

# An ASP Approach for Arteries Classification in CT-scans<sup>\*</sup>

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**Abstract.** Automated segmentation of CT scans is the first step in the pipeline for the interpretation and identification of potential pathologies in human organs. Several methods based on Machine Learning are currently available, even if their precision is still outperformed by medical doctors. In this field there are some intrinsic limitations to ML approaches, such as the cost and time to acquire high quality annotated scans for training; a considerably high variability of organs morphology due to age, health conditions, genetics; acquisition noise. This paper outlines a new methodology based on Answer Set Programming, which returns reliable, easy-to-program and explainable interpretations. In particular, we focus on the CT scan analysis and retrieval of tree-like structure, corresponding to main blood vessels (arteries) arrangement. The structure is compared to the knowledge base of vessels contained in anatomy text-books. The mapping of vessels names is computed by an ASP program. This preliminary step produces a robust input to a reasoner for the multi-organ labeling and localization problem.

**Keywords:** Answer set programming · CT scan · Image processing · Blood vessels classification

## 1 Introduction

In Italy, according to the registry of tumor [1], there have been 373 thousands new diagnosis of malign cancer in 2018. The survival rate at 5 years is still very low, *e.g.*, 20% for liver tumours and only 8% for pancreas neoplasia. Unfortunately, while surgery is the only curative treatment, a small subset of patients are diagnosed at a sufficiently early stage such that surgery is still a viable option, mainly because at such stage cancer is often asymptomatic.

The screening process typically involves three main categories of examinations: ultrasound (US), computed tomography (CT) scans and magnetic resonance (MR). They are performed in this specific order and in case of detected

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anomalies, the next examination is prescribed. Such investigations are ordered by increasing running cost, increasing sensitivity and decreasing accessibility.

Usually CT scans show a very good sensitivity for cancer, but in case of small tumours (less than 2 cm) sensibility and specificity often drop because cancer is still indistinguishable from healthy tissue. Moreover, radiologist experience and training make a difference in spotting smaller tumours. Consequently, the diagnosis is very challenging, and an early stage tumour can hide behind acquisition noise, even if other diagnostic modalities (i.e., MR) could highlight the problem.

In recent years, several lines of research have been dedicated to support the radiologists' work and to help them in processing and assessing the amount of data coming from CT scans. The goal is typically to train a system that suggests potential abnormalities during the experts' analyses. In Section 2.2 a short overview is provided. The automated support for diagnosis is a challenging process, because of a combination of unique domain-specific features:

- **Acquisition noise:** radiologists train their eyes to selectively remove noise from the images and to capture the tiniest *shadow* that could be associated to tumours;
- **Patients anatomy:** compared to text-books, abdominal organs are subject to a high variability in terms of size, shape, position, ageing, genetics, etc.;
- **Annotated models:** the cost for the creation of clean, complete and annotated model to be fed to automatic training requires some hours for a single scan. For effective training a large set of cases is needed;
- **Need for an explanation:** a radiologist can support its diagnosis with a set of deductions coming from the observation of CT scans. This should be provided by the automated process as well, as mentioned in [9].

Machine learning approaches do not yet outperform human experts, as opposed to other fields of AI applications, partly because of the above mentioned issues. We argue that such scenario will not drastically mutate in the future and therefore a different methodology could be more suitable and should be investigated.

Our project is about the development of a software that could help radiologists with the detection of early stage tumors and to avoid delayed diagnosis and treatment. The key idea is to build a system that relies on medical knowledge (anatomy and radiology) and reasons on it. Constraint programming [14] and Answer Set Programming [5] are the type of technologies suitable for this task. In particular, they produce a solution model that is compatible with a knowledge base and an input instance. Moreover, they can provide a high level proof that can be interpreted by experts, for both model improvement and diagnosis support.

The challenging goal is to build Logic Programming (LP) programs that embed the reasoning tasks that radiologists activate during the interpretation of a scan. Typically, they refer to the text-book knowledge and they map it to the patient at hand. Differently from atlas based approaches, where a model is stretched to fit the instance, radiologist aggregate low level features found in the

scan and combine them according to a high level reasoning. As an example, many high level properties are retained among all human beings: liver is connected to aorta through the same set of vessels connections, despite their size, length and placement. In such scenario, liver identification can be easily tracked by following the correct *junctions* along the vessel network.

In general, radiologists interleave different types of activities during the visualization of scans: low level features and landmarks recognition in the scan, localization and labeling of organs and analysis of organs features. The process is often performed by looking at a single 2D scan slice at a time and then jumping among neighbor slices, creating an animation motion that helps in the removal of noise and in visualizing and highlighting 3D features. Usually, the 3D models reconstructions from raw data, available in all scan visualizer software, are not suitable for cancer diagnosis.

Our expected result is to develop a software that could warn a radiologist about some potential issues, in the attempt to reduce false negative CT exams. The analysis could provide insightful information about relationships between organs and suggest whether the patient is a candidate for surgical treatment. Finally, the software should be integrated into the Picture Archive and Communication System (PACS)[10], which is the standard for handling medical imaging data, in order to load it seamlessly in the radiologist workflow.

This paper presents the preliminary models and results achieved so far. Section 2 covers the essential topics discussed in the paper. We shortly depict the main pipeline for the complete tool in Section 3 and we focus on the arteries detection and classification, namely the problem of assigning the anatomical name to each vessel in the scan. In Section 3.1 we briefly discuss the vessel extraction and in Section 3.2 we present an ASP model for the vessels' labelling. We show some preliminary results in Section 4 and we conclude in Section 5.

## 2 Background

In this section we review the basic notions that are covered by the project. We briefly review CT scans, some examples in automated organ recognition and some basics of Answer Set Programming.

### 2.1 CT scan

Computer Assisted Tomography (in short CT) scan [8] is a well established X-ray based acquisition procedure for a general evaluation of pathologies and traumas. A patient's body is acquired through a sequence of X-ray images that are shot from different positions such that they are orthogonal to a central axis (ideally placed from feet to the head). Each image shows the cumulative absorption of X-rays caused by body's content along a specific point of view, as seen in common 2D X-rays shots. Given the CT scanner controlled setup, a set of acquisitions can provide information about each single position in the body: a deconvolution procedure is run to determine the radiometric absorption of each

*voxel* (volume element). Typically, the size of a voxel is  $1 \text{ mm}^3$ . Such volumetric information is arranged in a 3D matrix, where each cell contains a scalar number which corresponds to the radiometric absorption of that specific voxel. The unit of measure is the HU (Hounsfield Unit). Different chemical elements, as well as different body structures, show different X-ray absorption. Therefore, 3D images can be used to observe organs, vessels, bones etc. Some structures show similar intensity or absorption levels and a trained radiologist is able to discriminate finer details in order to assess potential abnormalities. For example, typical tumours are less dense than healthy tissues and therefore they absorb less X-rays. This fact can be visualized on a 3D image as a darker area compared to the neighborhood, assuming to depict values with shades of gray ranging from black (low absorption, *e.g.*, air) to white (high absorption, *e.g.*, bones).

Radiological images are saved with a standard file format called DICOM [6]. This image format is uncompressed and it contains 16 bit of information for each voxel (volume element). Each image usually provides a range of around 3000 distinct values among voxels. Since human vision is capable of distinguish much less variability (especially on a gray scale), an image may hide some relevant piece of information that is not visible to the eyes, even when enhancing tools are used by post processing software. Furthermore, CT images are affected by intrinsic noise related to the acquisition process and deconvolution of density, which may interfere with finer analysis.

## 2.2 Related work

Artificial Intelligence, ranging from vision to machine learning, has been applied to CT scans, given the valuable richness of information and the high demand for increased accuracy in interpretation and diagnosis. The overall goal is not to substitute the radiologist, but to provide them with a tool that can assist their interpretation process, by highlighting regions of attention and presenting reasons that support the warning.

Starting from low level vision problems, organ segmentation (see [15, 21, 18] for some examples and [11] for a survey) is a fundamental problem, where a program is asked to return a binary matrix, where the value 1 is assigned to voxels that belong to a specific organ/tissue. The extension of the request to multi-organ segmentation is rather trivial, while its implementation becomes more complex but it takes advantage of mutual classification choices. The state of the art methods lacks from satisfactory precision (up to 86% of volume correctly classified for pancreas), since the boundaries of organs are often mis-classified. Unfortunately, such regions are often the place where cancer can grow from (*e.g.*, the tail of the pancreas) and radiologists are still able to outperform the tools.

The circulatory system (including arteries and veins) can be identified by techniques similar to organ segmentation, adapted to the line-shaped structures [20, 12, 17]. In order to ease the identification of tiniest details, typical analyses require a contrast medium to be ingested by the patient before the scan. Built on top of feature extraction problem, an interesting goal is to correctly label

each vessel with its medical name. This can help in referencing the area of investigation and it can also help surgical preparation.

On the high-level end, another fundamental problem is direct cancer detection (e.g., [2]) customized for a selected organ. In this case, starting from a correct organ segmentation, the 3D voxels are analyzed in terms of texture and other features, typically by neural networks and classifiers.

### 2.3 ASP

A general program  $P$  in the language ASP is a set of rules  $r$  of the form:

$$a_0 \leftarrow a_1, \dots, a_m, \text{not } a_{m+1}, \dots, \text{not } a_n$$

where  $0 \leq m \leq n$  and each element  $a_i$ , with  $0 \leq i \leq n$ , is an *atom* of the form  $p(t_1, \dots, t_k)$ ,  $p$  is a predicate symbol of arity  $k$  and  $t_1, \dots, t_k$  are terms built using variables, constants and function symbols. Negation-as-failure (naf) literals are of the form *not*  $a$ , where  $a$  is an atom. Let  $r$  be a rule, we denote with  $h(r) = a_0$  its *head*, and  $B^+(r) = \{a_1, \dots, a_m\}$  and  $B^-(r) = \{a_{m+1}, \dots, a_n\}$  the positive and negative parts of its *body*, respectively; we denote the body with  $B(r) = \{a_1, \dots, \text{not } a_n\}$ . A rule is called a *fact* whenever  $B(r) = \emptyset$ ; a rule is a *constraint* when its head is empty ( $h(r) = \text{false}$ ); if  $m = n$  the rule is a *definite rule*. A *definite program* consists of only definite rules.

A term, atom, rule, or program is said to be *ground* if it does not contain variables. Given a program  $P$ , its *ground instance* is the set of all ground rules obtained by substituting all variables in each rule with ground terms. In what follows we assume atoms, rules and programs to be *grounded*. Let  $M$  be a set of ground atoms ( $\text{false} \notin M$ ) and let  $r$  be a rule: we say that  $M \models r$  if  $B^+(r) \not\subseteq M$  or  $B^-(r) \cap M \neq \emptyset$  or  $h(r) \in M$ .  $M$  is a *model* of  $P$  if  $M \models r$  for each  $r \in P$ . The *reduct* of a program  $P$  w.r.t.  $M$ , denoted by  $P^M$ , is the definite program obtained from  $P$  as follows: (i) for each  $a \in M$ , delete all the rules  $r$  such that  $a \in B^-(r)$ , and (ii) remove all naf-literals in the the remaining rules. A set of atoms  $M$  is an *answer set* [5] of a program  $P$  if  $M$  is the minimal model of  $P^M$ . A program  $P$  is *consistent* if it admits an answer set.

We will make use of ASP to describe a model which will allow to classify the vessels extracted from the CT-scans. In fact, thanks to the declarative nature of ASP, it is possible to define concise and accurate anatomical rules (that follows “rigid” patterns) that allow a precise labelling even in presence of errors or uncertainty often produced by the acquisition noise.

## 3 The methodology outline

Our system has been designed to take advantage of the best technologies for each of the three phases is composed of. It starts with a filtering process, in order to attenuate acquisition noise, and a low level feature extraction. The second phase, based on Logic Programming (LP), labels each body part in the

scan by reasoning on the set of features. Finally, organ evaluations can take place inside predicted organs volumes (here, original scan data are used in place of the filtered version for improved detection precision).

Our vision is to build a system that is based, in the second phase, on LP. We believe that such technology proposes some distinctive advantages that can outperform other approaches. The other two phases already show promising results in the literature.

The main advantage of LP is the capability of including a knowledge base, which can be build from anatomy textbooks and from radiologists interviews about their empirical interpretation procedures. Such knowledge can be translated into a set of clear rules that drive the search of a model matching the set of patient’s low level features. For example, a rule can state that a specific artery extends on a specific area and it branches from another artery. A low-level feature can be a tubular shape with its interconnections. Since vessels form a tree-like structure, the process of matching boils down to a constrained graph coloring problem.

Rather than training a classifier, the presence of a knowledge base allows to i) interact with Medical Doctors on a simple and natural language like level; ii) integrate the model with information extracted from already existing medical ontologies [3, 16]; iii) receive an explanation in terms of used rules to justify the answers; iv) consequently, update and refine the rules in a scientist-in-the-loop process; v) avoid to build a system that invests its training time for implicitly learning the anatomical general rules directly from low-level features. In particular, information retrieval from ontologies could allow us to extract anatomical information regarding specific vessels (through specific queries). The extracted piece of information, associated to the anatomy of the vessel (*e.g.*, its average length or radius) and/or the nomenclature of some of its component, will be then integrated to our knowledge base. As already said, thanks to the declarative nature of the model, this integration would be relatively easily achieved.

Our system’s interpretation phase mimics the same mental procedure a radiologist follows when she/he observes a CT scan. We interviewed radiologists during some scans interpretations and asked them to report on the logics behind their actions and findings. In particular, the procedure appears to be stratified from a coarse to fine approach. There is a preference in ruling out geometric properties first (low-level features) and combine them to identify organs and pathologies. Such strategy allows to decouple feature extraction from the reasoning phase. Therefore, off the shelf algorithm from computer vision can be employed and next specific LP programs can reason about features. In popular machine learning approaches the two steps are often merged together.

The first radiologist action is to localize main landmarks and to find a reference in the body. Even if organs position, size and shape can individually differ, there are some structural properties that are always constant (or more precisely, there is a set of known structural conformations that occur with some distribution among population). Vessel organization and structure possess this property and they are exploited as a 3D map that gives directions to organs. The correct

classification of arteries (which are more visible compared to veins, even without a contrast drug) allows to reach main organs and unlock further deductions about neighborhood, boundaries etc. Here, radiologists use a global approach that takes advantage of the whole scan, starting from some safe landmarks. This phase resembles a constrained graph coloring, which merges radiometric properties of organs, anatomy information and low level features extracted from the scan.

We give a brief description of filtering and feature extraction in Section 3.1 and we focus on the the arteries classification problem in Section 3.2. Our future plan is to extend the LP analysis to the multi-organ classification phase.

### 3.1 Filtering and feature extraction

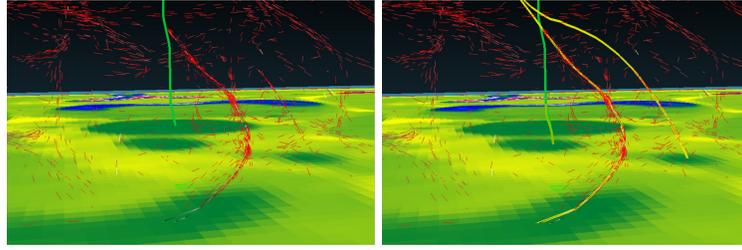
In the literature, filtering is fundamental to remove acquisition noise and compensate for spurious interference (e.g. a titanium implant) [19, 13]. Total variation is a rather effective filtering technique and it is anisotropic and edge preserving [7], so that shapes and boundaries are maintained at the correct position and contrast. We implemented an interleaved Total Variation and median filter in order to enhance arteries shape for the goals of our paper.

Unlike [12, 20], where contrast medium in the arteries allows a simple thresholding on the image, we opted for a finer analysis. For each voxel we compute the principal axis (main eigenvector) in density arrangement and connect voxels that are oriented along compatible and strong 1D arrangements. Such procedure returns pieces of reliable tubular fragments that are merged in a bottom up process. The ones that are also connected to the thoracic Aorta (the main artery connected to the heart), are the candidates for labeling. Such set of arteries are managed as a forest of trees that branch from the Aorta. Additional features are added to tree branches, e.g. estimated diameter and body quadrant spanned.

Figure 1, on the left, depicts a slice of the CT scan, where voxels values are plotted with a rainbow palette. Each voxel's principal direction is printed with short red lines centered at density local barycenter. It can be seen that clusters of coherent lines are positioned along arteries (dark green color regions). In the same Figure on the right, the local cues are merged and tracked. The resulting yellow lines cover the arteries barycenters. The vertical green line depicts the Aorta.

### 3.2 ASP vessels classification

We focus now on the automated process that examines the graph produced by the feature extraction phase and associates the largest subset of arcs to the corresponding anatomical names. We introduce an Answer Set Programming model that, exploiting anatomical rules and relations, performs a labeling of the main arteries that separate from the thoracic Aorta. This is a minimal test-bed domain that is sufficient to contain the general issues in finding the correct labeling. Nevertheless, the program can be extended to cover additional regions with the effort of coding new set of modular rules. Since all the rules can be



**Fig. 1.** Detection of voxels 1D directions (left) and vessel tracking (right)

expanded and modified (thanks to the nature of declarative programming), we focus on the structure of the program rather than the accuracy of the rules of knowledge base in use.

Given the presence of possible errors due to acquisition noise, filtering and extraction of low-level features, the ASP model needs to identify the best classification while allowing the presence of both missing and incorrect information. For example, some major artery could not be detected because the junction with Aorta is outside the scan and/or some set of voxels could resemble an important vessel while only being a cluster of acquisition noise or a surface of an organ.

Let us note that in this proof of concept, the set of rules in use is based onto anatomical relationships retrieved from atlas depictions. Some work will be dedicated to enrich such information thanks to a critical review by radiologists.

In particular, we focus on the set of arteries that separate from the Aorta. Branching of such arteries along sub-trees, except for the branches of the *celiac trunk*, are not yet considered.

**Domain Knowledge** Let us present the organization of knowledge as extracted by the procedure described above.

We prepare some **facts** that constitute the knowledge base. Such knowledge base covers all the vessels we are interested in and that are going to be assigned or discarded by the ASP model. In particular, the factual domain knowledge is formed of three main different types of facts

- **m\_art**(ID, Z, A, R): it describes a **main artery** vessel, i.e. a vessel that separates from the Aorta ;
- **b\_art**(ID, R): it describes a **bifurcation artery** vessel, i.e. any vessel that branches from a main artery vessel;
- **edge**(ID1, ID2): it encodes the tree parent-child relationship between two connected arteries.

The parameters of the predicates have the following meaning:

- ID/ID1/ID2: the unique id associated to a single vessel;
- Z: an integer that contains the position along the z axis (i.e. the slice number) where a connection takes place. Intuitively, a higher value is closer to the head and a lower number is closer to feet;

- **A**: the angle, in degrees, formed by the vessel when it separates from the aorta (where the 0 corresponds with left side of the body and increases clockwise);
- **R**: the radius, in voxels, of the vessel at the separation from the Aorta.

The domain knowledge is automatically extracted. In case of additional geometrical properties, the procedure can be extended to produce such data.

**The model** The ASP model objective is to associate the vessels, identified through the domain knowledge, to their anatomical description. The program also needs to discern between vessels that represents actual anatomical features from the ones that are false positives.

To perform an accurate labeling we created a model comprised of anatomical rules that describe some fundamental properties that help the characterization of a specific label. In particular, several properties associated to each single label are stored: i) the relative (w.r.t. the other vessels) z-height of a vessel; ii) its radius; iii) its branching direction angle; iv) its number of entering/exiting edges; and v) its interconnections with other vessels.

To achieve an optimal classification, we search for a model that verifies the highest number of rules. The model is reinforced by the presence of multiple properties for each vessel and the knowledge base uncertainty, errors and missing information can be handled as well. The program needs to be functional even when some major piece of information is missing (*e.g.*, the edge between the Aorta and one of its main branches), and that is why we chose an optimization problem on the number of rules rather than imposing strict constraints on labeling.

Let us present a simplified version of the ASP model. For the sake of readability we show only two arteries' description. The classification of the remaining ones follows the same pattern with according anatomical rules.

First of all, let us start by introducing some predicates that are used to identify anatomical characteristics (*i.e.*, arteries' radius and direction) with different degrees of precision. Not all the predicates are included for the sake of readability.

```

rad_small (R) :- rad(R), R > 0,    R ≤ 20.
rad_big   (R) :- rad(R), R > 20.

rad_1     (R) :- rad(R), R > 0,    R ≤ 5.
rad_2     (R) :- rad(R), R > 5,    R ≤ 10.
...
rad_8     (R) :- rad(R), R > 40.

quad_1    (A) :- angle(A), A > 0,   R ≤ 90.
...
quad_4    (A) :- angle(A), A > 270. R ≤ 360.

semiquad_1 (A) :- angle(A), A > 0,   A ≤ 45.
...
semiquad_8 (A) :- angle(A), R > 315. A ≤ 360.

```

where `rad(1..60)` and `angle(1..360)` are facts.

Intuitively the predicates `rad_small(R)` and `rad_big(R)` are used to classify the radius in two main groups to perform a first partition of the vessels. Then, thanks to predicates, `rad_{1/2..8}(R)` it is possible to refine this characterization as in the model of the *celiac trunk artery*. The predicates related to the direction angle follow the same principle: the predicates `quad_{1/2/3/4}(A)` give a coarse classification of the angles while the predicates `semiquad_{1/2..8}(A)` refine it.

We present now the model of the *celiac trunk* (referred to as `celiac`) and of the *left gastric* (referred to as `gast`) arteries. While the former is a branch of the Aorta (and is therefore a `m_art`) the latter is a `b_art` being a bifurcation of the *celiac trunk* itself. As before, we present a simplified version of the model.

```

p_b_art (ID,      R  ) :- id(ID), rad(R), b_art_in(ID, R).
p_m_art (ID, Z, A, R  ) :- id(ID), height(Z), angle(A), rad(R),
                           m_art(ID, Z, A, R).

artery (ID,      N) :- id(ID), name(N), b_art(ID, -, N).
artery (ID,      N) :- id(ID), name(N), m_art(ID, -, -, N).

m_art (ID, Z, A, R, N) :- art_gen(ID, N), name(N), p_m_ar(ID, Z, A, R),
                          N = celiac, quad_1(A), rad_big(R).

conf_r (celiac, 0) :- m_art(-, -, A, -, celiac), semiquad_2(A).
conf_r (celiac, 1) :- m_art(-, -, -, R, celiac), rad_6(R).
conf_r (celiac, 2) :- m_art(ID, -, -, -, celiac), edge(aorta, ID).
conf_r (celiac, 3) :- m_art(ID1, -, -, -, celiac), b_art(ID2, -, gast),
                          edge(ID1, ID2).

conf_r (celiac, 4) :- m_art(-, -, -, Z1, celiac),
                          m_art(-, -, -, Z2, sup_mese), Z1 > Z2.
conf_r (celiac, 5) :- m_art(-, -, -, Z1, celiac),
                          m_art(-, -, -, Z2, inf_mese), Z1 > Z2 + 30.

b_art (ID,      R, N) :- art_gen(ID, N), name(N), p_m_ar(ID, Z, A, R),
                          N = gast, rad_big(R).

conf_r (gast, 0) :- m_art(-, -, -, R, celiac), rad_6(R).
conf_r (gast, 1) :- b_art(ID2, -, gast), m_art(ID1, -, -, -, celiac),
                          edge(ID1, ID2).
conf_r (gast, 2) :- b_art(ID2, -, gast), K = 1,
                          K = #count{ID2 : edge(ID1, ID2)}.

```

Where the predicates `id(ID/ID1/ID2)` and `height(Z/Z1/Z2)` are extracted from the domain knowledge.

The general idea behind the presented model is to generate, for each artery fact in the knowledge base (`m_art` and `b_art`), a predicate that associates the `id` of the artery to a `name`. This first association follows some loose anatomical rules that associate the artery labels only to vessels that respect such rules.

That is why predicates `m_art` and `b_art` only use the less precise radius and angle descriptors (*i.e.*, `rad_{big/small}` and `quad_{1/.../4}`). If a vessel does not satisfy such general rule, it is surely not involved in such label. When the IDs are associated to the `names`, the program checks which of the various confidence rules (`conf_r`) are satisfied for a certain artery. These sets of satisfied rules will be then used to give a *score* to each model instantiation; the more rules are satisfied, the more the labeling is optimal. Let us show how this optimization problem is encoded in our ASP program.

```
0{art_gen(ID,N) : name(N)}1:- id(ID).
rule_count(K):- K = #count{N,R : conf_r(N,R)}.
#maximize{K : rule_count(K)}.
```

These lines of code tell the solver Clingo [4] to select the generation of predicates `art_gen` such that the various associations `ID-name` satisfy the highest number of confidence rules. Line `0 {art_gen(ID,N) : name(N)} 1` allows to skip some association `ID-name` because, as already said, the knowledge base could miss the description of all the vessels.

## 4 Results

The results of the features extraction on a filtered CT scan (Figure 1) have been converted into facts of the knowledge base for the ASP model presented in Section 3.2. As we already said, the model is comprised of rules extracted from atlas by non medical experts and is, therefore, still not completely accurate.

Our preliminary test of our model focuses on labeling the thoracic aorta, its main branches and some of the sub-arteries of such branches. We modelled a total of 20 arteries.

The model correctly classified the Aorta and its main branches. On the other hand the classification of the sub-arteries is not as accurate, since we did not include a large set of rules in the model. However, the knowledge coming from the extracted vessels is richer and we believe further information can be exploited and used for labelling the whole set of arteries.

Moreover, the features extraction has not been properly tuned. We prefer to keep some spurious arteries rather than missing some true positives. Therefore, wrong `edges` predicates are present, thus increasing the number of candidate vessels that can be labeled as sub-arteries.

All the experiments were performed on a 2.20GHz Intel Core i7-8750H machine with 16 GB of memory and with Ubuntu 18.04.5 LTS. The ASP program was executed exploiting the multi-thread (eight threads in parallel) capabilities of Clingo. The average number of found models is 15, while the average running times of the program were 0.06 and 124.75 seconds to find the optimal model and to conclude the search, respectively. We also measured the  $accuracy = \frac{\text{correctly labeled arteries}}{\text{total number of arteries}}$  for the optimal model. As we already mentioned, we were able to perform the complete test on a single CT scan, obtaining an accuracy of 70%. It is important to notice that the *accuracy* restricted



## 5 Conclusion

This paper presents a Declarative Programming methodology for CT scan automated interpretation. We focus on arteries detection and classification and we introduced an ASP model to label the vessels. This model relies on anatomical rules to identify the best association of detected vessels with their anatomical name. The implemented ASP program allows to identify the main arteries that branch out from the Aorta and some of their bifurcations. Our preliminary results show that the methodology is viable. More work will be dedicated to increase the knowledge base on the complete set of thoracic arteries, to extract a larger set of descriptors and to tune the labelling to different CT scans.

The program contains a set of anatomical rules that are easily modifiable; currently, we populate the rules with simple spatial relationships derived from anatomical atlases. This is a key feature that allows, in future versions, to integrate the experience of radiologists in the model, making it more accurate. Moreover, we presented a version of the program with only “positive” rules: that is, rules that, if activated, contribute to the support of a desired property. The program can be easily expanded to also introduce “negative” rules that penalize certain model’s instantiations, when activated. We plan to differentiate weights associated to rules, reflecting the relevance of certain properties, from anatomical or empirical viewpoint. Moreover, in a future version of the model, we plan to also add dependencies between the confidence rules. This last three future works will need supervision of expert radiologists that could help us in recognizing both “negative” anatomical rules and the weight of the confidence rules.

Finally, being the model based on declarative programming, it is possible to interface with tools that would parse the output of the model in natural language. This will allow to produce an explanation for the labeling and confidence rules choices. Having explainable AI techniques [9] is, in fact, a desiderata when introducing automated tools in environments where the health of the patients is taken into consideration. Introducing tools that explain the results will allow a more confident usage of the program from the medical operators and an easier error pruning/detection.

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