# Vessel12 Challenge
# Algorithm Description

Hans Meine, Markus Hüllebrand, Christina Stöcker

April 12, 2012

# 1 Description of 'FME_LungVessels' Submission

This submission is a fully automatic lung vessel segmentation method, developed for this challenge in a few days of work, and tested only on the challenge data so far. It has not been particularly tuned to the evaluation scheme, though – we have included several steps that lowered the area-under-ROC, while improving the visual impression (i.e. fewer tumors / other structures included in result mask).

Section 2 covers another experimental submission that targets a better ROC area.

## 1.1 Overview of Main Steps

The method consists of the following main steps:

- Preprocessing: Computation of Frangi's vesselness measure ($\sigma = 1$mm),
  resulting in the vesselness image $V(\vec{x})$

- Identification of seed points $\vec{s}_i$
  (described below in detail, think of filtered local maxima of $V(\vec{x})$)

- Region Growing on $V(\vec{x})$, starting from $\vec{s}_i$

- Excluding airway walls by using the dilated result of a simple bronchi segmentation method for masking

For the "probabilistic segmentation mask" $P(\vec{x})$, we output masks for different threshold values of the Region Growing:

$$P(\vec{x}) = \max\left(g \cdot R_{\theta(g)}(\vec{x})\right)$$

where $R_\theta(\vec{x})$ is a binary result mask (0 for background, 1 for vessel voxels) resulting from Region Growing in direction of descending vesselness values, stopping at the vesselness threshold $\theta$. Every possible gray value $g \in [1 \ldots 255]$ is linearly mapped to a threshold $\theta(g) = \theta_{\max} \cdot {}^g/_{255}$ ($\theta_{\max}$ was set to 100 for the submission).

We use a Region Growing variant that directly computes the "fuzzy connectivity" values for every pixel (the value at which it was first reached), without explicitly running the algorithm for each threshold.

## 1.2 Vessel Seed Points

The Region Growing is based on a (large) set of scattered seedpoints $\vec{s}_i$, which are defined as follows: Local maxima of $V$ whose value $V(\vec{s}_i) > V_{\min}$ is larger than a threshold $V_{\min}$ which was set to the 97% quantile of $V$.

Additionally, the seed points were *spatially* filtered: In order to suppress artifacts near the lung boundary, we used a morphologically shrinked (eroded) lung mask in order to use only seed points

that are at least 15mm away from the outer lung boundary. In order not to suppress seeds around the hilus, we used the *convex hull* of the input lung mask as the basis for the erosion. This effectively retained useful seeds at the root of the vessel system, while suppressing seeds near the lung border, where we had problems with artifacts due to high-density structures within the lung mask.

As stated above, we make use of a simple bronchi segmentation method in order to mask out big airways from the result mask; we also exclude seeds within this bronchi mask.

## 1.3   Run Time

All experiments were run on a standard development workstation with an Intel® Core™ i7-950 processor (3 GHz). Overall, the runtime of our experimental prototype is roughly around 5 minutes. Here are some singled out components:

- Airway/bronchi segmentation: 15-30 seconds

- Vesselness computation: 80-180 seconds

- Marker computation (dominated by convex hull) and region growing: 150-220 seconds

# 2   Description of 'FME_Vesselness' Submission

We noticed that many of our algorithmic improvements reduced the ROC area for the available example data. Thus, we submitted the preprocessed input data as additional result, out of curiosity for the evaluation results on this "raw", nearly unprocessed data.

In this case, we have employed a multi-scale vesselness, the computation of which took about 7-8 minutes (4 scales: 0.9, 1.6, 2.3, and 3 mm).