

Algorithm for the modelling of the lung/bronchial tree coupling customised (V3)

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Abstract - An accurate description of the morphometry of the lung and airways is essential to enable numerical simulations, related to the respiratory system, that are in line with the morphometric observations. The structure of the lung is governed both by its respiratory functions and by the inherent hierarchy of the bronchial tree, making it the complex organ that it is. The airways, defined by an asymmetric dichotomous tree, allow the transport of air to the blood exchange zones and thus the supply of oxygen. In this paper, we present a scalable algorithm for generating individual-specific 3D models of the bronchial tree, based on morphological structures of the lung lobes and the first three generations of airways. These structures are the result of further work to extract them from a person's CT-Scan, using a Deep Learning method of multi-class segmentation. The algorithm we present is based on mesh preprocessing, calculating the centre of the largest ball inscribed in a volume by an octree method, and applying physiological constraints. The statistical study of our model, correlated with the different morphometric data, allows us to validate the accuracy and fidelity aspects. The result is a 3D mesh of the lung surface and the bronchial tree that is suitable for numerical simulations.

Index terms - respiratory system, lungs, bronchial tree, 3D modeling, space-filling, mesh processing, octree

1 Introduction

Numerical simulations are commonly used to describe and analyse phenomena related to the respiratory system, and in particular related to intra-bronchial activity. For instance, they have been used to study gas exchange with the blood, aerosol deposition [14, 15] or gas transport in relation to a disease [17, 11, 2]. Consequently, it is essential to have a detailed and realistic model of the main morphological structures of the lungs, including the lobes and the bronchial tree. Several studies exist on specific pathologies, yet most of the works

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assume generic respiratory system models that do not necessarily reflect the morphology of the actual patients.

Obtaining an accurate model of the respiratory system is not an easy task, as the latter is a complex set of organs whose main function is to supply oxygen to the vascular system. This system includes the airways, which are used to transport oxygen from the environment into the bloodstream, the lungs, which contain part of the airways, and the diaphragm, which carries out the physiological processes of inspiration and expiration. The airways can be divided into upper and lower; both allow for air from the outside to pass into the alveoli, where various gas exchanges with the blood capillaries take place. The upper respiratory tract consists of the nose, nasal cavity, mouth, pharynx and larynx. Their role is to filter, warm and humidify the inspired air. They are also responsible for the sensory functions of taste and smell, and are also producing sound. The lower airways, which we seek to model, are defined as a complex asymmetric dichotomous tree. This tree consists of the trachea, bronchi, bronchioles, acini and alveoli. The passage from the trachea to the bronchioles constitutes the conducting airways, which allow the delivery of air to and from the respiratory airways, composed of the acini and alveoli.

The first morphometric measurements were obtained using casts as reported in the work of Weibel *et al.* [24, 25] or Horsfield *et al.* [7, 6, 4, 5, 3]. Based on his own observations, Weibel *et al.* described a simplified structure of the airway anatomy, called Weibel's A-model [25], whose symmetrical structure has been the most widely used. The use of symmetric models improves the computational time required to solve the ventilation equations. Since each path is similar, the governing equations are also identical, therefore it is sufficient to solve them once. However, this simplification provides a global view which is not close enough to reality and discards the effects of asymmetry.

Like Weibel *et al.*, Horsfield and Cumming have also defined a model, based on their observations, which is, this time, asymmetrical. This model also differs from the first one with a reversed numbering of the branches. Indeed, Weibel *et al.* define an ordered numbering where the trachea is of order one and the underlying branches have an increasingly higher order. Whereas in Horsfield's numbering, order one is associated with the terminal branch of the tree and the order of the parent branch is incremented by one relative to that of the daughter branch with the highest order. However, the limitation of this model is that it does not take into account the spatial position of the branches.

Later on, following the increase of available computing power, three-dimensional asymmetric branching models were developed, such as Kitaoka's model [9]. This model is based on Murray's law [13] which relates the through-flow rate to the diameter of a segment of a living organ. It is a system of branching ducts that is based on two principles, the first one is that the amount of air flow through a branch is proportional to the volume of the region served, and the second is that the terminal branches of the tree are homogeneously arranged within the organ. The algorithm is defined by a series of 9 basic rules for the generation of the tree structure, on top of that 4 additional rules have been defined to correct the length, diameter and branching angle. This allows for a more isotropic division of the space, while optimising the flow through the bronchial tree. This model also has the advantage of being fully deterministic, but the examples presented were generated in an idealised chest cavity, and therefore suffer from a lack of realism. It can be seen that the morphometric data do not correspond with the observations of Weibel *et al.* or Horsfield *et al.*.

Shortly after the model of Kitaoka *et al.*, one more algorithm was developed with a different approach, which turns out to be the most successful model to date (Tawhai *et al.* [20, 8]).

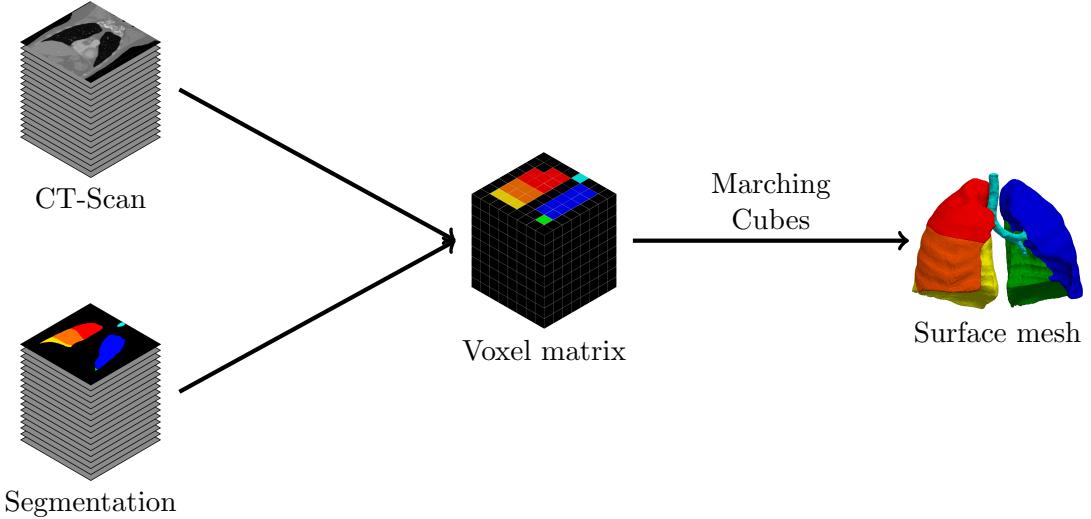


Figure 1: Extraction of the surface meshes from data

This model is based on the work of Wang *et al.* [23], which describes a method of subdividing a two-dimensional space defined by a point cloud. The papers from Tawhai *et al.* describe the modifications made to the Wang *et al.* model to move from the dimension two to the higher dimension and to adapt some parameters to better fit the morphological data. One of the main changes is the use of a point grid to define the point cloud instead of a Monte Carlo method. As with the Kitaoka *et al.* algorithm, the Tawhai model is defined by a list of rules for the growth of the bronchial tree in the volume, and corrections on the branch length or angle to make sure that the generated tree is close enough to the morphometric data. This algorithm was a source of inspiration for more recent models [1, 12].

In this paper we build upon the algorithms of Tawhai *et al.* and Kitaoka *et al.*. Indeed, these models are quite old and computer tools have evolved enormously over the last two decades, which makes it possible to define new methods of computation and geometric representation. We then worked on an updated version of this model, in order to free ourselves from the constraints linked to the point cloud, and to focus on the use of morphological structures. Moreover, the parameters of a branch were modified to correspond more closely to the constraints set out in the article of Kitaoka *et al.* and more in accordance with the function of these airways, i.e. gas transport.

2 Data and extractions of the morphological structures

As we said, the bronchial tree growth algorithm is the main focus of this paper but it is important, for the algorithm to be effective, to have a good definition of the morphological structures of the lung lobes and the early generations of the bronchial tree. In this section, we will discuss the data and methods used to obtain this morphological structures.

Patient data - As the model we are developing is patient specific, we need to have a dataset on which we can extract the morphological structures in order to test the algorithm.

For this we used data from a large public medical imaging library, the Lung Image Database Consortium, known as LIDC-IDRI. This library includes over a thousand lung patient data

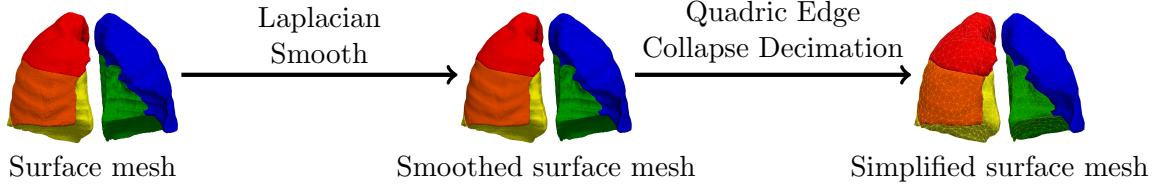


Figure 2: Simplification of the lobes surface meshes

sets and has been used repeatedly for deep learning and artificial intelligence challenges, such as LUNA16 [16]. In this competition, CT-Scan from 50 patients were provided, and annotations were made public thanks to the work of Tang *et al.* [19]. These annotations are in the form of a matrix where each element of the matrix is defined by a label corresponding to a morphological structure, for example, label 1 refers to the left upper lobe.

Extraction of the meshes - The extraction of surface meshes is a fairly simple task, using the marching cubes algorithm [10]. Based on the CT-Scan metadata, it is then possible to know the size of the voxels contained in the segmentation matrix, we can then apply the method of marching cubes, very often used in the medical field, to pass from a volumetric set, i.e. a group of voxel with the same value, to an isosurface or a surface mesh. Once the surface mesh is obtained, we distinguish two cases : the surface meshes of the pulmonary lobes and the surface mesh of the bronchial tree (Cf. Fig. 1).

Simplification of the lobar meshes - For the first morphologies, the next step consists in smoothing the meshes and then simplifying them, which corresponds to reducing the number of faces and therefore the number of nodes and edges. The obtained result, after using the method of marching cubes, shows the different slices of the CT-Scan. To get a smoother result, we apply a Laplacian smooth, which allows to reduce the noise of the marching cubes while preserving the morphology. Then, we use a simplification method, "Quadric Edge Collapse Decimation", we then switch from a mesh with more than 100000 faces to a mesh with only a few thousand (Cf. Fig. 2). This reduction decreases the computational effort required to generate a bronchial tree.

Skeleton of the bronchial tree - For the morphology of the bronchial tree, the process is different, the main purpose being to extract the skeleton representing the first three generations of the airways (Cf. Fig 3). To generate this skeleton, we use the "Mean Curvature Flow Skeleton" method, developed by Tagliasacchi and al [18] and implemented in the CGAL library [21], which was also used for some steps in the bronchial tree growth algorithm. This method is based on mesh contraction, and differs in the management of intersections. With the contraction method, the intersection are not well approximated, for a three-branches intersection, the skeleton could be represented with three connected nodes instead of one intersection point. With the "Mean Curvature Flow Skeleton", this approximation is better managed by applying an edge collapse method, which results in a better defined skeleton without bad intersection approximation. With this method, it is also possible to get the diameter associated with each branch, and that will be an important parameter for the bronchial tree generation.

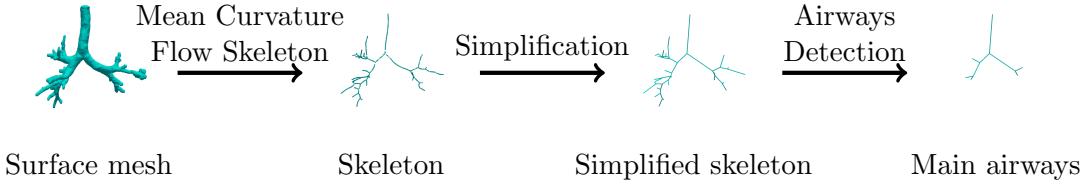


Figure 3: Extraction of the skeleton from the bronchial tree mesh

Nevertheless, the skeleton remains too complex because it follows perfectly the curve of the bronchial tree's surface mesh. We then proceeded to a simplification, by keeping only the intersections and extremities nodes. For this we only take the node with only one intersection and those with at least three intersections and reconnect them together by following the connection. This simplified version allows us to work only on segments and not curves, which will make it easier to define the initial cutting planes.

Then we have to classify them, to identify the major branches : trachea, pulmonary airways and lobar airways. For this, we search the morphological structure associated to each terminal branch of the simplified skeleton, either by checking if the end point of the branch is in a lobar mesh, or by determining the lobar mesh that intersects the half line of the branch. The tree can then be retraced by attributing to each mother branch the organs irrigated by the daughter branches, thus making it possible to know which lobes are irrigated by a branch. The identification of the main branches is now trivial by looking at the organs served by each branch.

This last step concludes the part on the extraction of the initial conditions, which are the simplified surface meshes of the pulmonary lobes and the skeleton on the bronchial tree from trachea to the lobar branch.

3 Generation of the bronchial tree

As previously explained, our algorithm for generating the bronchial tree is based on two current models, with the intention of combining the two approaches while updating some methods. Our reflection on the subject allowed us to set up a hybrid model using the subdivision principles of Tawhai *et al.* algorithm [20, 8], while taking into account the rules developed by Kitaoka *et al.* [9] to optimise the flow through the branches of the tree.

Rules for the generation of the bronchial tree - As with the two models mentioned, we have created a deterministic model based on a series of steps. The algorithm will repeat these steps for each volume of a generation which are then described as follows :

1. Separation of the surface mesh by the cutting plane into two new closed surface meshes (Cf. Fig 4a).
2. Calculation of the barycentre and the center of the largest inscribed sphere (centroid) for each new mesh (Cf. 4b).
3. Definition of the initial daughter branch, according to the reference point (barycentre or centroid) (Cf. 4c).

4. Application of morphological parameters on the branch (diameter, length and branching angle).
5. Checking the parameters of the branch to see if it is terminal.
6. Calculate the cutting plane of new closed surface meshes, if their associated branch isn't terminal.
7. Statistical analysis on the new branches.
8. Saving of the generation created in the form of a tubular mesh, a skeleton, volumes associated with the branches.
9. Repeat the operation with all the new closed surface meshes whose associated branch isn't terminal (Cf. 4d).

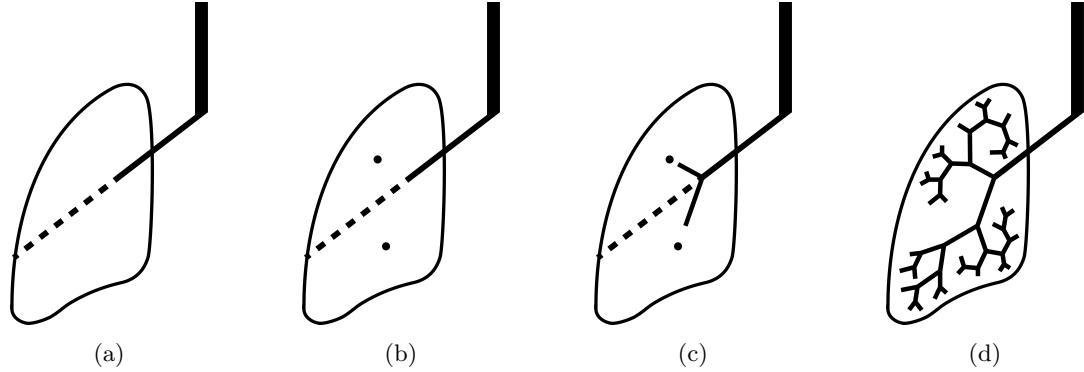


Figure 4: Bronchial tree generation in 2D, with our model. (a) Subdivision of the closed area mesh with the cutting plane. (b) Calculation of the barycentre and centroid. (c) Generation of daughter branches. (d) Repetition of the steps

Mesh division - One of the first notable changes is that, unlike the algorithm of Tawhai *et al.*, we have chosen not to use a point cloud to define a volume. Indeed, the Tawhai *et al.* model generates an arbitrary grid of points at the beginning of the algorithm. This grid allows to approximate the volume where the tree will grow, but this method does not necessarily allow to keep a good precision throughout the growth. Instead, we use the closed area mesh and mesh processing methods, from the CGAL library [21], to proceed to a subdivision of a surface mesh by a plane, and thus obtain two new closed surface meshes.

Barycentre - Since the point grid is not defined in our algorithm, the computation of the barycentre is also different. Instead of calculating the barycentre by averaging the points defining the volume, the calculation is based on the closed surface mesh and is defined by :

$$\begin{aligned}
 C &= \frac{\sum_i^{N_{faces}} \frac{1}{3}(p_{i0} + p_{i1} + p_{i2}) \times \frac{1}{2}\|(p_{i1} - p_{i0}) \wedge (p_{i2} - p_{i0})\|}{\sum_i^{N_{faces}} \frac{1}{2}\|(p_{i1} - p_{i0}) \wedge (p_{i2} - p_{i0})\|} \\
 &= \frac{\sum_i^{N_{faces}} C_i \times A_i}{\sum_i^{N_{faces}} A_i}
 \end{aligned} \tag{1}$$

With C as the barycentre of the closed surface mesh, C_i as the barycentre of the i -th face, A_i as the area of the i -th face and p_{ij} as the j -th node of the i -th face.

However, the closed surface meshes, used during the growth of the bronchial tree, can be non-convex. The barycentre is then not necessarily included in the mesh, or is too close to the edges of the mesh. We then calculated an other point that is included in the mesh, who is the center of the largest sphere included in the mesh, which we will rename the centroid in the following.

Centroid - We then developed a method to compute the centroid of a closed surface mesh, based on an 2D algorithm. This 2D algorithm has been developed by V. Agafonkin, using quadtrees [22], which are widely used for spatial indexing problems, but also for image compression and even for physical simulation. The concept of quadtree is to subdivide, recursively, a two-dimensional space into four cells. We have worked on the transition from the 2D algorithm to a 3D version. For this, we apply the principle of octrees, which is the 3D adaptation of quadtrees. This involves subdividing a three-dimensional space into height cells. The algorithm works as follows: (1) The bounding box of the mesh is generated, and is the initial cell. (2) The cell is divided into 8 cells. (3) For each cell, the signed distance, $dist_{mesh}$, between the cell's barycentre and the mesh is calculated. It is positive if the barycentre is inside the mesh and negative if the barycentre is outside. (4) The cells are added to a queue list according to their potential, defined by $potential = radius + dist_{mesh}$. The $radius$ being the half-diagonal of the cell. (5) Steps (2), (3), and (4) are repeated for the cell in the tail list that maximises the potential until the cell size is small enough. For our model, we have defined the size limit as a function of the size of the bounding box as :

$$H_{lim} = \frac{H_{Bbox}}{256} \quad (2)$$

Where H_{lim} is the size limit of a cell, and H_{Bbox} , the size of the initial cell, the bounding box of the mesh. This limits calculation times and maintains good accuracy.

Definition of the initial daughter branch - Now that we have the barycentre and centroid of the closed surface mesh, we can define a first version of the daughter branch. In the Tawhai *et al.* model, this branch is defined using the barycentre but, as we explained earlier, in some non-convex volumes, this barycentre will not be included or will be too close to the edges, which implies a bad development of the branches of the following generations and it is then more complicated to fill the space of the lung while keeping good morphometric properties. For this reason, we thought of taking into account the signed distance of the barycentre from the closed surface mesh and compared this with the signed distance of the centroid from the closed surface mesh. Indeed, if the signed distance of the barycentre is greater than 0.5 times the signed distance of the centroid, then we use the barycentre to define the initial branch, otherwise it will be oriented towards the centroid. However, we have left it up to the user to choose between using the barycentre, the centroid or both.

Diameter - We can now define the morphometric parameters associated with this initial branch, starting with the diameter which as the branch generation grows, sees its diameter decrease with it. In both Tawhai *et al.* and Kitaoka *et al.* algorithms, this parameter is defined according to the diameter of the mother branch.

In Tawhai *et al.* algorithm, the calculation uses the Homothety Ratio (HR), which can be found in several articles [20, 8, 1, 12], is the relationship that allows the diameter of a daughter branch to be calculated as a function of the mother branch. It is expressed as :

$$D_{child} = 2^{-0.33} D_{mother} \quad (3)$$

However, there is another method, based on Murray's law [13], which was described, in the paper of Kitaoka *et al.*, by :

$$D_{child} = D_{mother} \times r^{\frac{1}{n}} \quad (4)$$

With $r = \frac{V_{child}}{V_{mother}}$ which corresponds to the ratio of the mesh volumes associated with the parent and daughter branches. As for the variable n , its value varies according to the articles but Kitaoka *et al.* fixes it at 2.8.

In order to respect the laws of flow conservation in the bronchial tree, we chose to use the second ratio, especially as it is easily calculable and applicable with our algorithm.

Branching angle - Before defining the length of the branch, it is important to check that the branch is correctly oriented, which is the same as checking that the branch angle is in agreement with the morphometric data. The branching angle is defined as the angle between the mother branch and the daughter branch. Using the branch initialization, a branching angle can then be calculated by applying the following formula :

$$\theta_{init} = \arccos\left(\frac{v_{mother} \cdot v_{init}}{\|v_{mother}\| \times \|v_{init}\|}\right) \quad (5)$$

The angle correction will thus depend on this value. In fact, in most articles [20, 8, 1, 12], an angle limit is set and the angles above it are adjusted to this threshold value. In the case of the algorithm of Tawhai *et al.*, this value is set at 60°. We also chose to use the threshold method to define whether a branching angle should be corrected, but this time we relied on the method of Kitaoka *et al.*, which sets this value at 80°. Then we do not correct the branching angle according to the threshold value, but according to the theoretical branching angle that results from the relationship between the flow rate and the branching angle. As for the diameter, Kitaoka *et al.* define the branching angle by :

$$\theta_{theoric} = \arccos\left(\frac{1 + r^{4/n} - (1 - r)^{4/n}}{2r^{2/n}}\right) \quad (6)$$

With $r = \frac{V_{child}}{V_{parent}}$ and $n = 3$. Nevertheless, the variable n can vary according to the type of simulated flow, if it is a laminar flow, $n = 3$, if the flow is turbulent, $n = 2, 33$. In our algorithm, this coefficient depends on the generation of the branch, the first generation will have a turbulent flow while the smaller branches will have a laminar flow.

We then rotate the initial branch around the vector normal to that branch and the mother branch. The purpose of the rotation is to adjust the branching angle to match the theoretical value. This rotation is performed with a rotation matrix, whose simplified form is described by :

$$R = P + \cos(\theta_{rot})(I - P) + \sin(\theta_{rot})Q \quad (7)$$

Where :

$$P = \begin{pmatrix} u_x^2 & u_x u_y & u_x u_z \\ u_x u_y & u_y^2 & u_y u_z \\ u_x u_z & u_y u_z & u_z^2 \end{pmatrix}; I = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}; Q = \begin{pmatrix} 0 & -u_z & u_y \\ u_z & 0 & -u_x \\ -u_y & u_x & 0 \end{pmatrix} \quad (8)$$

$$u = v_{mother} \wedge v_{init} \quad (9)$$

u is the normal vector of the initial branch and the mother branch. The rotation angle is obtained by computing : $\theta_{rot} = \theta_{theoric} - \theta_{init}$. To obtain the branch with the right branching angle, we apply the rotation matrix on the vector of the initial branch : $v_{daughter} = Rv_{init}$.

Length - Finally to conclude with the morphometric parameters, we will now define the length of the branch. The length of the branch can be related to the diameter of the branch using the following relationship :

$$\frac{L}{D} = 3 \quad (10)$$

It is, however, more natural to have a distribution of this ratio in accordance with a normal distribution of expectation 3 and standard deviation 1. For this Tawhai *et al.* defined the length of the branch as 40% of the length of the segment between the end of the mother branch and the barycentre.

We have used the same principle, but modified some aspects. We define a ray using the vector associated with the daughter branch, and then we calculate the different intersection points between this ray and the associated surface mesh. There may be several points of intersection due to the fact that some surface meshes are non-convex. These points of intersection are then sorted according to their distance from the end of the mother branch, and the length of the daughter branch is defined as 25% of the length of the nearest point of intersection.

We then check that the relationship between the diameter and the length is respected, if this is not the case and the length is too great, we will then correct this. We progressively reduce the length of the branch until the ratio is less than 6, as defined by Kitaoka *et al.*

Terminal branch - Once the morphometric parameters of the branch are obtained, it is necessary to know if this branch is considered as terminal in order to continue the growth or not. In the articles of Tawhai *et al.*, a branch is defined as terminal if its length is less than a threshold value, or if the volume served does not contain enough points. In the model of Kitaoka *et al.*, if the flow is too small then the branch is considered as terminal, which in the end has a link with the diameter of the branch.

In our algorithm, we made a similar choice to the one used by Kitaoka *et al.* by using the diameter, with a threshold fixed at 0.4mm, since we know the initial diameter of the trachea, we can deduce a theoretical diameter of the terminal branch. According to the work of Horsfield *et al.* [7, 6, 4, 5, 3], the mean generation for a terminal branch is around 17, and the ratio between the diameter of the mother branch and the diameter of the daughter branch is $(\frac{1}{2})^{\frac{1}{3}}$, so we have the following relation:

$$d_{terminal} = \frac{d_{trachea}}{2^{\frac{17}{3}}} \quad (11)$$

Plane Center	Plane Vector	Direction of Branch	Correction Branching Angle
Barycentre	Sister	Barycentre	Activated
Centroid	Mother	Centroid	Activated after a fixed generation
End Branch		Hybrid	Deactivated

Table 1: Adjustable parameters for bronchial tree generation

Definition of the cutting plane - In the papers of Tawhai *et al.* [8, 20], two different versions of the definition of the cutting plane can be found. In both versions the plane is centred on the end of the branch, in the 2000 paper, the plane is defined using the branch and the mother branch, while the second, 2004 paper uses the sister branch instead of the mother branch. More recently, models such as Bordas *et al.* [1] or Montesantos *et al.* [12] have also based their work on the model of Tawhai *et al.* by centering the design on the barycentre. For the model we have generated, we have used the same definition as the latest paper by Tawhai *et al.*, which means that the plane will be centered on the end of the branch, using the director vector of the branch and its sister branch.

There are several methods to compute a plane, for our work we have taken the one using a point and a vector which will be the normal vector of the plane. The vector chosen is the normal vector of the branches, and for the point we have chosen the end of the mother branch. The equation of the plane is then :

$$a(x - x_0) + b(y - y_0) + c(z - z_0) = 0 \quad (12)$$

With (a, b, c) , the coordinates of the normal vector and (x_0, y_0, z_0) , the coordinates of the end of the mother branch.

Modularity of the algorithm We have presented the different steps and default parameters of our algorithm, however we still have the possibility to modify some elements of our algorithm as shown in the Table 1.

We then generated a bronchial tree with the different parameters listed, making a total of 54 different trees, the morphological parameters of these numerous trees are listed in Tables 6, 7, 8.

4 Results

Based on our previous observations, we have thus defined default parameters, namely that the plane is defined by the end of the branch, the director vector of the branch and the sister branch. As for the direction to orient the branch, we use the method alternating between the barycentre and the centroid, depending on whether the former is far enough from the edges of the closed surface mesh. In addition, the correction of the branch angle is also applied. The algorithm was used on the surface meshes of the lobes extracted from the data of a patient from the LIDC-IDRI library during the LUNA16 challenge [16] and from the annotations of Tang *et al.* [19]. The result is a mesh, as shown in Fig 5, representing the bronchial tree obtained.

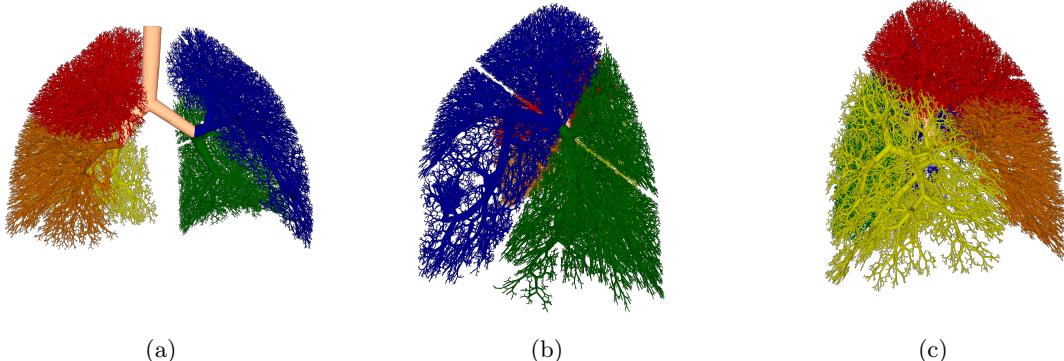


Figure 5: Bronchial tree generation in 2D, with our model. (a) Subdivision of the closed area mesh with the cutting plane. (b) Calculation of the barycentre and centroid. (c) Generation of daughter branches. (d) Repetition of the steps

This method produces a tree with approximately 240,000 branches, half of which are terminal branches. This terminal branches appear from the 11th generation to the 26th generation, with an average of 17.1 generations.

As we said the branching angle correction is also used in this model in order to have an optimised model for the gas transport in the tree. This correction allows to have an average branching angle equal to 37.86° with a distribution of the angles, which can be seen in the Fig 6a, quite concentrated on this average value while having an equal distribution on the more distant values. This is due to the heterogeneity of the subdivision which is provided by the use of the hybrid method. Indeed, by using the centroid as a direction in some cases, the cutting plane will then separate the closed surface mesh in a more heterogeneous way, and the theoretical branching angle will then be different from 37.5° .

However, this heterogeneity has no influence on the morphometric measurements of the tree, indeed by observing the Fig 6b, 6c, 6d, we can see that the length, diameter and ratio are consistent with the expected data. Again, this is due to the implementation of the model, which takes into account the volume of the closed surface mesh, and using this information deduces from the Eq 4 the value of the diameter of the branch. The length is then deduced from this diameter by ensuring that the ratio between these two is between 1 and 6.

5 Discussion

In this paper, we have developed an algorithm to generate a bronchial tree, using a closed surface mesh. This mesh is the conclusion of another project, allowing to segment, from CT-Scan, the lung lobes and the first generations of the bronchial tree.

This algorithm is based on the work of Kitaoka *et al.* [9] and Tawhai *et al.* [20, 8], which provides a good approximation of the bronchial tree. These models are both space filling algorithms but differ in their basic principle. The first one aims to fit perfectly in the geometry where the tree will grow, while the second one wants to optimise the flows in the branches. It was therefore important for us to try to combine these two models, while updating the tools and calculation methods, since these two models were created two decades ago. We have, for example, used the closed surface mesh, in the absence of a point grid, for the subdivision of the space, which allows us to have a better quantification of the volume

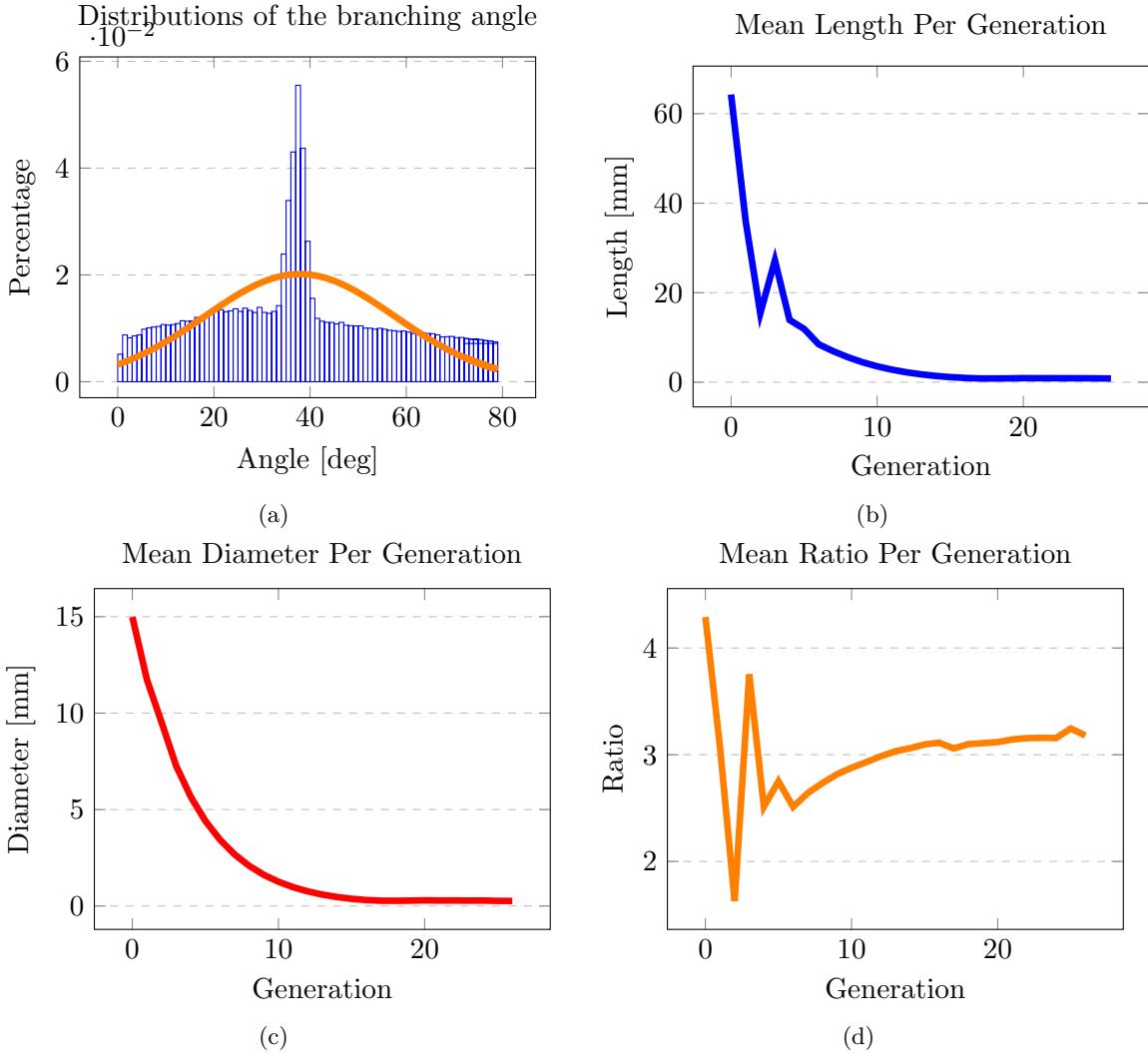


Figure 6: Graphs of the morphometric parameters of the bronchial tree obtained with the default parameters.
 (a) Distributions of the branching angle. (b) Mean length. (c) Mean Diameter. (d) Mean ratio.

associated with each branch and to apply the theoretical properties that a branch must have in order to be in agreement with the algorithm of Kitaoka *et al.*.

We have also introduced some new features, such as the fact that we do not necessarily use only the barycentre to define a branch but also the centroid. This ensures that in non-convex regions of the mesh, the branch will always fit into the mesh. The algorithm also adapts according to the generation of a branch, indeed between the beginning and the end of the bronchial tree, the type of flow is not the same, in the first generations the flow is turbulent and will progressively evolve towards a laminar flow in the smaller branches. This has an impact on the morphological properties of a branch since the calculation of the diameter between the mother and daughter branches is different, as is the theoretical branching angle. The algorithm is also very flexible, with the possibility of choosing from various parameters, in particular the choice of the centre or the second branch of the cutting plane, but also the point towards which the daughter branch is defined. There is also the possibility of applying

or not the correction of the angle for the branches.

In this section we will present different models that were all generated on the same patient, with the angle correction applied after a fixed generation, but with different generation parameters. All the statistics on these different trees are in the appendices, we will only discuss here the data that show the differences between the models.

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Terminal Generation	Mean Branching Angle
Barycenter	Sister	Barycenter	18	16.649	37.053
Barycenter	Sister	Centroid	18	16.6379	30.998
Barycenter	Sister	Hybrid	18	16.646	37.579
Barycenter	Mother	Barycenter	18	16.653	34.984
Barycenter	Mother	Centroid	18	16.640	25.058
Barycenter	Mother	Hybrid	18	16.649	34.851
Centroid	Sister	Barycenter	31	17.784	33.183
Centroid	Sister	Centroid	31	17.844	31.326
Centroid	Sister	Hybrid	31	17.827	32.822
Centroid	Mother	Barycenter	29	17.725	31.022
Centroid	Mother	Centroid	31	18.062	27.213
Centroid	Mother	Hybrid	32	17.817	30.905
End	Sister	Barycenter	26	16.978	37.671
End	Sister	Centroid	37	19.416	30.779
End	Sister	Hybrid	26	17.100	37.860
End	Mother	Barycenter	18	16.648	34.924
End	Mother	Centroid	32	17.889	28.032
End	Mother	Hybrid	28	16.774	34.946

Table 2: Statistical data of bronchial tree without branching angle correction

Based on the table, we can notice that the direction parameter, i.e. the point towards which the daughter branch is defined, is the parameter that has the most influence on the average branching angle of the tree. Indeed, if we compare the models three by three, where only the direction differs, we observe significant differences between the angles. For example, the Barycentre.Sister.Barycentre model has an average angle of 37°, while the Barycentre.Sister.Centroid model has an angle of only 31°, for the model using the hybrid version, the average angle observed is very close to the average angle with the barycentre version. This difference is reduced by taking into account the influence of the centre of the plane, and is even less present when comparing the results according to the cutting plane vector.

However, this data does not provide information on the asymmetry of the tree, and for this it is necessary to refer to the number of generations obtained, and the average generation of the terminal branches. Indeed, by observing the number of generations calculated, one can have an idea of the asymmetry of the bronchial tree obtained. For example, models using the barycentre to define the centre of the plane will have a less pronounced asymmetry than those using the centroid. This can be justified by the fact that the subdivision centred

on the barycentre gives two more homogeneous surface meshes in terms of volume than the subdivision centred on the centroid, which gives two more heterogeneous surface meshes. Thus, in the first case, the daughter branches will be more similar and will therefore tend to converge more quickly to a terminal branch, whereas in the second case, the daughter branches will be less similar and therefore the path to a terminal branch will converge less quickly.

Another important point concerned the filling of the volumes. After the first trees were generated we found that the models using the barycentre had more difficulty filling the non-convex areas of the lung, which the models using the centroid did more easily. Based on this conjecture, we defined the hybrid method of calculating the signed distance between the barycentre and the centroid with the closed surface mesh. Using this information we can then choose the point to be used for the direction of the new branch. And using this method we then have a happy medium between symmetry of the surface subdivision and assymetry of the bronchial tree. Nevertheless, the number of terminal and non-terminal branches in all models is almost constant.

As explained, some data are not present in the table, as they were not relevant to show the differences between the models. This is the case for morphological data such as length, diameter or the ratio between these two. It can be seen that whatever the model used (see table in appendix), these three values are always quite similar, with respectively 1.1 mm for the length, 0.36mm for the diameter, and 3.1 for the ratio. This is quite understandable given that the diameter is defined as a function of the mother branch and the volume left by the daughter branch, as explained in the paragraph on "diameter". And it is according to the diameter and the ratio that the length of the branch is defined, which is why the ratio between these two data respects the morphometric data. The same is true when we look at the number of terminal or non-generated branches. With values that oscillate between 230,000 and 255,000 branches generated, half of which are considered terminal.

6 Conclusion

We presented a bronchial tree generation algorithm that combines the benefits of the respective models of Kitaoka et al. and Tawhai et al. while introducing new methods to improve the accuracy and speed of calculations. The model obtained has morphometric data in agreement with the observed findings, such as an average branching angle close to 37.5° or a length to diameter ratio equal to 3. The diameter of each branch is calculated so that the flow at each branch is preserved, as is the branching angle. The choice of the barycentre or centroid according to their signed distance from the closed surface mesh allows a better filling, especially in the non-convex zones of the lung.

We were then able to go further in the number of branches generated while keeping an average generation comparable to those obtained by the two basic models used. In addition, the mesh obtained is completely usable for numerical simulations.

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7 Annexe

In this section, we will present a large number of results obtained with different methods, due to the fact that our algorithm is scalable. This will also show the influence of parameters such as the centre of the cutting plane, the second vector to define the cutting plane or the point used to define a new branch. We will also be able to highlight the advantage brought by the branching angle correction algorithm.

7.1 Influence of the center of the plane

To begin with, we will look at the impact of the centre of the plane on the generation of the bronchial tree. For this purpose, we have made nine different models which all use the sister branch as the second vector used to define the cutting plane, and they are grouped by the direction of branch definition. Then we got, in each group, a model whose cutting plane is centred on the barycentre, on the centroid or on the end of the branch. In order to better see the effects of this choice, the models presented do not use the branching angle correction. As we have done previously, we do not refer to the length, diameter and branch ratio of the trees obtained because these are in all the models used always very similar as can be seen in the Table 6, 7, 8.

The Table 3 will group together the statistical data that allow the models to be differentiated. The first observation that can be made is that the models using the barycentre and the centroid to define the cutting plane are very different in terms of the results obtained but that their results are very similar whatever the point defining the branch. Whereas the model using the end of the branch to define the cutting plane will be influenced by the point used to define the branch.

Indeed, if we look at the first group where the branch is defined by the barycentre, we observe that the models whose plane is defined by the centre or the end of the branch have very similar results with a maximum generation of 18, an average generation for the terminal branches of 16.65 and a branching angle of about 48.6. The model using the centroid for the cutting plane is quite different from the other two with 31 generations obtained, an average generation of the terminal branches equivalent to 17.8 and a branching angle lower by 1.5, compared to the other two.

Taking the second group, i.e. when the centroid is used to define the branch, we can make the same conjecture as with the first group, only the model defined by the end of the branch will be closer to the one defined by the centroid this time. However, there are some discrepancies, notably in the number of generations obtained, with 30 generations for the model with the centroid for the cutting plane and 37 generations for the one centered on the end of the branch. This difference is the result of the first subdivision on the closed surface meshes of the lobes, which will give different volumes from one model to another, and which then results in very similar models in terms of average generation of the terminal branches as well as average branching angle. The average terminal branch generation for the latter two models is 17.9 which is slightly higher than the average observed in the models of Weibel *et al.* [24, 25], Horsfield *et al.* [7, 6, 4, 5, 3], Kitaoka *et al.* [9] and Tawhai *et al.* [20, 8].

If we now pay attention to the last group, when the branch is defined either by the barycentre or by the centroid, we have this time a rather intriguing phenomenon. We can observe that the model centred on the barycentre and on the end of the branch have similarities, in terms of morphometric data, with an average generation of terminal branches equivalent to

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Terminal Generation	Mean Branching Angle
Barycentre	Sister	Barycentre	18	16.649	48.524
Centroid	Sister	Barycentre	31	17.801	47.149
End	Sister	Barycentre	18	16.644	48.707
Barycentre	Sister	Centroid	18	16.631	47.603
Centroid	Sister	Centroid	30	18.030	49.625
End	Sister	Centroid	37	17.858	49.039
Barycentre	Sister	Hybrid	18	16.647	49.078
Centroid	Sister	Hybrid	34	17.848	47.053
End	Sister	Hybrid	30	16.757	49.431

Table 3: Statistical data of bronchial tree without branching angle correction and with different center of cutting plane

16.7 ± 0.05 and an average branching angle of 49.25 ± 0.2 . However there is an important difference with a maximum generation of 18 for the model using the barycentre against 30 generation for the model using the hybrid version, which is then in this case closer to the results obtained with the centroid model.

This phenomenon is quite understandable, when we use the barycentre for the cutting plane, i.e. either those centred on the barycentre or those centred on the end of the branch and using the barycentre to define the branch, will give a more homogeneous subdivision of the closed surface mesh, i.e. the two surface meshes obtained after the subdivision will have a volume closer to each other. And therefore the convergence to a terminal branch will be faster, that is why the three models have a maximum generation equal to 18.

Conversely, the models centred on the centroid, namely those centred on the centroid and the one defined by the end of the branch for the plane and the centroid for the branch, will give two more heterogeneous volumes, the convergence towards the terminal branch will then be less rapid, and in the non-convex regions of the lung, this convergence will be even less important, which is why we find a large number of generations, always greater than 30, but the number of branches among these generations is not very large.

This leaves only the end-of-branch algorithm and the hybrid version, which is a perfect combination of the other two versions, because the cutting plane will then be defined either by the barycentre in volumes with low non-convexity, or by the centroid in those with high non-convexity. So we have a fairly large convergent in the areas where we use the barycentre as a direction, and we will look for more distant generations in the areas that use the centroid.

7.2 Influence of the second branch to define the cutting plane

We will now focus on the second vector used to define the cutting plane, we have two possible choices, either we use the mother branch or the sister branch. To observe the effects of this parameter, we proceed as for the centre of the plane, using groups of models with similar parameters except for the second vector. We thus have 6 models which all use the end of the branch as the centre of the cutting plane, as they are quite similar to those using the

barycentre or the centroid respectively when using these points to define the branch and they make a difference with the hybrid version. And we have just three different groups depending on the point used to define the branch.

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Terminal Generation	Mean Branching Angle
End	Sister	Barycentre	18	16.644	48.707
	Mother	Barycentre	18	16.645	47.837
End	Sister	Centroid	37	17.858	49.039
	Mother	Centroid	32	17.962	47.477
End	Sister	Hybrid	30	16.757	49.431
	Mother	Hybrid	37	16.809	48.290

Table 4: Statistical data of bronchial tree without branching angle correction

If we look at the Table 4, for the models using the barycentre to define the branch, we observe two very similar models, except for the average branching angle, where we have a difference of a little less than one degree. This difference is again due to the fact that the subdivision centred on the barycentre will give two very homogeneous volumes and therefore whether it is the parent or the daughter branch, which is used to define the cutting plane, has no great influence on the model generated.

Looking at the results for the second group, namely the models using the centroid to define the branch, we can see a difference of 5 generations obtained, with 37 generations for the model using the sister branch, and 32 generation for the model using the mother branch. This difference, which on paper looks important, is not so important because it may be a branch that takes less time to converge and therefore will give us more generations. If we combine this information with the average generation of the terminal branches, which are very close whatever the second branch used, we confirm the hypothesis of a branch taking more generations to converge towards a terminal branch. As for the branching angles, we notice that there is a difference of about 1.5. These differences remain minimal, however, and are the result of the divergences generated by the more heterogeneous subdivision of the planes centred on the centroid.

This hypothesis is confirmed using the models using the hybrid version, where we can see that the number of generations obtained is, once again, quite different with 30 generations for the version using the sister branch against 37 generations for the version using the mother branch. As for the model using the centroid, we will have some branches, in the areas with important non-convexity, which will tend towards a terminal branch more slowly. But if we take into account the average generation of the terminal branches, we have a difference that is negligible. This also shows that the difference in generations obtained is not indicative of a great difference in the bronchial trees obtained. There is, however, still a difference of about one degree in the mean branching angle which, in view of the other groups, seems to be influenced by the choice of the second vector.

This choice has an impact on the subdivisions that will be different from one model to another, but the difference is not very important on the bronchial trees obtained, with an average angle generally different by about one degree.

Nevertheless, referring to the Tables 7, 8, where the angle correction algorithm is applied, one can see more pronounced differences in branching angles between the methods with the sister branch and those with the mother branch. With the use of the sister branch, the results are closer to the observed reality.

7.3 Influence of the point used to define a daughter branch

The last parameter, on which we wanted to see the effects, is the point used to define the daughter branch, i.e. either the barycentre or the centroid, or alternating between the two points according to the distance signed with the closed surface mesh (so-called hybrid method).

By taking up the tables 3, 4, we can observe that the point used to define the branch is going to have an important influence when we use the end of the branch to define the cutting plane. If we take into account the models where the plane is centred on the barycentre, we can see that the results are for the most part very similar with a slight difference in the average branching angles, and it is the same with the models where the plane is centred on the barycentre. However, by using the Tables 7, 8, it can be seen that when the branching angle correction is applied, this difference is more pronounced, with a generally smaller branching angle when the branches are directed towards the centroid. In any case, trees centred on the barycentre tend, especially in meshes with high non-convexities, not to fill the whole space because the barycentre will then be located quite close to the mesh, or even outside it in some cases, and the filling is then less efficient.

With bronchial trees whose branches are defined by the centroid, the filling of the volumes will be more efficient, because we are looking for the point whose signed distance from the mesh is maximum, so that we can be sure that we can correctly define the following generations, if necessary. But we notice that the branching angle is generally lower when we use the branching angle correction.

With the hybrid version, we manage to take advantage of both methods because in convex regions, such as the inside of the lungs, the branch will go towards the barycentre, and in more complex regions, the centroid will allow us to go deeper and obtain a better filling. However, as the non-complex regions are less important, we will have morphometric data close to those using the barycentre method, which are more in keeping with reality.

7.4 Influence of the angle correction

Finally, we will now look at the branching angle correction algorithm and observe the differences between the models whose plane is centred on the end of the branch and those using the sister branch. The Table 5 thus groups some statistical data for the bronchial trees obtained.

We can easily observe the advantage of using the branching angle correction, when the latter is not applied we will have average branching angles of about 49 ± 0.4 whereas, with the angle correction, we will have, for the models whose branch is directed towards the barycentre or the hybrid version, branching angles equivalent to 37.75 ± 0.1 and, for the models with the branches directed towards the centroid, equivalent to 30.9 ± 0.2 .

If we look at the number of generations as well as the average generation of the terminal branches, we can also see a difference, notably for the algorithms using the centroid which, without correction of the angle, has an average generation equal to 17.858 generation whereas

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Terminal Generation	Mean Branching Angle
<i>Without branching angle correction</i>					
End	Sister	Barycentre	18	16.644	48.707
End	Sister	Centroid	37	17.858	49.039
End	Sister	Hybrid	30	16.757	49.431
<i>With branching angle correction</i>					
End	Sister	Barycentre	26	16.978	37.671
End	Sister	Centroid	37	19.416	30.779
End	Sister	Hybrid	26	17.100	37.860
<i>With branching angle correction applied after a fixed generation</i>					
End	Sister	Barycentre	26	16.964	37.741
End	Sister	Centroid	37	19.021	31.113
End	Sister	Hybrid	31	17.117	37.865

Table 5: Statistical data of bronchial tree without branching angle correction

with the correction this average is higher than 19 generation. For the other two methods, there was a slight increase of about 0.3 generation, which does not have a real impact on the results obtained. However, for the algorithms using the barycentre, we can see that the number of generations has strongly increased, going from 18 generations without the correction to 26 generations with the correction. This difference is also explained by the choice of the centre of the plane which, here, is the end of the branch, and then when a branch is corrected the cutting plane is different from the one centred on the barycentre, this brings a less heterogeneous subdivision and then the convergence of the branches is less fast. Taking into account the tables 6, 7, 8, we can see that when the cutting plane is centred on the barycentre or even on the centroid, the differences between the models with and without the correction algorithm, are only on the average branching angle and not on the average generation of the terminal branches or on the number of generations obtained. This can be explained by the fact that the subdivision of the closed surface meshes are very similar, they remain, in all cases, centred on the same point with a branch that has been modified but that remains in the same basic plane, so that the cutting planes are all quite similar.

7.5 Tables of the different possible models

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Generation	Mean			Number Branches	Mean Terminal Length	Mean Diameter	Mean Ratio	Mean Branching Angle
					Number Branches	Mean Terminal Length	Mean Diameter					
Barycentre	Sister	Barycentre	18	16.649	233504	116745	1.161	0.361	3.271	48.524		
Barycentre	Sister	Centroid	18	16.631	229913	114940	1.201	0.363	3.325	47.603		
Barycentre	Sister	Hybrid	18	16.647	233992	116992	1.159	0.361	3.268	49.078		
Barycentre	Mother	Barycentre	18	16.653	233759	116874	1.167	0.361	3.290	48.103		
Barycentre	Mother	Centroid	18	16.638	230718	115334	1.216	0.363	3.367	44.416		
Barycentre	Mother	Hybrid	18	16.649	233955	116974	1.170	0.361	3.294	48.272		
Centroid	Sister	Barycentre	31	17.801	235843	117903	1.186	0.364	3.310	47.149		
Centroid	Sister	Centroid	30	18.030	239073	119521	1.241	0.364	3.438	49.625		
Centroid	Sister	Hybrid	34	17.848	236724	118353	1.190	0.364	3.317	47.053		
Centroid	Mother	Barycentre	30	17.662	235327	117650	1.188	0.364	3.314	47.847		
Centroid	Mother	Centroid	34	18.086	239599	119764	1.242	0.364	3.444	47.238		
Centroid	Mother	Hybrid	30	17.759	236548	118267	1.190	0.364	3.317	48.180		
End	Sister	Barycentre	18	16.644	229707	114850	1.165	0.363	3.265	48.707		
End	Sister	Centroid	37	17.858	239371	119653	1.242	0.364	3.447	49.039		
End	Sister	Hybrid	30	16.757	228758	114375	1.173	0.364	3.277	49.431		
End	Mother	Barycentre	18	16.645	233282	116638	1.169	0.361	3.288	47.837		
End	Mother	Centroid	32	17.962	239178	119549	1.243	0.364	3.440	47.477		
End	Mother	Hybrid	37	16.809	232084	116032	1.175	0.362	3.299	48.290		

Table 6: Mean morphological parameters of bronchial tree without branching angle correction

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Generation	Mean			Number Branches	Mean Terminal Length	Mean Diameter	Mean Ratio	Mean Branching Angle
					Number Branches	Mean Terminal Length	Mean Diameter					
Barycentre	Sister	Barycentre	18	16.649	233557	116768	1.099	0.361	3.088	37.053		
Barycentre	Sister	Centroid	18	16.637	231241	115610	1.148	0.362	3.182	30.998		
Barycentre	Sister	Hybrid	18	16.646	233859	116928	1.100	0.361	3.088	37.579		
Barycentre	Mother	Barycentre	18	16.653	233833	116906	1.110	0.361	3.117	34.984		
Barycentre	Mother	Centroid	18	16.640	231808	115845	1.152	0.362	3.184	25.058		
Barycentre	Mother	Hybrid	18	16.649	234076	117032	1.113	0.361	3.120	34.851		
Centroid	Sister	Barycentre	31	17.784	235013	117486	1.123	0.364	3.131	33.183		
Centroid	Sister	Centroid	31	17.844	238088	119029	1.147	0.364	3.190	31.326		
Centroid	Sister	Hybrid	31	17.827	236421	118203	1.126	0.364	3.135	32.822		
Centroid	Mother	Barycentre	29	17.725	236647	118300	1.123	0.364	3.130	31.022		
Centroid	Mother	Centroid	31	18.063	239742	119784	1.113	0.364	3.103	27.213		
Centroid	Mother	Hybrid	32	17.817	237729	118850	1.120	0.364	3.125	30.905		
End	Sister	Barycentre	26	16.978	239326	118805	1.091	0.361	3.077	37.671		
End	Sister	Centroid	37	19.416	254951	123845	1.088	0.365	3.056	30.779		
End	Sister	Hybrid	26	17.100	238341	118249	1.094	0.361	3.080	37.860		
End	Mother	Barycentre	18	16.648	233805	116899	1.111	0.361	3.117	34.924		
End	Mother	Centroid	32	17.889	238980	119431	1.113	0.364	3.104	28.032		
End	Mother	Hybrid	28	16.774	231267	115623	1.115	0.362	3.120	34.946		

Table 7: Mean morphological parameters of bronchial tree with branching angle correction

Plane Center	Plane Vector	Branch Direction	Max Generation	Mean Generation	Mean			Number Branches	Mean Terminal Length	Mean Diameter	Mean Ratio	Mean Branching Angle
					Number Branches	Terminal Length	Diameter					
Barycentre	Sister	Barycentre	18	16.648	233518	116754	1.099	0.361	3.089	37.064		
Barycentre	Sister	Centroid	18	16.633	230382	115179	1.148	0.363	3.178	31.462		
Barycentre	Sister	Hybrid	18	16.646	233886	116939	1.100	0.361	3.090	37.724		
Barycentre	Mother	Barycentre	18	16.654	234015	117002	1.104	0.360	3.104	36.074		
Barycentre	Mother	Centroid	18	16.639	231598	115760	1.152	0.362	3.183	26.789		
Barycentre	Mother	Hybrid	18	16.650	234238	117113	1.107	0.361	3.108	35.921		
Centroid	Sister	Barycentre	32	17.771	234870	117414	1.124	0.364	3.135	32.973		
Centroid	Sister	Centroid	33	17.947	237560	118763	1.145	0.364	3.185	31.393		
Centroid	Sister	Hybrid	33	17.947	237560	118763	1.145	0.364	3.185	31.393		
Centroid	Mother	Barycentre	29	17.679	236435	118198	1.118	0.364	3.122	32.326		
Centroid	Mother	Centroid	35	18.050	239281	119565	1.110	0.364	3.100	27.651		
Centroid	Mother	Hybrid	32	17.769	237787	118882	1.116	0.363	3.118	31.944		
End	Sister	Barycentre	26	16.964	239348	118812	1.091	0.361	3.079	37.741		
End	Sister	Centroid	37	19.021	254885	123951	1.085	0.364	3.054	31.113		
End	Sister	Hybrid	31	17.117	238529	118318	1.095	0.361	3.083	37.865		
End	Mother	Barycentre	18	16.648	233931	116956	1.106	0.361	3.107	35.829		
End	Mother	Centroid	33	17.933	239432	119666	1.109	0.364	3.097	28.106		
End	Mother	Hybrid	32	16.829	232737	116358	1.109	0.362	3.109	35.744		

Table 8: Mean morphological parameters of bronchial tree with branching angle correction applied after a fixed generation