Multiple hypothesis tracking based extraction of airway trees from CT data
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MULTIPLE HYPOTHESIS TRACKING BASED EXTRACTION OF AIRWAY TREES FROM CT DATA

Using statistical ranking of template-matched hypotheses

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Abstract

Segmentation of airway tree from CT scans of lungs has important clinical applications, in relation to the diagnosis of chronic obstructive pulmonary disease (COPD). Here we present a method based on multiple hypothesis tracking (MHT) and template matching, originally developed for vessel segmentation, to extract airway trees. Idealized tubular templates are constructed and ranked using scores assigned based on the image data. Several such regularly spaced hypotheses are used in constructing a hypothesis tree, which is then traversed to obtain improved segmentation results.

Introduction

COPD is a leading cause of mortality worldwide, characterised by:
- Destruction of the lung tissues (emphysema)
- Morphological changes to the airways

Objective: Develop segmentation methods, with improved specificity and sensitivity, to study morphological changes of airways trees from CT.

Existing methods:
- Airway tree segmentation is a challenging problem
- Most methods try to strike a balance between specificity and sensitivity.
- Room for improvement on both fronts
- Single hypothesis / greedy algorithms
- Inconsistent decisions
- Only the best hypothesis is propagated
- Sensitive to noise
- Highly local solutions

Template matching-based MHT

Method based on [1], proposed for tracking small vessels:
- Designed to track small tubular structures
- Uses a scale-dependent score threshold
- Semi-automatic

Model

- Probability images obtained from trained KNN classifiers (K = 21), airways (p = 1)
- Method in [1] is modified, while retaining the image model:
- Template function (T) used to map probability variations to a profile function (p):
  \[ T(x, x_0, v) = \beta \cdot \exp\left( -\frac{d^2}{2\sigma^2} \right) \]
  \[ d^2 = \frac{1}{c} \left( \frac{\partial^2(T(x, x_0, v))}{\partial x^2} \right)^2 \]
- Centerlines of segmentation results are compared with reference segmentations, to quantify estimation error:

\[ \text{Error} = \sum_{i,j} \left| C_{\text{ref}} - C_{\text{op}} \right| \]

Error distance:

\[ d_{ij} = \sqrt{\sum_{k} (x_{ij} - y_{jk})^2} \]

\( C_{\text{ref}}, C_{\text{op}} \) are centerlines of reference, output segmentations, with \( n_{\text{ref}}, n_{\text{op}} \) points respectively, \( d_{ij} \) is Euclidean distance

Results

- Single seed point automatically placed at the origin of trachea, thus fully automatic
- Set of 32 images split into training, test sets
- Danish Lung Cancer Screening Trial data used [2]
- Probability images from KNN classifier
- Centerlines of segmentation results are compared with reference segmentations, to quantify estimation error:

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References