDy, imageDz,
                    smoothBlocksProcess)

    # Moving smoothed file for next iterations

    beginImageStack = 0
    endImage = beginImageStack
    for zBlock in 0:(imageDepth / imageDz - 1)
        startImage = endImage
        endImage = startImage + imageDz
        for xBlock in 0:(imageWidth / imageDx - 1)
            for yBlock in 0:(imageHeight / imageDy - 1)

                f_V = string(modelDirectory, "/smoothed_output_", xBlock, "-", yBlock, "_",
                            startImage, "_", endImage, "_vtx.stl")
                f_FV = string(modelDirectory, "/smoothed_output_", xBlock, "-", yBlock, "_",
                             startImage, "_", endImage, "_faces.stl")

```



```

< final file merge 53a > ≡
    if parallelMerge
        @time Model2Obj.mergeObjParallel(string(outputDirectory, "MODELS"))
    else
        @time Model2Obj.mergeObj(string(outputDirectory, "MODELS")) ◇

```

Fragment referenced in 38a.

## 6 GenerateBorderMatrix

This module has the responsibility for the generation of the border matrix operator for models boundary computation.

### 6.1 Module imports

These are modules needed for this part of the package and the public functions exported

```

< modules import GenerateBorderMatrix 53b > ≡
    import LARUtils, Lar2Julia
    import JSON

    export computeOriented3Border, writeBorder, getOriented3BorderPath, getBorderMatrix
    ◇

```

Fragment referenced in 99b.

### 6.2 Get border matrix from file

As we have already seen in previous sections, we need to compute boundaries for every block of the model grid. This can be done using the topological boundary operator from LAR package (which has been ported into Julia as we can see in Section 7.5). However, the resulting matrix depends only on grid sizes; so it could be reused for other models. Consequently first time we need a border operator we compute it and then save it on disk for next conversions. This function does that work searching for a file containing the border and, if it does not exist, calculate and save it:

```

< get Border matrix 53c > ≡

```

```

function getOriented3BorderPath(borderPath, nx, ny, nz)
    """
    Try reading 3-border matrix from file. If it fails matrix
    is computed and saved on disk in JSON format

    borderPath: path of border directory
    nx, ny, nz: image dimensions
    """

    filename = string(borderPath, "/border_", nx, "-", ny, "-", nz, ".json")
    if !isfile(filename)
        border = computeOriented3Border(nx, ny, nz)
        writeBorder(border, filename)
    end
    return filename

end ◇

```

Fragment referenced in 99b.

### 6.3 Write border matrix on file

We have already seen that for performance reasons border operator matrix is saved on file; here we will see code used for this scope. Firstly, we have defined a function `writeBorder`, which takes as parameters the border matrix (computed in subsection 6.4) and the output file path.

$\langle \textit{write Border matrix 54} \rangle \equiv$

```

function writeBorder(boundaryMatrix, outputFile)
    """
    Write 3-border matrix on json file

    boundaryMatrix: matrix to write on file
    outputFile: path of the outputFile
    """

    row = findn(boundaryMatrix)[1]
    col = findn(boundaryMatrix)[2]
    data = nonzeros(boundaryMatrix)

    matrixObj = MatrixObject(0, 0, row, col, data)

    outfile = open(string(outputFile), "w")

```

```

        JSON.print(outfile, matrixObj)
        close(outfile)
    end ◇

```

Fragment referenced in 99b.

We can see that, in final JSON file, we write an object called `MatrixObject` which has the following definition:

```

⟨ Matrix object for JSON file 55a ⟩ ≡
    type MatrixObject
        ROWCOUNT
        COLCOUNT
        ROW
        COL
        DATA
    end ◇

```

Fragment referenced in 99b.

The most important fields of this object are the last three ones; the first two contain all coordinates of the non-zero elements, the last contains all non-zero elements of the sparse matrix. So considering the full matrix  $V$  we will have that  $S[ROW[k], COL[k]] = V[k]$ .

## 6.4 Compute border matrix

Here we can see code used for computation of the border operator, which calls the functions in `Lar2Julia` module.

```

⟨ compute border matrix 55b ⟩ ≡
    # Compute the 3-border operator
    function computeOriented3Border(nx, ny, nz)
        """
        Compute the 3-border matrix
        """
        V, bases = LARUtils.getBases(nx, ny, nz)
        return Lar2Julia.signedCellularBoundary(V, bases)
    end ◇

```

Fragment referenced in 99b.



## 6.5 Transform border matrix

Last function we will see, extracts the `MatrixObject` in Section 6.3 converting it into a common Julia csc sparse matrix

```
< transform border matrix in csc format 56 > ≡
function getBorderMatrix(borderFilename)
    """
    Get the border matrix from json file and convert it in
    CSC format
    """
    # Loading borderMatrix from json file
    borderData = JSON.parsefile(borderFilename)

    # Converting Any arrays into Int arrays
    row = Array{Int64, length(borderData["ROW"])}
    col = Array{Int64, length(borderData["COL"])}
    data = Array{Int64, length(borderData["DATA"])}

    for i in 1: length(borderData["ROW"])
        row[i] = borderData["ROW"][i]
    end

    for i in 1: length(borderData["COL"])
        col[i] = borderData["COL"][i]
    end

    for i in 1: length(borderData["DATA"])
        data[i] = borderData["DATA"][i]
    end
    return sparse(row, col, data)
end ◊
```

Fragment referenced in 99b.

## 7 Lar2Julia

This module contains functions used in LAR library which are converted using Julia syntax. Next versions of the software will contain more and more functions from the original LAR library (which is written in python)

## 7.1 Module imports

These are modules used for `Lar2Julia` and the public functions

```
< modules import Lar2Julia 57a > ≡  
import JSON  
  
using Logging  
  
export larBoundaryChain, cscChainToCellList, relationshipListToCSC ◇
```

Fragment referenced in 100a.

## 7.2 Get boundary chain from a model

Now we will observe how to compute the boundary chain of a LAR model given the list of non-empty cells and the boundary operator stored as a csc sparse matrix. This algorithm is very simply: firstly we need to convert the list of cells into a sparse array containing the LAR model. So, the resulting array (which will be called `cscChain`) will contain a one for every `cscChain[i][1]  $\forall i \in$  brcCellList`. Next, we just have to compute the product between the two sparse matrices and convert all values of the result into one of these: `{-1; +1; 0}` using function `cscBinFilter`.

```
< get boundary chain 57b > ≡  
function larBoundaryChain(cscBoundaryMat, brcCellList)  
    """  
    Compute boundary chains  
    """  
  
    # Computing boundary chains  
    n = size(cscBoundaryMat)[1]  
    m = size(cscBoundaryMat)[2]  
  
    debug("Boundary matrix size: ", n, "\t", m)  
  
    data = ones{Int64, length(brcCellList)}  
  
    i = Array{Int64, length(brcCellList)}  
    for k in 1:length(brcCellList)  
        i[k] = brcCellList[k] + 1  
    end  
  
    j = ones{Int64, length(brcCellList)}
```

```

debug("cscChain rows length: ", length(i))
debug("cscChain columns length: ", length(j))
debug("cscChain data length: ", length(brcCellList))

debug("rows ", i)
debug("columns ", j)
debug("data ", data)

cscChain = sparse(i, j, data, m, 1)
cscmat = cscBoundaryMat * cscChain
out = cscBinFilter(cscmat)
return out
end

function cscBinFilter(CSCm)
    k = 1
    data = nonzeros(CSCm)
    sgArray = copysign(1, data)

    while k <= nnz(CSCm)
        if data[k] % 2 == 1 || data[k] % 2 == -1
            data[k] = 1 * sgArray[k]
        else
            data[k] = 0
        end
        k += 1
    end

    return CSCm
end ◇

```

Fragment referenced in 100a.

### 7.3 Get oriented cells from a chain

Another operation that could be useful (even if it is not actually used in the package) consists in getting of “+1” oriented cells from a chain. For obtaining this result, it is necessary to get all non-zeros element from the sparse Julia array (remembering that if the user manually write a zero into the array it will be returned from `nonzeros` function anyway) and then returning only indices of cells that have a “+1” in nonzero element array.

$\langle \textit{get oriented cells from a chain 58} \rangle \equiv$

```

function cscChainToCellList(CSCm)
    """
    Get a csc containing a chain and returns
    the cell list of the "+1" oriented faces
    """
    data = nonzeros(CSCm)
    # Now I need to remove zero element (problem with Julia nonzeros)
    nonzeroData = Array{Int64, 0}
    for n in data
        if n != 0
            push!(nonzeroData, n)
        end
    end

    cellList = Array{Int64, 0}
    for (k, theRow) in enumerate(findn(CSCm)[1])
        if nonzeroData[k] == 1
            push!(cellList, theRow)
        end
    end
    return cellList
end

```

Fragment referenced in 100a.

## 7.4 Transform relationships from arrays of arrays to a sparse matrix

Another function which can be useful for our purposes is conversion between different representations of the LAR relationships. For example we often use a representation based on list of list of int but if we want to apply topological operators (such as the incident operators) we need to convert it into a matrix of values. In Figure 16 we can see an example of a LAR relationship with different representations.

```

⟨ transform relationships to csc 59 ⟩ ≡
function relationshipListToCSC(larRelation)
    """
    Get a LAR relationship
    and convert it into a CSC matrix
    """

    # Build I and J arrays for creation of
    # sparse matrix
    data = Array{Int, 0}

```

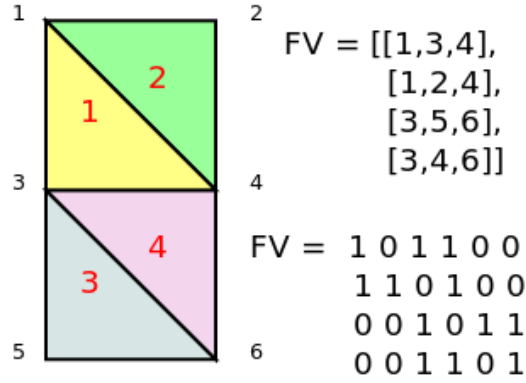


Figure 16: Different representations for faces of a simple LAR model. the first one is based on a list of list of int, while the other is a simple matrix where for every value we have  $FV[i][j] = 1 \iff \text{face } i \text{ contains the vertex } j$

```

I = Array{Int, 0}
J = Array{Int, 0}
for (k,row) in enumerate(larRelation)
    for col in row
        push!(I, k)
        push!(J, col)
        push!(data, 1)
    end
end

return sparse(I, J, data)
end ◊

```

Fragment referenced in 100a.

## 7.5 Compute the boundary operator

Here we see how to compute the boundary operator using topological algebra. First of all we need two helper functions for computation of convex combination of an array of vectors and for transposition of Julia sparse matrix.

```

⟨convex combination of an array of vectors 60⟩ ≡
function convexCombination(vectors)
    """
    Compute the convex combination of an

```

```

array of vectors

vectors: An array of vectors
"""
# Computing sum of all vectors
sum = [0.0, 0.0, 0.0]
for v in vectors
    sum += v
end
return sum/length(vectors)
end ◇

```

Fragment referenced in 65.

$\langle \text{sparse matrix transposition 61a} \rangle \equiv$

```

function cscTranspose(CSCm)
"""
    Compute the transpose matrix of a
    sparse CSC matrix
"""
    rows, columns = findn(CSCm)
    data = nonzeros(CSCm)
    return sparse(columns, rows, data, size(CSCm)[2], size(CSCm)[1])
end ◇

```

Fragment referenced in 65.

Now we can see how to compute the simple *boundary* operator (without orientation) for the array of *cells* and *facets* of our model. According to this algorithm, we should just compute the sparse matrix representation of the cells and facets multiply the latter with the transposed of the first. Finally we have to maintain only the max values for every row returning a matrix with only ones and zeros.

$\langle \text{non-oriented boundary 61b} \rangle \equiv$

```

function boundary(cells, facets)
"""
    Take the usual LAR representation of d-cells
    and (d-1)-facets and returns the
    boundary operator in csc format

    cell, facets: d-cells and (d-1)-facets in BRC format

```

```

"""
cscCV = relationshipListToCSC(cells)
cscFV = relationshipListToCSC(facets)
cscFC = cscFV * cscTranspose(cscCV)
return cscBoundaryFilter(cscFC)
end ◇

```

Fragment referenced in 65.

$\langle \text{boundary filter 62} \rangle \equiv$

```

function cscBoundaryFilter(CSCm)
"""
Matrix filtering to produce the boundary
matrix. It returns only max values for
every row

CSCm: a matrix in the CSC format
"""

# Now I iterate on all rows of the matrix
# saving only the max values on the row in a
# new sparse matrix
rows = Array{Int, 0}()
columns = Array{Int, 0}()
data = Array{Int, 0}()

# I need to compute the transposed matrix
# for improving performances. In fact Julia
# use only column-stored arrays so it is
# inefficient to iterate over rows
transCSCm = cscTranspose(CSCm)

for k in 1 : size(transCSCm)[2]
    matrixColumn = transCSCm[:, k]
    maxColumnValue = maximum(matrixColumn)
    rowIndices, _ = findn(matrixColumn)
    for rowIndex in rowIndices
        if transCSCm[rowIndex, k] == maxColumnValue
            push!(rows, k)
            push!(columns, rowIndex)
            push!(data, 1)
        end
    end
end
end
end

```

```

        return sparse(rows, columns, data, size(CSCm)[1], size(CSCm)[2])
    end ◇

```

Fragment referenced in 65.

Now we can compute the *oriented boundary operator*, which returns a sparse matrix with values in the Abelian group  $\{-1, 0, 1\}$

```

⟨ oriented boundary operator 63 ⟩ ≡
function signedCellularBoundary(V, bases)
    """
    Compute the signed cellular boundary
    for polytopal complexes

    V: the array of vertices
    bases: the bases of a LAR model

    Warning: At the end of this function the bases arrays
    will be modified for performance reasons
    """
    # First of all I need to convert LAR bases in Julia
    # 1-based indexing

    for i in 1 : length(bases)
        for j in 1 : length(bases[i])
            for z in 1 : length(bases[i][j])
                bases[i][j][z] += 1 # This will change the reference to bases arrays!!
            end
        end
    end

    cscBoundary = boundary(bases[end], bases[end - 1])
    rows, columns = findn(cscBoundary)
    pairs = map((x,y) -> return[x, y]), rows, columns)
    dim = length(bases) - 1
    signs = Array{Int, 0}
    chain = incidenceChain(bases)

    for pair in pairs
        flag = reverse(pair)
        for k in 1 : dim - 1
            cell = flag[end]
            append!(flag, collect(chain[k + 1][cell][2]))
        end
    end
end

```



```

flagMat = Array(Float64, dim + 1, dim + 1)

for k in 0 : dim
    vertices = Array{Array{Int}, 0}
    for v in bases[dim - k + 1][flag[k + 1]]
        push!(vertices, V[v])
    end
    vert = convexCombination(vertices)
    for j in 1 : dim
        flagMat[j, k + 1] = vert[j]
    end
    flagMat[dim + 1, k + 1] = 1
end

# I have used a transposed flagMat to better
# exploit caching, now I can use the right version
flagMat = transpose(flagMat)
flagSign = sign(det(flagMat))
push!(signs, flagSign)
end
transposedPairs = transpose(pairs)
return sparse(map(((x)->return x[1])), pairs), map(((x)->return x[2])), pairs), signs)
end ◊

```

Fragment referenced in 65.

As we can see, we also need an incidence operator between cells and facets

```

⟨ incidence operator 64 ⟩ ≡
function larIncidence(cells, facets)
    """
    The incidence operator between cells
    and facets of a LAR model

    cells, facets: cells and facets BRC representation
    of a LAR model
    """
    # The cell-face incidence operator
    cscCellFacet = boundary(facets, cells)
    larCellFacet = Array{Array{Int}, length(cells)}

    # Using a transposed matrix for caching exploitation
    transCscCellFacet = cscTranspose(cscCellFacet)

```

```

columns, rows = findn(transCscCellFacet)
data = nonzeros(transCscCellFacet)
for i in 1 : length(data)
    if data[i] == 1
        if(!isdefined(larCellFacet, rows[i]))
            larCellFacet[rows[i]] = []
        end
        append!(larCellFacet[rows[i]], collect(columns[i]))
    end
end
return larCellFacet
end

function incidenceChain(bases)
    """
    Compute 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,...]

    bases: bases of a LAR cellular complex
    """
    pairsOfBases = zip(bases[2 : end], bases[1 : end - 1])
    relations = Array{Array{Array{Int}}, 0}
    tasks = Array{RemoteRef, 0}
    for (cells, facets) in pairsOfBases
        task = @spawn larIncidence(cells, facets)
        push!(tasks, task)
    end

    for task in tasks
        push!(relations, fetch(task))
    end

    return reverse(relations)
end ◇

```

Fragment referenced in 65.

$\langle \text{boundary computation 65} \rangle \equiv$   
 $\langle \text{convex combination of an array of vectors 60} \rangle$   
 $\langle \text{sparse matrix transposition 61a} \rangle$   
 $\langle \text{boundary filter 62} \rangle$

*⟨ non-oriented boundary 61b ⟩*

*⟨ incidence operator 64 ⟩*

*⟨ oriented boundary operator 63 ⟩* ◇

Fragment referenced in 100a.

## 8 LARUtils

This module contains functions used for manipulation of LAR models

### 8.1 Module imports

These are modules used in LARUtils and the functions exported

```
⟨ modules import LARUtils 66a ⟩ ≡  
    using Logging  
  
    export ind, invertIndex, getBases, removeDoubleVerticesAndFaces,  
           computeModelAndBoundaries  
    ◇
```

Fragment referenced in 100b.

### 8.2 Transformation from matrix to array

First utility functions we will see, transform a matrix into an array and vice versa. We have already seen in section 5.4.1 uses of this linearized matrices; now we can focus on code for transformation.

```
⟨ conversion from matrix to array 66b ⟩ ≡  
    function ind(x, y, z, nx, ny)  
        ""  
        Transform coordinates into linearized matrix indexes  
        ""  
        return x + (nx + 1) * (y + (ny + 1) * (z))  
    end ◇
```

Fragment referenced in 100b.

Here we have defined also the inverse transformation from the array to the matrix, which is useful for obtaining vertices coordinates from a cell

```

⟨ conversion from array to matrix 67a ⟩ ≡
function invertIndex(nx,ny,nz)
    ""
    Invert indexes
    ""
    nx, ny, nz = nx + 1, ny + 1, nz + 1
    function invertIndex0(offset)
        a0, b0 = trunc(offset / nx), offset % nx
        a1, b1 = trunc(a0 / ny), a0 % ny
        a2, b2 = trunc(a1 / nz), a1 % nz
        return b0, b1, b2
    end
    return invertIndex0
end ◇

```

Fragment referenced in 100b.

### 8.3 Get bases of a LAR model

For generation of LAR models from an array of non-empty cells, we need to define a function for obtaining a base for every model, which will contain all LAR relationships:

- **V**: the array of vertices of a LAR model
- **VV**: the relationship between a vertex and itself
- **EV**: the relationship between an edge and its vertices
- **FV**: the relationship between a face and its vertices
- **CV**: the relationship between a cell and its vertices

From a geometrical point of view these bases create a chain composed from  $nx \times ny \times nz$  square cells (where nx ny and nz are the grid size).

Now we will see in details how to obtain all LAR relationships.  
First of all we need to compute vertices for the geometry:

```

⟨ compute vertices 67b ⟩ ≡

```

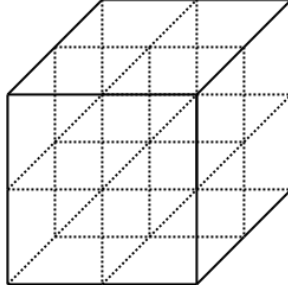


Figure 17: LAR bases geometry for a  $2 \times 2 \times 2$  grid

```
# Calculating vertex coordinates (nx * ny * nz)
V = Array{Int64}[]
for z in 0:nz
  for y in 0:ny
    for x in 0:nx
      push!(V,[x,y,z])
    end
  end
end
end ◇
```

Fragment referenced in 70c.

So we assume that our cube geometry has only integers coordinates that can vary from (0,0,0) to (nx,ny,nz)

Next we have to compute the CV relationship:

```
< compute CV 68 > ≡
# Building CV relationship
CV = Array{Int64}[]
for z in 0:nz-1
  for y in 0:ny-1
    for x in 0:nx-1
      push!(CV,the3Dcell([x,y,z]))
    end
  end
end
end ◇
```

Fragment referenced in 70c.

For every coordinate in the space delimited by the grid size, it is called function `the3Dcell`, which get the coordinate values returning a cell in the three-dimensional space:

```

⟨ compute three-dimensional cells 69a ⟩ ≡
  function the3Dcell(coords)
    x,y,z = coords
    return [ind(x,y,z,nx,ny), ind(x+1,y,z,nx,ny), ind(x,y+1,z,nx,ny),
            ind(x,y,z+1,nx,ny), ind(x+1,y+1,z,nx,ny), ind(x+1,y,z+1,nx,ny),
            ind(x,y+1,z+1,nx,ny), ind(x+1,y+1,z+1,nx,ny)]
  end
  ◇

```

Fragment referenced in 70c.

Now we have to compute the FV relationship, which will be widely used in this package:

```

⟨ compute FV 69b ⟩ ≡
  # Building FV relationship
  FV = Array{Int64}[]
  v2coords = invertIndex(nx,ny,nz)

  for h in 0:(length(V)-1)
    x,y,z = v2coords(h)

    if (x < nx) && (y < ny)
      push!(FV, [h,ind(x+1,y,z,nx,ny),ind(x,y+1,z,nx,ny),ind(x+1,y+1,z,nx,ny)])
    end

    if (x < nx) && (z < nz)
      push!(FV, [h,ind(x+1,y,z,nx,ny),ind(x,y,z+1,nx,ny),ind(x+1,y,z+1,nx,ny)])
    end

    if (y < ny) && (z < nz)
      push!(FV, [h,ind(x,y+1,z,nx,ny),ind(x,y,z+1,nx,ny),ind(x,y+1,z+1,nx,ny)])
    end

  end
  ◇

```

Fragment referenced in 70c.

Finally we have the VV relationship (which is trivial)

```

< compute VV 70a > ≡
    # Building VV relationship
    VV = map((x)->[x], 0:length(V)-1) ◇

```

Fragment referenced in 70c.

and the EV relationship

```

< compute EV 70b > ≡
    # Building EV relationship
    EV = Array{Int64}[]
    for h in 0:length(V)-1
        x,y,z = v2coords(h)
        if (x < nx)
            push!(EV, [h,ind(x+1,y,z,nx,ny)])
        end
        if (y < ny)
            push!(EV, [h,ind(x,y+1,z,nx,ny)])
        end
        if (z < nz)
            push!(EV, [h,ind(x,y,z+1,nx,ny)])
        end
    end ◇

```

Fragment referenced in 70c.

This is the complete code for the function `getBases`

```

< get LAR bases 70c > ≡
    function getBases(nx, ny, nz)
        """
        Compute all LAR relations
        """

        < compute three-dimensional cells 69a >

        < compute vertices 67b >

        < compute CV 68 >

        < compute FV 69b >
    end

```

```

    < compute VV 70a >

    < compute EV 70b >

    # return all basis
    return V, (VV, EV, FV, CV)
end ◇

```

Fragment referenced in 100b.

## 8.4 Double vertices and faces removal

Another useful function for our models is *removal of double vertices and faces*. In fact, when we produce a LAR model getting only full cell from the geometry in Figure 17 we could obtain double vertices (and consequently double faces). Figure 18 shows an example of a model with these vertices:

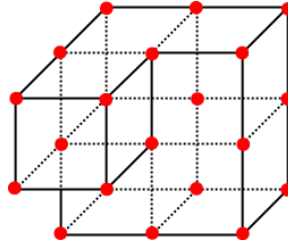


Figure 18: A sample model taken from a  $2 \times 2 \times 2$  grid with double vertices between faces in red (remember that we have only the boundaries faces for the model as we have seen in section 5.4.1)

As we can see, for every model there are a lot of double vertices, so we need to remove them for obtaining a compact representation and for next smoothing of the objects. First of all we have to identify double vertices, so it can be useful to define an order between them. Unfortunately Julia does not define a function for order array containing coordinates (which is format used in  $V$  array); so we have to define first a custom ordering function:

```

< vertices comparator function 71 > ≡
function lessThanVertices(v1, v2)
    """
    Utility function for comparing vertices coordinates
    """

    if v1[1] == v2[1]

```



```

        if v1[2] == v2[2]
            return v1[3] < v2[3]
        end
        return v1[2] < v2[2]
    end
    return v1[1] < v2[1]
end ◇

```

Fragment referenced in 74.

Now we can remove double vertices from the  $V$  array simply ordering them and removing all consecutive equal vertices. This procedure is more complex than a simple call to Julia `unique` function for removal of double elements because we need the new vertices indices for renaming faces (as we can see later)

```

⟨removal of double vertices 72⟩ ≡
function removeDoubleVertices(V)
    """
    Remove double vertices from a LAR model

    V: Array containing all vertices of the model
    """

    # Sort the vertices list and returns the ordered indices
    orderedIndices = sortperm(V, lt = lessThanVertices, alg=MergeSort)

    orderedVerticesAndIndices = collect(zip(sort(V, lt = lessThanVertices),
                                             orderedIndices))

    newVertices = Array{Array{Float64}, 0}()
    indices = zeros{Int, length(V)}
    prevv = Void
    i = 1
    for (v, ind) in orderedVerticesAndIndices
        if v == prevv
            indices[ind] = i - 1
        else
            push!(newVertices, v)
            indices[ind] = i
            i += 1
            prevv = v
        end
    end
    return newVertices, indices
end ◇

```

Fragment referenced in 74.

As we can see the algorithm does the following steps:

1. Sort of vertices list
2. Set the current vertex index counter to 1
3. For every couple (*vertex*, *index* into V array) do:
  - (a) If the current *vertex* is equal to the previous one put into the indices array at position *index* the value for the current vertex index count
  - (b) If the current *vertex* is not equal to the previous one save it into a new V array, insert the indices array at position *index* the current index count and increment it by one

So at the end of this function the array *newVertices* will contain all unique vertices, while the *indices* array will contain the correct index for every vertex into *newVertices* and the index corresponding to the saved vertex for every deleted vertex.

Now we can use these informations for renaming all faces.

```
<renaming of faces 73>  $\equiv$ 
function reindexVerticesInFaces(FV, indices, offset)
    """
    Reindex vertices indices in faces array

    FV: Faces array of the LAR model
    indices: new Indices for faces
    offset: offset for faces indices
    """

    for f in FV
        for i in 1: length(f)
            f[i] = indices[f[i] - offset] + offset
        end
    end
    return FV
end  $\diamond$ 
```

Fragment referenced in 74.

Here we can observe a *offset* parameter, which is necessary only if we are renaming faces whose indices doesn't start from zero; actually in `ImagesToLARModel` it is always equal to zero.

Finally for removing double faces, we only have to call `unique` function on renamed faces. This is the final code

$\langle \text{removal of double vertices and faces 74} \rangle \equiv$   
 $\langle \text{vertices comparator function 71} \rangle$

```
function removeDoubleVerticesAndFaces(V, FV, facesOffset)
    """
    Removes double vertices and faces from a LAR model

    V: Array containing all vertices
    FV: Array containing all faces
    facesOffset: offset for faces indices
    """

    newV, indices = removeDoubleVertices(V)
    reindexedFaces = reindexVerticesInFaces(FV, indices, facesOffset)
    newFV = unique(FV)

    return newV, newFV

end

 $\langle \text{removal of double vertices 72} \rangle$ 

 $\langle \text{renaming of faces 73} \rangle \diamond$ 
```

Fragment referenced in 100b.

## 8.5 Creation of a LAR model

Now we can see code used for creation of a LAR model given the sparse array containing full cells of our block (`objectBoundaryChain` as we had seen in Section 7.2). We also need the following parameters:

- **imageDx, imageDy, imageDz**: The grid size
- **xStart, yStart, zStart**: The coordinate offsets for the current block vertices
- **facesOffset**: The offset for faces of this block

First thing to do is define models that will be returned from the function:

```

⟨ models definition 75 ⟩ ≡
  V_model = Array(Array{Int}, 0)
  FV_model = Array(Array{Int}, 0)

  V_left = Array(Array{Int},0)
  FV_left = Array(Array{Int},0)

  V_right = Array(Array{Int},0)
  FV_right = Array(Array{Int},0)

  V_top = Array(Array{Int},0)
  FV_top = Array(Array{Int},0)

  V_bottom = Array(Array{Int},0)
  FV_bottom = Array(Array{Int},0)

  V_front = Array(Array{Int},0)
  FV_front = Array(Array{Int},0)

  V_back = Array(Array{Int},0)
  FV_back = Array(Array{Int},0) ◇

```

Fragment referenced in 79.

We can see from Figure 19 that our grid is divided into seven parts.

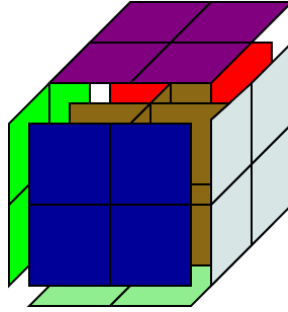


Figure 19: Decomposition of a LAR model into seven parts: the inside model (brown), the left boundary (green), the right boundary (light blue), the top boundary (purple), the bottom boundary (light green), the front boundary (blue), the back boundary (red)

We need this decomposition because we are interested in boundaries of the entire model, while we currently have boundaries only for blocks. So we need to split the inner parts

of a single block model, as we need to freely merge boundaries between adjacent blocks removing the common faces. Function for boundaries merging are shown in subsection 8.6.

After model definition we have to get the cells indices from the block boundary chain and for every non-empty cell we have found, choose the correct model for it. We can observe that every boundary face has a fixed coordinate; for example all faces on the top boundary have the maximum z-coordinate, or faces on right boundary have the maximum y-coordinate (as shown in Figure 20)

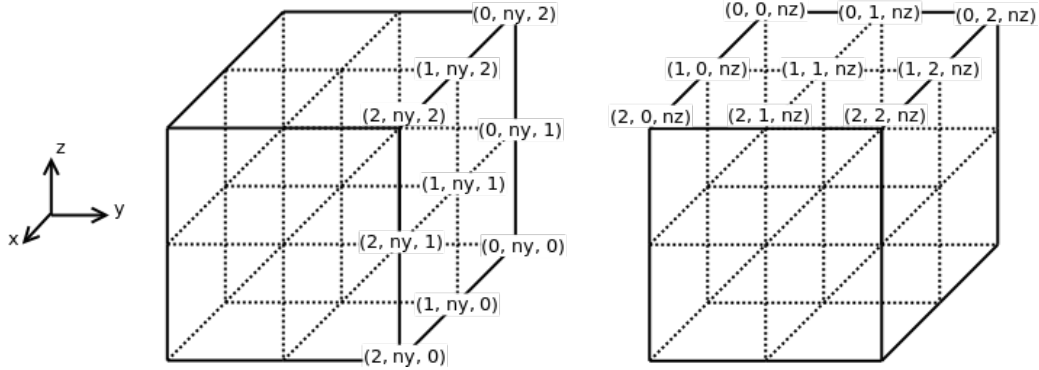


Figure 20: Boundaries coordinates for top and right boundaries of a  $2 \times 2 \times 2$  grid. We can observe that every boundary has a fixed coordinate

So we can define a series of functions for checking the membership of a given face to a boundary exploiting these fixed coordinates:

```

< check membership of a face to a boundary 76 > ≡
function isOnLeft(face, V, nx, ny, nz)
    """
    Check if face is on left boundary
    """

    for(vtx in face)
        if(V[vtx + 1][2] != 0)
            return false
        end
    end
    return true

end

function isOnRight(face, V, nx, ny, nz)
    """

```

```

Check if face is on right boundary
"""

for(vtx in face)
  if(V[vtx + 1][2] != ny)
    return false
  end
end
return true

end

function isOnTop(face, V, nx, ny, nz)
  """
  Check if face is on top boundary
  """

  for(vtx in face)
    if(V[vtx + 1][3] != nz)
      return false
    end
  end
  return true
end

function isOnBottom(face, V, nx, ny, nz)
  """
  Check if face is on bottom boundary
  """

  for(vtx in face)
    if(V[vtx + 1][3] != 0)
      return false
    end
  end
  return true
end

function isOnFront(face, V, nx, ny, nz)
  """
  Check if face is on front boundary
  """

  for(vtx in face)
    if(V[vtx + 1][1] != nx)
      return false
    end
  end
end

```

```

        end
    end
    return true
end

function isOnBack(face, V, nx, ny, nz)
    """
    Check if face is on back boundary
    """

    for(vtx in face)
        if(V[vtx + 1][1] != 0)
            return false
        end
    end
    return true
end ◇

```

Fragment referenced in 79.

After choosing of the right model, we have to insert our face into it. We can do it with the following function, which takes vertices and faces of the base and the model, the face, and the offset of the current face for the model chosen:

```

⟨ add a face to a model 78 ⟩ ≡
function addFaceToModel(V_base, FV_base, V, FV, face, vertex_count)
    """
    Insert a face into a LAR model

    V_base, FV_base: LAR model of the base
    V, FV: LAR model
    face: Face that will be added to the model
    vertex_count: Indices for faces vertices
    """

    new_vertex_count = vertex_count
    for vtx in FV_base[face]
        push!(V, [convert{Int}(V_base[vtx + 1][1] + xStart),
                  convert{Int}(V_base[vtx + 1][2] + yStart),
                  convert{Int}(V_base[vtx + 1][3] + zStart)])
        new_vertex_count += 1
    end
    push!(FV, [vertex_count, vertex_count + 1, vertex_count + 3])
    push!(FV, [vertex_count, vertex_count + 3, vertex_count + 2])
end

```

```

    return new_vertex_count
end ◇

```

Fragment referenced in 79.

As we can see, for every face we put into the model FV array two faces, in fact our final representation is not based on square faces but on triangular faces.

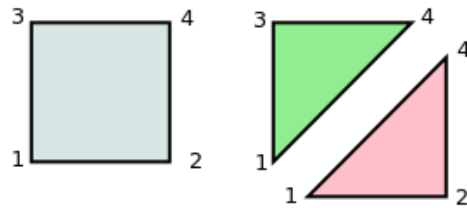


Figure 21: Triangulation of a single face

This is the complete code for creation of a model

```

⟨ LAR model creation 79 ⟩ ≡
  ⟨ check membership of a face to a boundary 76 ⟩

function computeModelAndBoundaries(imageDx, imageDy, imageDz,
                                   xStart, yStart, zStart,
                                   objectBoundaryChain)
    """
    Takes the boundary chain of a part of the entire model
    and returns a LAR model splitting the boundaries

    imageDx, imageDy, imageDz: Boundary dimensions
    xStart, yStart, zStart: Offset of this part of the model
    objectBoundaryChain: Sparse csc matrix containing the cells
    """

    ⟨ add a face to a model 78 ⟩

    ⟨ models definition 75 ⟩

    V, bases = getBases(imageDx, imageDy, imageDz)
    FV = bases[3]

    vertex_count_model = 1
    vertex_count_left = 1

```



```

vertex_count_right = 1
vertex_count_top = 1
vertex_count_bottom = 1
vertex_count_front = 1
vertex_count_back = 1

# Get all cells (independently from orientation)
b2cells = findn(objectBoundaryChain)[1]

debug("b2cells = ", b2cells)

for f in b2cells
    old_vertex_count_model = vertex_count_model
    old_vertex_count_left = vertex_count_left
    old_vertex_count_right = vertex_count_right
    old_vertex_count_top = vertex_count_top
    old_vertex_count_bottom = vertex_count_bottom
    old_vertex_count_front = vertex_count_front
    old_vertex_count_back = vertex_count_back

    # Choosing the right model for vertex
    if(isOnLeft(FV[f], V, imageDx, imageDy, imageDz))
        vertex_count_left = addFaceToModel(V, FV, V_left, FV_left,
                                             f, old_vertex_count_left)
    elseif(isOnRight(FV[f], V, imageDx, imageDy, imageDz))
        vertex_count_right = addFaceToModel(V, FV, V_right, FV_right,
                                             f, old_vertex_count_right)
    elseif(isOnTop(FV[f], V, imageDx, imageDy, imageDz))
        vertex_count_top = addFaceToModel(V, FV, V_top, FV_top,
                                             f, old_vertex_count_top)
    elseif(isOnBottom(FV[f], V, imageDx, imageDy, imageDz))
        vertex_count_bottom = addFaceToModel(V, FV, V_bottom, FV_bottom,
                                             f, old_vertex_count_bottom)
    elseif(isOnFront(FV[f], V, imageDx, imageDy, imageDz))
        vertex_count_front = addFaceToModel(V, FV, V_front, FV_front,
                                             f, old_vertex_count_front)
    elseif(isOnBack(FV[f], V, imageDx, imageDy, imageDz))
        vertex_count_back = addFaceToModel(V, FV, V_back, FV_back,
                                             f, old_vertex_count_back)
    else
        vertex_count_model = addFaceToModel(V, FV, V_model, FV_model,
                                             f, old_vertex_count_model)
    end
end
end

```

```

# Removing double vertices
return [removeDoubleVerticesAndFaces(V_model, FV_model, 0)],
[removeDoubleVerticesAndFaces(V_left, FV_left, 0)],
[removeDoubleVerticesAndFaces(V_right, FV_right, 0)],
[removeDoubleVerticesAndFaces(V_top, FV_top, 0)],
[removeDoubleVerticesAndFaces(V_bottom, FV_bottom, 0)],
[removeDoubleVerticesAndFaces(V_front, FV_front, 0)],
[removeDoubleVerticesAndFaces(V_back, FV_back, 0)]
end ◇

```

Fragment referenced in 100b.

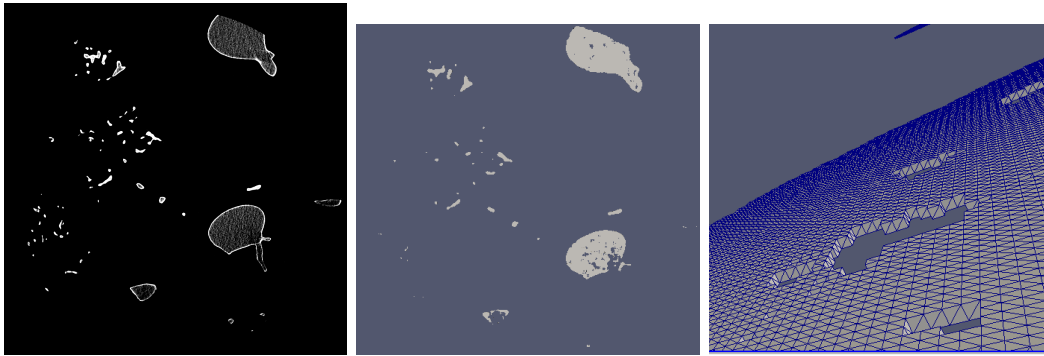


Figure 22: Creation of a sample model. (a) The original image (b) The three-dimensional model (c) The three-dimensional model (detail with triangular faces)

## 8.6 Removing double faces and vertices from boundaries

In previous section, we have seen how to create a LAR model from the chain list. However this model contains all borders between blocks, while we are only interested in borders for the entire image. So, we will see functions for boundaries merging with removal of double faces and vertices from both sides.

The algorithm for the removal is very simply. First of all we need to remove double vertices from models in the usual way using `removeDoubleVertices` function and re-indexing all faces. Next we count all elements in re-indexed faces array removing elements with more than one occurrence and create an array of faces with an explicit representation of vertices (*FV\_vertices*). Now we can safely remove double vertices on the other side of the boundary without losing the correct indexing in the faces. Finally we can create the final faces array with only remaining vertices comparing coordinates in *FV\_vertices* with the

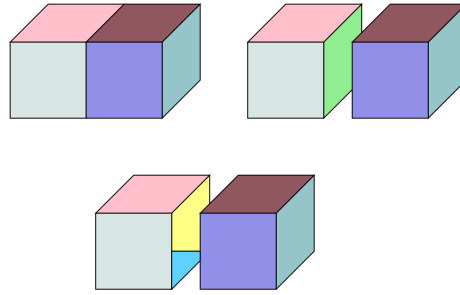


Figure 23: Removal of double faces from boundaries. (a) Two adjacent blocks (b) The same blocks exploded on x axis (c) Result of the removal on the exploded blocks

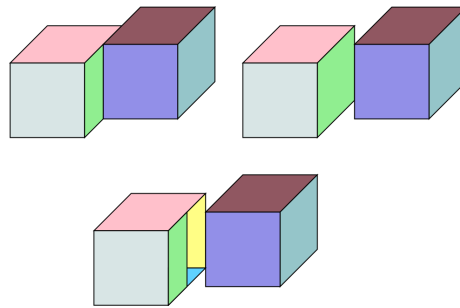


Figure 24: Same as Figure 23 with another model

ones in the last vertices array.

Code for this function is the following:

```
< Removal of double vertices and faces from boundaries 82 > ≡
function removeVerticesAndFacesFromBoundaries(V, FV)
    """
    Remove vertices and faces duplicates on
    boundaries models

    V,FV: lar model of two merged boundaries
    """

    newV, indices = removeDoubleVertices(V)
    uniqueIndices = unique(indices)

    # Removing double faces on both boundaries
    FV_reindexed = reindexVerticesInFaces(FV, indices, 0)
    FV_unique = unique(FV_reindexed)

    FV_cleaned = Array(Array{Int}, 0)
```

```

for f in FV_unique
  if(count((x) -> x == f, FV_reindexed) == 1)
    push!(FV_cleaned, f)
  end
end

# Creating an array of faces with explicit vertices
FV_vertices = Array{Array{Array{Float64}}, 0}

for i in 1 : length(FV_cleaned)
  push!(FV_vertices, Array{Array{Float64}, 0})
  for vtx in FV_cleaned[i]
    push!(FV_vertices[i], newV[vtx])
  end
end

V_final = Array{Array{Float64}, 0}
FV_final = Array{Array{Int}, 0}

# Saving only used vertices
for face in FV_vertices
  for vtx in face
    push!(V_final, vtx)
  end
end

V_final = unique(V_final)

# Renumbering FV
for face in FV_vertices
  tmp = Array{Int, 0}
  for vtx in face
    ind = findfirst(V_final, vtx)
    push!(tmp, ind)
  end
  push!(FV_final, tmp)
end

return V_final, FV_final
end ◇

```

Fragment referenced in 100b.

## 9 Smoother

This module contains functions used for smoothing LAR models

### 9.1 Get adjacent vertices

As we will see in next subsection, for executing a smoothing algorithm we need to know adjacent vertices to a given one. So we need a *VV relationship*, where for every vertex index  $i$ , we have a list of adjacent vertices.

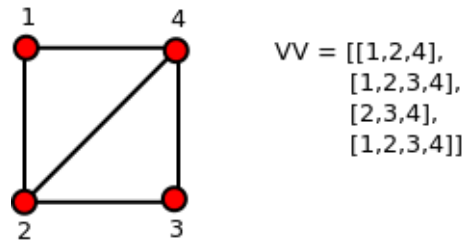


Figure 25: *VV relationship* for a simple model

Algorithm is very simple and exploit the following property: *for triangular faces all vertices are linked together*. So, for every vertex  $v$  in a face  $f$ , we just have to add to  $VV[v]$  all the vertices of  $f$ .

```

⟨get adjacent vertices 84⟩ ≡
function adjVerts(V, FV)
    """
    Compute the adjacency graph of vertices
    of a LAR model

    V, FV: LAR model

    Returns the list of indices of vertices adjacent
    to a vertex
    """
    VV = Array{Array{Int},length(V)}
    for i in 1:length(FV)
        for v in FV[i]
            if(!isdefined(VV,v))
                # Adding a new array for this vertex
                VV[v] = Array{Int}[]
            end
            push!(VV[v], FV[i][1], FV[i][2], FV[i][3])
            VV[v] = unique(VV[v])
        end
    end

```

```

    end
    return VV
end ◊

```

Fragment referenced in 102.

## 9.2 Laplacian smoothing

There are many different algorithms for mesh smoothing. The simpler and the one we used in this library is **laplacian smoothing**. For each vertex in a mesh, a new position is chosen according to local information (such as the coordinates of neighbors) and the vertex is moved there. If that mesh is topologically a rectangular grid (so each internal vertex is connected to four neighbors) then this operation produces the *Laplacian* of the mesh.

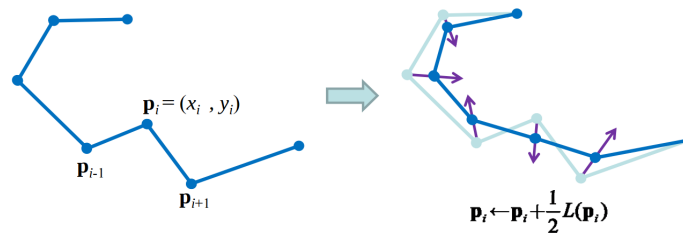


Figure 26: Laplacian smoothing (picture taken from the *Geometry Processing Algorithms* course at Stanford University)

As we can see from Figure 26, with substitution of every vertex position with the mean of the neighbors positions, we can obtain a curve with smoothed edges. This procedure can be repeated many times, so we can obtain a smoother model. For example, in Figure 28, we can see this algorithm applied on a sample mesh with three iterations.

This is the code for the smoothing function; it takes a single LAR model and returns the smoothed model.

```

⟨laplacian smoothing 85⟩ ≡
function smoothModel(V, FV)
    """
    Execute a Laplacian smoothing on a LAR model returning
    the new smoothed model

    V, FV: LAR model
    """

    VV = adjVerts(V, FV)

```

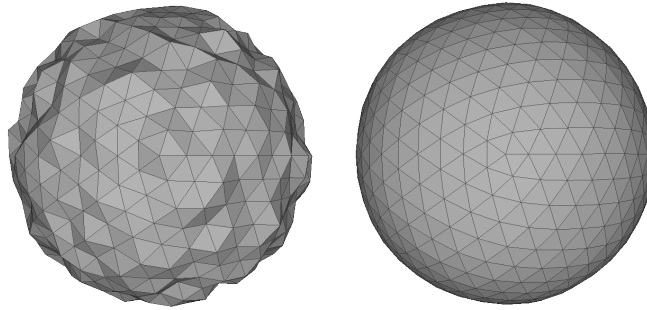


Figure 27: Laplacian smoothing for a sample mesh. (a) Original mesh (b) Mesh after three iterations of the smoothing algorithm (picture taken from a *Digital Geometry Processing* course at IMPA)

```

newV = Array(Array{Float64},0)
V_temp = Array(Array{Float64},0)

for i in 1:length(VV)
    adjs = VV[i]
    # Get all coordinates for adjacent vertices
    coords = Array(Array{Float64}, 0)
    for v in adjs
        push!(coords, V[v])
    end

    # Computing sum of all vectors
    sum = [0.0, 0.0, 0.0]
    for v in coords
        sum += v
    end

    # Computing convex combination of vertices
    push!(newV, sum/length(adj))
end

return newV, FV
end ◇

```

Fragment referenced in 102.

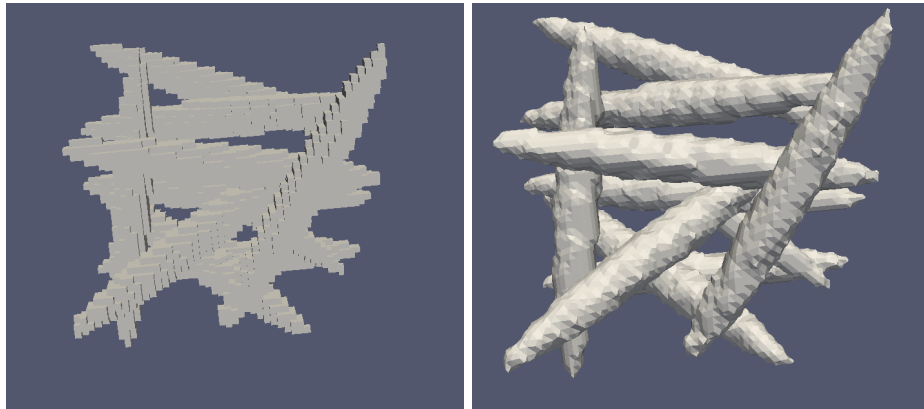


Figure 28: Smoothing of a sample model made with ImagesToLARModel

## 10 Model2Obj

This module contains functions used for reading/writing LAR models into obj files on disk

### 10.1 Writing models to file

Up to now we have seen how to manipulate LAR models obtaining a three-dimensional representation for our stack of images. However we have not seen how to visualize them using external software yet. We have chosen the *wavefront obj file format* for external visualization, which is very simple and common. The syntax used is the following:

- All vertices are described with their coordinates and written on a single row according to the following syntax: `v xCoord yCoord zCoord`
- All faces are described with their vertex index (calculated from their row) according to the following syntax: `f vertex1 vertex2 ...vertexn`

In Figure 29 there is an example of an obj file

We can see that this kind of representation is very similar to the LAR representation schema, so we just have to read every element of V and FV arrays and write them on disk. Because of we will use these informations a lot, it is more convenient to save the vertices and the faces on different files, so they can be loaded with less efforts. This is code used by the library:

```
<write obj files 87> ≡
function writeToObj(V, FV, outputFilename)
    """
    Take a LAR model and write it on obj file
```



```

v 0 0 0
v 1 0 0
v 0 1 0
v 1 1 0
v 0 0 1
v 1 0 1
v 1 1 1
f 1 2 4 3
f 5 6 8 7
f 1 2 6 5

```




Figure 29: Obj sample file

```

V: array containing vertices coordinates
FV: array containing faces
outputFilename: prefix for the output files
"""

if (length(V) != 0)
    outputVtx = string(outputFilename, "_vtx.stl")
    outputFaces = string(outputFilename, "_faces.stl")

    fileVertex = open(outputVtx, "w")
    fileFaces = open(outputFaces, "w")

    for v in V
        write(fileVertex, "v ")
        write(fileVertex, string(v[1], " "))
        write(fileVertex, string(v[2], " "))
        write(fileVertex, string(v[3], "\n"))
    end

    for f in FV

        write(fileFaces, "f ")
        write(fileFaces, string(f[1], " "))
        write(fileFaces, string(f[2], " "))
        write(fileFaces, string(f[3], "\n"))
    end

    close(fileVertex)
    close(fileFaces)

end

```

end ◇

Fragment referenced in 101a.

## 10.2 Merging block models

Now we have seen how to write on disk a LAR model using the *wavefront obj file format*, however, as we have already seen, we have a lot of models from every block; so we need a function for the creation of the final merged model. The code which executes this task is very simple; this is the function:

⟨ *serial file merge* 89 ⟩ ≡

```
function mergeObj(modelDirectory)
    """
    Merge stl files in a single obj file

    modelDirectory: directory containing models
    """

    files = readdir(modelDirectory)
    vertices_files = files[find(s -> contains(s, string("_vtx.stl")), files)]
    faces_files = files[find(s -> contains(s, string("_faces.stl")), files)]
    obj_file = open(string(modelDirectory, "/", "model.obj"), "w") # Output file

    vertices_counts = Array{Int64, length(vertices_files)}
    number_of_vertices = 0
    for i in 1:length(vertices_files)
        vtx_file = vertices_files[i]
        f = open(string(modelDirectory, "/", vtx_file))

        # Writing vertices on the obj file
        for ln in eachline(f)
            splitted = split(ln)
            write(obj_file, "v ")
            write(obj_file, string(convert{Int, round(parse(splitted[2]) * 10)), " "))
            write(obj_file, string(convert{Int, round(parse(splitted[3]) * 10)), " "))
            write(obj_file, string(convert{Int, round(parse(splitted[4]) * 10)), "\n"))
            number_of_vertices += 1
        end
        # Saving number of vertices
        vertices_counts[i] = number_of_vertices
        close(f)
    end
end
```

```

for i in 1 : length(faces_files)
  faces_file = faces_files[i]
  f = open(string(modelDirectory, "/", faces_file))
  for ln in eachline(f)
    splitted = split(ln)
    write(obj_file, "f ")
    if i > 1
      write(obj_file, string(parse(splitted[2]) + vertices_counts[i - 1], " "))
      write(obj_file, string(parse(splitted[3]) + vertices_counts[i - 1], " "))
      write(obj_file, string(parse(splitted[4]) + vertices_counts[i - 1]))
    else
      write(obj_file, string(splitted[2], " "))
      write(obj_file, string(splitted[3], " "))
      write(obj_file, splitted[4])
    end
    write(obj_file, "\n")
  end
  close(f)
end
close(obj_file)

# Removing all tmp files
for vtx_file in vertices_files
  rm(string(modelDirectory, "/", vtx_file))
end

for fcs_file in faces_files
  rm(string(modelDirectory, "/", fcs_file))
end

end ◇

```

Fragment referenced in 101a.

As we can see, we take all files contained into the model folder (distinguishing between files containing vertices from those containing faces) and write all their lines into the final model file. However this is simply for vertices files, while it is a bit complicated for faces, because it is necessary to change their indexes according to the current vertices positions into the file. So we need to memorize the offset for every file counting the number of vertices added at every time we open a new file containing vertices. Moreover we can see that we convert vertices coordinates into integer values; this is useful because some softwares do not read float vertices coordinates, so we first make the model ten times bigger (so we still have the first decimal number) and then round it.

The creation of this final model is quite slow, so we can try to speedup the entire software parallelizing it. In the next part we will see how this can be done.

### 10.2.1 Parallel merging of obj files

Now we will see how to parallelize the final file merging. However this is useful only for certain conditions; in fact in traditional filesystems the disk can be accessed from only one process at the same time, so parallelizing this task is totally useless. However for parallel filesystems it is a different matter because we can have parallel writes on storage.

The first simple algorithm we can think for parallel file merging, takes two files for every process and merge them creating a unique file. Then, this process can be repeated until we have only one final file. In Figure 30 there is a simple schema for this algorithm.

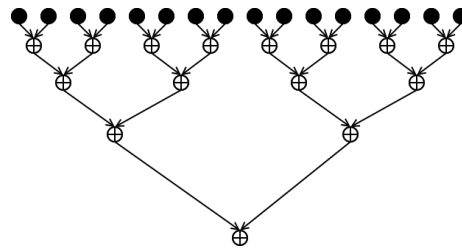


Figure 30: The first parallel algorithm for file merge. Black circles represent the original files, while circles with the cross, represent merged files

How we can see in that figure, if we have a process for every merge operation and sixteen files, we will have eight processes for the first merge, four processes for the second merge steps, two processes for the third step and one process for the final merge. Speaking in a general way, told  $n$  the number of files we want to merge, we will use  $\lfloor n/2 \rfloor$  processes for every step. Probably if we would not have a balanced tree we could use the number of processes in a more efficient way for all our steps. In Figure 31 there is a non-balanced tree where the number of processes for every merge step is maximized.

Now we can examine the code used for obtaining this result. First of all we need a function for assigning files to the right process creating the tree in Figure 31:

```
< assign tasks 91 > ≡
function assignTasks(startInd, endInd, taskArray)
    """
    This function choose the first files to merge
    creating a tree where number of processes is maximized

    startInd: starting index for array subdivision
    endInd: end index for array subdivision
    taskArray: array containing indices of files to merge for first
```

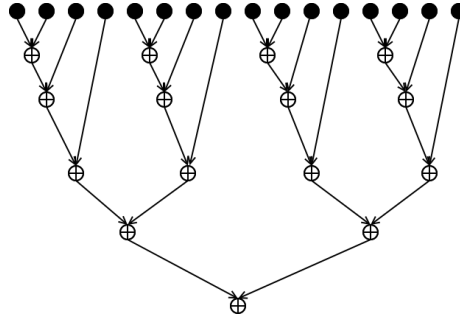


Figure 31: A better algorithm for file merge

```

"""
if (endInd - startInd == 2)
    push!(taskArray, startInd)
elseif (endInd - startInd < 2)
    if (endInd % 4 != 0 && startInd != endInd)
        # Stop recursion on this branch
        push!(taskArray, startInd)
    end
    # Stop recursion doing nothing
else
    assignTasks(startInd, startInd + trunc((endInd - startInd) / 2), taskArray)
    assignTasks(startInd + trunc((endInd - startInd) / 2) + 1, endInd, taskArray)
end
end ◇

```

Fragment referenced in 101a.

Now we need some functions for merging files; in particular we have to merge vertices files (contemporary counting the offsets for the faces) and faces files. This is the code for the first function:

```

⟨merge vertices file 92⟩ ≡
function mergeVerticesFiles(file1, file2, startOffset)
    """
    Support function for merging two vertices files.
    Returns the number of vertices of the merged file

    file1: path of the first file
    file2: path of the second file
    startOffset: starting face offset for second file

```

```

"""

f1 = open(file1, "a")

f2 = open(file2)
debug("Merging ", file2)
number_of_vertices = startOffset
for ln in eachline(f2)
    write(f1, ln)
    number_of_vertices += 1
end
close(f2)

close(f1)

return number_of_vertices
end ◇

```

Fragment referenced in 101a.

As we can see the algorithm is very simple; what we do is appending the content of the second file into the first one and returns the number of appended vertices, which will be used as offsets for faces. This is the code for concatenation of faces files:

```

⟨ merge faces file 93 ⟩ ≡
function mergeFacesFiles(file1, file2, facesOffset)
    """
    Support function for merging two faces files

    file1: path of the first file
    file2: path of the second file
    facesOffset: offset for faces
    """

    f1 = open(file1, "a")

    f2 = open(file2)
    for ln in eachline(f2)
        splitted = split(ln)
        write(f1, "f ")
        write(f1, string(parse(splitted[2]) + facesOffset, " "))
        write(f1, string(parse(splitted[3]) + facesOffset, " "))
        write(f1, string(parse(splitted[4]) + facesOffset, "\n"))
    end
end

```

```

close(f2)

close(f1)
end ◇

```

Fragment referenced in 101a.

These concatenation functions, are called by the `mergeObjProcesses`, which is executed by a single Julia process:

```

⟨parallel merge obj process function 94⟩ ≡
function mergeObjProcesses(fileArray, facesOffset = Nothing)
    """
    Merge files on a single process

    fileArray: Array containing files that will be merged
    facesOffset (optional): if merging faces files, this array contains
        offsets for every file

    if it is merging vertices files it returns the offset
    for the corresponding faces
    """

    if(contains(fileArray[1], string("_vtx.stl")))
        # Merging vertices files
        offsets = Array{Int, 0}
        push!(offsets, countlines(fileArray[1]))
        vertices_count = mergeVerticesFiles(fileArray[1], fileArray[2], countlines(fileArray[1]))
        rm(fileArray[2]) # Removing merged file
        push!(offsets, vertices_count)
        for i in 3: length(fileArray)
            vertices_count = mergeVerticesFiles(fileArray[1], fileArray[i], vertices_count)
            rm(fileArray[i]) # Removing merged file
            push!(offsets, vertices_count)
        end
        return offsets
    else
        # Merging faces files
        mergeFacesFiles(fileArray[1], fileArray[2], facesOffset[1])
        rm(fileArray[2]) # Removing merged file
        for i in 3 : length(fileArray)
            mergeFacesFiles(fileArray[1], fileArray[i], facesOffset[i - 1])
            rm(fileArray[i]) # Removing merged file
        end
    end
end

```

```

    end
end ◇

```

Fragment referenced in 101a.

The function can be called for both faces and vertices files; for the last case, however, we need to specify the *facesOffset* parameter.

Now we can put together the above functions with the following code:

```

⟨ merge obj helper function 95 ⟩ ≡
function mergeObjHelper(vertices_files, faces_files)
    """
    Support function for mergeObj. It takes vertices and faces files
    and executes a single merging step

    vertices_files: Array containing vertices files
    faces_files: Array containing faces files
    """
    numberOfImages = length(vertices_files)
    taskArray = Array{Int, 0}()
    assignTasks(1, numberOfImages, taskArray)

    # Now taskArray contains first files to merge
    numberOfVertices = Array{Int, 0}()
    tasks = Array{RemoteRef, 0}()
    for i in 1 : length(taskArray) - 1
        task = @spawn mergeObjProcesses(vertices_files[taskArray[i] : (taskArray[i + 1] - 1)])
        push!(tasks, task)
    end

    # Merging last vertices files
    task = @spawn mergeObjProcesses(vertices_files[taskArray[length(taskArray)] : end])
    push!(tasks, task)

    for task in tasks
        append!(numberOfVertices, fetch(task))
    end

    debug("NumberOfVertices = ", numberOfVertices)

    # Merging faces files
    tasks = Array{RemoteRef, 0}()
    for i in 1 : length(taskArray) - 1

```



```

        task = @spawn mergeObjProcesses(faces_files[taskArray[i] : (taskArray[i + 1] - 1)],
                                         numberOfVertices[taskArray[i] : (taskArray[i + 1] - 1)])
        push!(tasks, task)
    end

    #Merging last faces files
    task = @spawn mergeObjProcesses(faces_files[taskArray[length(taskArray)] : end],
                                     numberOfVertices[taskArray[length(taskArray)] : end])

    push!(tasks, task)

    for task in tasks
        wait(task)
    end

    end ◇

```

Fragment referenced in 101a.

As we can see, this is the code for distribution of our work among all processes. We have chosen to spawn a new process following the tree in Figure 31, passing to the `mergeObjProcesses` function the files given to the task with the function `assignTasks`.

Finally we just have to define the main function for parallel merging

```

⟨ merge obj parallel 96 ⟩ ≡
function mergeObjParallel(modelDirectory)
    """
    Merge stl files in a single obj file using a parallel
    approach. Files will be recursively merged two by two
    generating a tree where number of processes for every
    step is maximized
    Actually use of this function is discouraged. In fact
    speedup is influenced by disk speed. It could work on
    particular systems with parallel accesses on disks

    modelDirectory: directory containing models
    """

    files = readdir(modelDirectory)

    # Appending directory path to every file
    files = map((s) -> string(modelDirectory, "/", s), files)

    # While we have more than one vtx file and one faces file

```

```

while(length(files) != 2)
  vertices_files = files[find(s -> contains(s,string("_vtx.stl")), files)]
  faces_files = files[find(s -> contains(s,string("_faces.stl")), files)]

  # Merging files
  mergeObjHelper(vertices_files, faces_files)

  files = readdir(modelDirectory)
  files = map((s) -> string(modelDirectory, "/", s), files)
end

mergeVerticesFiles(files[2], files[1], 0)
mv(files[2], string(modelDirectory, "/model.obj"))
rm(files[1])

end ◇

```

Fragment referenced in 101a.

### 10.3 Load models from files

Another important functionality for our library, consists in model loading from our faces and vertices files. This is useful when passing from a pipeline step to another one. For simplicity, we offer a unique function that loads an array of vertices files (with the corresponding array of faces files), merge the values into a unique model and returns it.

⟨ *Load models from file 97* ⟩ ≡

```

function getModelsFromFiles(arrayV, arrayFV)
  """
  Get a LAR models for two arrays of vertices
  and faces files

  arrayV: Array containing all vertices files
  arrayFV: Array containing all faces files
  """

  V = Array(Array{Float64}, 0)
  FV = Array(Array{Int}, 0)
  offset = 0

  for i in 1:length(arrayV)
    if isfile(arrayFV[i])
      f_FV = open(arrayFV[i])

```

```

    for ln in eachline(f_FV)
        splitted = split(ln)
        push!(FV, [parse(splitted[2]) + offset, parse(splitted[3]) + offset,
            parse(splitted[4]) + offset])
    end
    close(f_FV)

    f_V = open(arrayV[i])
    for ln in eachline(f_V)
        splitted = split(ln)
        push!(V, [parse(splitted[2]), parse(splitted[3]),
            parse(splitted[4])])
        offset += 1
    end
    close(f_V)
end
end
return V, FV
end ◇

```

Fragment referenced in 101a.

## 11 Exporting the library

### ImagesToLARModel

```

"src/ImagesToLARModel.jl" 98≡
module ImagesToLARModel

    < update load path 6 >

    < modules import ImagesToLARModel 7a >
    < load JSON configuration 10 >
    < load JSON configuration for data preparation 7b >
    < data preparation from JSON file 11 >
    < manual data preparation 12 >
    < Start conversion from JSON file 13a >
    < Start manual conversion 13b >
end
◇

```

## ImagesConversion

```
"src/ImagesConversion.jl" 99a≡  
    module ImagesConversion  
  
        ⟨ modules import ImagesConversion 34a ⟩  
  
        ⟨ main function for ImagesConversion 34b ⟩  
  
        ⟨ parallel block iteration 36 ⟩  
  
        ⟨ pixelsToVoxels function 43 ⟩  
  
        ⟨ start conversion of images 38b ⟩  
  
        ⟨ image conversion process 42 ⟩  
  
        ⟨ boundary merge process function 44b ⟩  
  
        ⟨ merge boundaries utility function 45 ⟩  
  
        ⟨ Block merge process function 47b ⟩  
  
        ⟨ Smooth block process function 49 ⟩  
  
        ⟨ execute smoothing function 50 ⟩  
  
    end  
    ◇
```

## GenerateBorderMatrix

```
"src/GenerateBorderMatrix.jl" 99b≡  
    module GenerateBorderMatrix  
  
        ⟨ Matrix object for JSON file 55a ⟩  
  
        ⟨ modules import GenerateBorderMatrix 53b ⟩  
  
        ⟨ compute border matrix 55b ⟩  
  
        ⟨ write Border matrix 54 ⟩
```

```

    ⟨ get Border matrix 53c ⟩

    ⟨ transform border matrix in csc format 56 ⟩
end
◇

```

## Lar2Julia

```

"src/Lar2Julia.jl" 100a≡
    module Lar2Julia

        ⟨ modules import Lar2Julia 57a ⟩

        ⟨ get boundary chain 57b ⟩

        ⟨ get oriented cells from a chain 58 ⟩

        ⟨ transform relationships to csc 59 ⟩

        ⟨ boundary computation 65 ⟩
    end
    ◇

```

## LARUtils

```

"src/LARUtils.jl" 100b≡
    module LARUtils

        ⟨ modules import LARUtils 66a ⟩

        ⟨ conversion from matrix to array 66b ⟩

        ⟨ conversion from array to matrix 67a ⟩

        ⟨ get LAR bases 70c ⟩

        ⟨ removal of double vertices and faces 74 ⟩

        ⟨ Removal of double vertices and faces from boundaries 82 ⟩
    end

```

```

    < LAR model creation 79 >
end
◇

```

## Model2Obj

```

"src/Model2Obj.jl" 101a≡
    module Model2Obj

        using Logging

        export writeToObj, mergeObj, mergeObjParallel

        < write obj files 87 >

        < serial file merge 89 >

        < assign tasks 91 >

        < merge vertices file 92 >

        < merge faces file 93 >

        < parallel merge obj process function 94 >

        < merge obj helper function 95 >

        < merge obj parallel 96 >

        < Load models from file 97 >
    end
    ◇

```

## PngStack2Array3dJulia

```

"src/PngStack2Array3dJulia.jl" 101b≡

```

```

module PngStack2Array3dJulia

  ⟨ modules import PngStack2Array3dJulia 14⟩
  ⟨ image resizing 19⟩

  ⟨ image clustering 22⟩

  ⟨ 3d model filtering 29⟩

  ⟨ Convert to png 18⟩
  ⟨ Get image data 30⟩
  ⟨ Pixel transformation 31⟩
end
◇

```

## Smoother

```

"src/Smoother.jl" 102≡
  module Smoother
  export smoothModel

  ⟨ get adjacent vertices 84⟩

  ⟨ laplacian smoothing 85⟩
end
◇

```

## 11.1 Installing the library

## 12 Conclusions

### 12.1 Results

### 12.2 Further improvements

## References

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

- [PDFJ15] Alberto Paoluzzi, Antonio DiCarlo, Francesco Furiani, and Miroslav Jirik, *CAD models from medical images using LAR*, Computer-Aided Design and Applications **13** (2015), To appear.
- [W3C] W3C, *Portable Network Graphics (PNG) Specification (Second Edition)*, Tech. report.

## A Utility functions

## B Tests

## Generation of the border matrix

```
"test/generateBorderMatrix.jl" 103≡
push!(LOAD_PATH, "../..")
import GenerateBorderMatrix
import JSON
using Base.Test

function testComputeOriented3Border()
    """
    Test function for computeOriented3Border
    """
    boundaryMatrix = GenerateBorderMatrix.computeOriented3Border(2,2,2)

    rowcount = boundaryMatrix[:shape][1]
    @test rowcount == 36
    colcount = boundaryMatrix[:shape][2]
    @test colcount == 8
    row = boundaryMatrix[:indptr]
    @test row == [0,1,2,3,4,5,7,8,9,11,12,13,15,17,18,19,20,22,23,24,26,27,29,30,32,34,35,37,39,
    col = boundaryMatrix[:indices]
    @test col == [0,0,0,1,1,0,1,1,2,0,2,2,3,1,3,2,3,3,2,3,0,4,4,4,1,5,5,4,5,5,2,6,4,6,6,3,7,5,7,
    data = boundaryMatrix[:data]
    @test data == [-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,-1,1,-1,1,1,-1,1,1

end

function testWriteBorder()
    """
    Test for writeBorder
    """
    boundaryMatrix = GenerateBorderMatrix.computeOriented3Border(2,2,2)
    filename = "borderFile"
```





```

end

function testCalculateClusterCentroids()
    """
    Test function for calculateClusterCentroids
    """
    path = "images/"
    image = 0
    centroids = PngStack2Array3dJulia.calculateClusterCentroids(path, image, 2)

    expected = [0, 253]
    centroids = vec(reshape(centroids, 1, 2))

    @test sort(centroids) == expected
end

function testPngstack2array3d()
    """
    Test function for pngstack2array3d
    """
    path = "images/"
    minSlice = 0
    maxSlice = 4
    centroids = PngStack2Array3dJulia.calculateClusterCentroids(path, 0, 2)
    image3d = PngStack2Array3dJulia.pngstack2array3d(path, minSlice, maxSlice, centroids)

    @test size(image3d)[1] == 5
    @test size(image3d[1])[1] == 50
    @test size(image3d[1])[2] == 200
end

function executeAllTests()
    @time testCalculateClusterCentroids()
    @time testPngstack2array3d()
    @time testGetImageData()
    println("Tests completed.")
end

executeAllTests()

◇

```

## Test for LAR utilities

```
"test/LARUtils.jl" 105≡
    push!(LOAD_PATH, "../..")
    import LARUtils
    using Base.Test

    function testInd()
        """
        Test function for ind
        """

        nx = 2
        ny = 2

        @test LARUtils.ind(0, 0, 0, nx, ny) == 0
        @test LARUtils.ind(1, 1, 1, nx, ny) == 13
        @test LARUtils.ind(2, 5, 4, nx, ny) == 53
        @test LARUtils.ind(1, 1, 1, nx, ny) == 13
        @test LARUtils.ind(2, 7, 1, nx, ny) == 32
        @test LARUtils.ind(1, 0, 3, nx, ny) == 28
    end

    function executeAllTests()
        @time testInd()
        println("Tests completed.")
    end

    executeAllTests()

    ◇
```